```
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTGAA 2195
              ||||||||||||||||||  |  ||
Db          1 TTTTTTTTTTTTTTTAAGATAAAA 24


RESULT 2245
CF319953
LOCUS       CF319953                 25 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-K11.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-K11, mRNA sequence.
ACCESSION   CF319953
VERSION     CF319953.1  GI:33691714
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-K11"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 2.1e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||||||  ||   |||
Db          1 TTTTTTTTTTTTTTTGTTGGGTTT 24


RESULT 2246
BH791022/c
LOCUS       BH791022                 25 bp    DNA     linear   GSS 02-APR-2002
DEFINITION  SALK_058381.35.95.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_058381.35.95.x, genomic
            survey sequence.
ACCESSION   BH791022
VERSION     BH791022.1  GI:19884432
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At4g36950.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_058381.35.95.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 2.1e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2759 ATAATAAAAGTATTCTTGTTAGAA 2782
              | ||| ||| |||||||||| ||||
Db         25 AAAATTAAAATATTCTTGTAAGAA 2


RESULT 2247
AZ316353
LOCUS       AZ316353                 26 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0034D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0034D09 F, genomic survey sequence.
ACCESSION   AZ316353
VERSION     AZ316353.1  GI:10364094
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0034  row: D  column: 09
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
```

```
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0034D09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||| ||||||||||||||
Db          1 AAAAAAAAAATAAAAAAAAAAAA 24


RESULT 2248
AU267694
LOCUS       AU267694                  26 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU267694 VS Dictyostelium discoideum cDNA clone VSH605 5', mRNA
            sequence.
ACCESSION   AU267694
VERSION     AU267694.1  GI:20526492
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSH605"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2771 TTCTTGTTAGAATTGAAAAAAAAAA 2794
                || ||||||  ||| |||||||||
Db          3 TTGTTGTTATTATTAAAAAAAAAA 26


RESULT 2249
AV739265
LOCUS       AV739265                  27 bp    mRNA    linear   EST 17-OCT-2000
DEFINITION  AV739265 CB Homo sapiens cDNA clone CBFAWE01 5', mRNA sequence.
ACCESSION   AV739265
VERSION     AV739265.1  GI:10856846
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
  TITLE     Homo sapiens CB library cDNA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CBFAWE01"
                     /tissue_type="cord blood"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="CB"
                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is
                     cloned randomly with the EcoRI digestion"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 27;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                ||||  |    ||||||||||||||||
Db          2 AGAAGGGGNGNAAAAAAAAAAAAAAA 27


RESULT 2250
AV741507
LOCUS       AV741507                  27 bp    mRNA    linear   EST 17-OCT-2000
DEFINITION  AV741507 CB Homo sapiens cDNA clone CBMAMC05 5', mRNA sequence.
ACCESSION   AV741507
VERSION     AV741507.1  GI:10859088
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
```

```
  TITLE     Homo sapiens CB library cDNA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CBMAMC05"
                     /tissue_type="cord blood"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="CB"
                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is
                     cloned randomly with the EcoRI digestion"

  Query Match              0.6%;  Score 17.6;  DB 1;  Length 27;
  Best Local Similarity   76.9%;  Pred. No. 2.4e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAAA 2801
              |  |||   | ||||||||||||||||
Db          2 GNCAGANGGGGAAAAAAAAAAAAAAA 27


RESULT 2251
AW250467/c
LOCUS       AW250467                  27 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822354.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822354 3',
            mRNA sequence.
ACCESSION   AW250467
VERSION     AW250467.1  GI:6593460
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822354.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 27
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 27 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM9  row: D  column: 3
            High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822354"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match              0.6%;  Score 17.6;  DB 1;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 2.4e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAA 2801
              ||||||  || || ||||||||||
Db         24 TAGAATATAAGAAGAAAAAAAAAA 1


RESULT 2252
T81587
LOCUS       T81587                    28 bp    mRNA    linear   EST 15-MAR-1995
DEFINITION  yd44c02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            IMAGE:111074 3' similar to gb:M31932 LOW AFFINITY IMMUNOGLOBULIN
            GAMMA FC RECEPTOR II-A PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   T81587
VERSION     T81587.1  GI:704594
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1171
            High quality sequence starts: 1 High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL This clone is available royalty-free
            through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)
            for further information. Trace considered overall poor quality
            Insert Length: 1171   Std Error: 0.00
            Seq primer: T3
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:466691"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:111074"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen 1NFLS"
```

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.6%; Score 17.6; DB 1; Length 28;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
             || | ||||| |||||| ||||||
Db          1 AAATAAAAAATAAAAAATAAAAAA 24
```

RESULT 2253
BQ583967/c
LOCUS BQ583967 29 bp mRNA linear EST 06-DEC-2002
DEFINITION S013297-024-004-B01-T7 MPIZ-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-004-B01 3-PRIME, mRNA sequence.
ACCESSION BQ583967
VERSION BQ583967.1 GI:26113544
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 29)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 4 row: B column: 01
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .29
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:182728"
/db_xref="taxon:161934"
/clone="024-004-B01"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17.6; DB 1; Length 29;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
             || | ||||| |||||| ||||||
Db         29 AAAAAAAAAAACAAAAAAAAAAAA 6
```

RESULT 2254
AZ492630/c
LOCUS AZ492630 29 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0326B22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0326B22 R, genomic survey sequence.
ACCESSION AZ492630
VERSION AZ492630.1 GI:10665537
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0326 row: B column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0326B22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.6; DB 1; Length 29;

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  Best Local Similarity   83.3%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   |||||||| ||||||||||
Db         28 AACAAAAAAAAAACAAAAAAAAAA 5


RESULT 2255
BQ586486
LOCUS       BQ586486                  29 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012391-024-012-J22-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-012-J22 5-PRIME, mRNA sequence.
ACCESSION   BQ586486
VERSION     BQ586486.1  GI:26116068
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 29   Std Error: 0.00
            Plate: 12  row: J  column: 22
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:186373"
                     /db_xref="taxon:161934"
                     /clone="024-012-J22"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
              |||    ||||||||||||||||
Db          6 AGAGACCAAAAAAAAAAAAAAAAA 29


RESULT 2256
CF331804/c
LOCUS       CF331804                  30 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-B04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-B04, mRNA sequence.
ACCESSION   CF331804
VERSION     CF331804.1  GI:33811833
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-B04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
              ||||  |||  ||||||||||||||
Db         24 AGAAAAGAAGGAAAAAAAAAAAAA 1


RESULT 2257
AU266959/c
LOCUS       AU266959                  33 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU266959 VS Dictyostelium discoideum cDNA clone VSH136 5', mRNA
            sequence.
ACCESSION   AU266959
VERSION     AU266959.1  GI:20525757
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .33
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                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSH136"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match              0.6%;  Score 17.6;  DB 1;  Length 33;
  Best Local Similarity   76.9%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   |||||||| |||||||||
Db         26 AAAAACNAAAAAAAAACNAAAAAAAAA 1


RESULT 2258
AZ345795
LOCUS       AZ345795                 19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080H09 R, genomic survey sequence.
ACCESSION   AZ345795
VERSION     AZ345795.1  GI:10425032
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: H  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080H09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
             || ||||||||||||||||
Db          1 TTAAAAAAAAAAAAAAAAA 19


RESULT 2259
AZ650575
LOCUS       AZ650575                 19 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0520P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0520P13 R, genomic survey sequence.
ACCESSION   AZ650575
VERSION     AZ650575.1  GI:11785200
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0520  row: P  column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0520P13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
              || |||||||||||||||||
Db          1 TTAAAAAAAAAAAAAAAAA 19
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RESULT 2260
AW248747
LOCUS AW248747 19 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821119.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821119 3', mRNA sequence.
ACCESSION AW248747
VERSION AW248747.1 GI:6591740
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821119.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 7 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM5 row: P column: 16
High quality sequence stop: 7.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821119"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||| ||||||||
Db          1 TTTTTTTTTTATTTTTTT 19
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RESULT 2261
AW248747/c
LOCUS AW248747 19 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821119.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821119 3', mRNA sequence.
ACCESSION AW248747
VERSION AW248747.1 GI:6591740
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821119.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 7 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM5 row: P column: 16
High quality sequence stop: 7.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821119"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2804
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Db         19 AAAAAAAATAAAAAAAAA 1
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RESULT 2262
CF291665
LOCUS       CF291665                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-D01, mRNA sequence.
ACCESSION   CF291665
VERSION     CF291665.1  GI:33660698
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-D01"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGA 19


RESULT 2263
CF291665/c
LOCUS       CF291665                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-D01, mRNA sequence.
ACCESSION   CF291665
VERSION     CF291665.1  GI:33660698
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-D01"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         19 TCAAAAAAAAAAAAAAAAA 1


RESULT 2264
CF291899
LOCUS       CF291899                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I08.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-I08, mRNA sequence.
ACCESSION   CF291899
VERSION     CF291899.1  GI:33660932
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-I08"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              | ||||||||||||||||||
Db          1 TGTTTTTTTTTTTTTTTTT 19
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RESULT 2265
CF291899/c
LOCUS       CF291899                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I08.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-I08, mRNA sequence.
ACCESSION   CF291899
VERSION     CF291899.1  GI:33660932
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-I08"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  |
Db         19 AAAAAAAAAAAAAAAAACA 1


RESULT 2266
CF292072
LOCUS       CF292072                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-M03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-M03, mRNA sequence.
ACCESSION   CF292072
VERSION     CF292072.1  GI:33661105
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-M03"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              | ||||||||||||||||||
Db          1 TGTTTTTTTTTTTTTTTT 19


RESULT 2267
CF292072/c
LOCUS       CF292072                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-M03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-M03, mRNA sequence.
ACCESSION   CF292072
VERSION     CF292072.1  GI:33661105
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-M03"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  |
Db         19 AAAAAAAAAAAAAAAAACA 1
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RESULT 2268
CF292144
LOCUS       CF292144                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-N17.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-N17, mRNA sequence.
ACCESSION   CF292144
VERSION     CF292144.1  GI:33661177
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-N17"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              | ||||||||||||||||||
Db          1 TGTTTTTTTTTTTTTTTTT 19


RESULT 2269
CF292144/c
LOCUS       CF292144                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-N17.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-N17, mRNA sequence.
ACCESSION   CF292144
VERSION     CF292144.1  GI:33661177
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-N17"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||| |
Db         19 AAAAAAAAAAAAAAAAACA 1


RESULT 2270
CF309636/c
LOCUS       CF309636                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-O08.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-O08, mRNA sequence.
ACCESSION   CF309636
VERSION     CF309636.1  GI:33681397
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2782 ATTGAAAAAAAAAAAAAAA 2800
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Db         19 ATTCAAAAAAAAAAAAAAA 1
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RESULT 2271
CF310688
LOCUS CF310688 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--05-H18, mRNA sequence.
ACCESSION CF310688
VERSION CF310688.1 GI:33682449
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
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/clone="ABF--05-H18"
/tissue_type="leaf"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  |
Db          1 AAAAAAAAAAAAAAAAACA 19
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RESULT 2272
CF310688/c
LOCUS CF310688 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--05-H18, mRNA sequence.
ACCESSION CF310688
VERSION CF310688.1 GI:33682449
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--05-H18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              | ||||||||||||||||||
Db         19 TGTTTTTTTTTTTTTTTT 1
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RESULT 2273
CF329136
LOCUS CF329136 19 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-F15, mRNA sequence.
ACCESSION CF329136
VERSION CF329136.1 GI:33806509
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-F15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTCTTT 19
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RESULT 2274
CF329136/c
LOCUS CF329136 19 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-F15, mRNA sequence.
ACCESSION CF329136
VERSION CF329136.1 GI:33806509
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-F15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||| ||||||||||||||||
Db         19 AAAGAAAAAAAAAAAAAA 1
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RESULT 2275
CF329137/c
LOCUS CF329137 19 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-F15.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-F15, mRNA sequence.
ACCESSION CF329137
VERSION CF329137.1 GI:33806511
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-F15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2174 TTTTTTTTTTTTTAACTTT 2192
              |||||||||||||| ||||
Db         19 TTTTTTTTTTTTTATCTTT 1
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RESULT 2276
CF334610
LOCUS CF334610 19 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-P13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-P13, mRNA sequence.
ACCESSION CF334610
VERSION CF334610.1 GI:33817556
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-P13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTTTTATTA 19
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RESULT 2277
AZ345499
LOCUS AZ345499 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080F06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080F06 F, genomic survey sequence.
ACCESSION AZ345499
VERSION AZ345499.1 GI:10424736
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: F column: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080F06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2157 TTTTTCTCCTTTTTTTTTT 2175
              |||||||| ||||||||||
Db          1 TTTTTCTCTTTTTTTTTTT 19
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RESULT 2278
AZ360314
LOCUS AZ360314 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0103G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0103G03 R, genomic survey sequence.
ACCESSION AZ360314
VERSION AZ360314.1 GI:10474014
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: G column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0103G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAAA 2803
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Db          1 GAAAAAAAGAAAAAAAAA 19
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RESULT 2279
AZ363907
LOCUS AZ363907 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0109I13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0109I13 R, genomic survey sequence.
ACCESSION AZ363907
VERSION AZ363907.1 GI:10477607
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 row: I column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0109I13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||| |||||||||
Db          1 TTTTTTTTATTTTTTTTT 19
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RESULT 2280
AZ363907/c
LOCUS AZ363907 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0109I13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0109I13 R, genomic survey sequence.
ACCESSION AZ363907
VERSION AZ363907.1 GI:10477607
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 row: I column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0109I13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||| |||||||||
Db         19 AAAAAAAAATAAAAAAAAA 1
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RESULT 2281
AZ447251
LOCUS AZ447251 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0244J19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0244J19 F, genomic survey sequence.
ACCESSION AZ447251
VERSION AZ447251.1 GI:10599050
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: J column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244J19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2170 TTTTTTTTTTTTTTTTAA 2188
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Db          1 TTTTTTTTTTTTTTTATAA 19
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RESULT 2282
AZ513919
LOCUS AZ513919 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0360E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0360E13 F, genomic survey sequence.
ACCESSION AZ513919
VERSION AZ513919.1 GI:10695235
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: E column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0360E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||| |||||||
Db          1 TTTTTTTTTTTCTTTTTTT 19
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RESULT 2283
AZ513919/c
LOCUS AZ513919 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0360E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0360E13 F, genomic survey sequence.
ACCESSION AZ513919
VERSION AZ513919.1 GI:10695235
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: E column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0360E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||| ||||||||||
Db         19 AAAAAAAGAAAAAAAAAA 1
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RESULT 2284
AZ645841
LOCUS AZ645841 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0511G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0511G04 R, genomic survey sequence.
ACCESSION AZ645841
VERSION AZ645841.1 GI:11775726
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: G column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511G04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
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  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              ||||||||| ||||||||||
Db          1 TTTTTTTTCTTTTTTTTTT 19


RESULT 2285
AZ645841/c
LOCUS       AZ645841                19 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0511G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0511G04 R, genomic survey sequence.
ACCESSION   AZ645841
VERSION     AZ645841.1  GI:11775726
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0511  row: G  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
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                     /db_xref="taxon:10090"
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                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||| ||||||||
Db         19 AAAAAAAAAAGAAAAAAAA 1


RESULT 2286
AZ650252
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DEFINITION  1M0520N17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0520N17 F, genomic survey sequence.
ACCESSION   AZ650252
VERSION     AZ650252.1  GI:11784550
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0520  row: N  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0520N17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Db          1 AAAACAAAAAAAAAAAAAA 19


RESULT 2287
AZ650252/c
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DEFINITION  1M0520N17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0520N17 F, genomic survey sequence.
ACCESSION   AZ650252
VERSION     AZ650252.1  GI:11784550
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0520  row: N  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="UUGC1M0520N17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

 Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
 Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
 Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||| ||||
Db         19 TTTTTTTTTTTTTTGTTTT 1


RESULT 2288
AZ654747
LOCUS       AZ654747                 19 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0529F08 F, genomic survey sequence.
ACCESSION   AZ654747
VERSION     AZ654747.1  GI:11791893
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0529  row: F  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

 Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
 Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
 Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
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Db          1 TTTTTATTTTTTTTTTTTT 19


RESULT 2289
AZ654747/c
LOCUS       AZ654747                 19 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0529F08 F, genomic survey sequence.
ACCESSION   AZ654747
VERSION     AZ654747.1  GI:11791893
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
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            University of Utah
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            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0529  row: F  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0529F08"
                     /sex="Male"
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                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
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                     polynucleotide kinase. Adaptor oligonucleotides were
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                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
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                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||| |||||
Db          19 AAAAAAAAAAAAATAAAAA 1


RESULT 2290
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LOCUS       AZ786336                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0031H17 R, genomic survey sequence.
ACCESSION   AZ786336
VERSION     AZ786336.1  GI:12923992
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0031  row: H  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
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                     /db_xref="taxon:10090"
                     /clone="UUGC2M0031H17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
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                     0.005 inch orifice at constant velocity. The sheared DNA
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                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
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                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTT 2175
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Db          1 TTTTTCTCTTTTTTTTTT 19
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RESULT 2291
CF308984/c
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DEFINITION  ABF--03-A01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-A01, mRNA sequence.
ACCESSION   CF308984
VERSION     CF308984.1  GI:33680745
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||| |||||
Db         20 AAAAAAAAAAAAACAAAAA 2

RESULT 2292
AZ375620
LOCUS       AZ375620                 20 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0129A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0129A08 F, genomic survey sequence.
ACCESSION   AZ375620
VERSION     AZ375620.1  GI:10489320
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0129  row: A  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0129A08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||| ||||||||||
Db          1 AAAAAAAATAAAAAAAAAA 19

RESULT 2293
AZ486787/c
LOCUS       AZ486787                 20 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0315D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0315D23 F, genomic survey sequence.
ACCESSION   AZ486787
VERSION     AZ486787.1  GI:10653904
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
```

```
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0315  row: D  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0315D23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||| ||
Db         20 AAAAAAAAAAAAAAAACAA 2

RESULT 2294
AZ579122
LOCUS       AZ579122                  20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0363G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0363G19 F, genomic survey sequence.
ACCESSION   AZ579122
VERSION     AZ579122.1  GI:11693583
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0363  row: G  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0363G19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||| ||||||||||||||||
Db          1 AAAACAAAAAAAAAAAAA 19

RESULT 2295
AZ949997
LOCUS       AZ949997                  20 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0213D24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0213D24 R, genomic survey sequence.
ACCESSION   AZ949997
VERSION     AZ949997.1  GI:13821224
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
```

```
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0213  row: D  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES              Location/Qualifiers
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                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0213D24"
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                      /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC2M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (female) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||| ||||||||||
Db          1 AAAAAAAATAAAAAAAAAA 19


RESULT 2296
CF299570
LOCUS       CF299570                20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-K09, mRNA sequence.
ACCESSION   CF299570
VERSION     CF299570.1  GI:33671331
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="7LEAF--03-K09"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTACT 19


RESULT 2297
CF301101/c
LOCUS       CF301101                20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-N04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-N04, mRNA sequence.
ACCESSION   CF301101
VERSION     CF301101.1  GI:33672862
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="7LEAF--05-N04"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||| ||||||||||||||||
Db         19 GAAGAAAAAAAAAAAAAAA 1
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```
RESULT 2298
CF333052
LOCUS       CF333052                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-M17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--01-M17, mRNA sequence.
ACCESSION   CF333052
VERSION     CF333052.1  GI:33814360
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /clone="JMT--01-M17"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              | ||||||||||||||||||
Db          2 TGTTTTTTTTTTTTTTTT 20


RESULT 2299
CF333052/c
LOCUS       CF333052                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-M17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--01-M17, mRNA sequence.
ACCESSION   CF333052
VERSION     CF333052.1  GI:33814360
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--01-M17"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  |
Db         20 AAAAAAAAAAAAAAAAACA 2


RESULT 2300
AZ343730/c
LOCUS       AZ343730                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0077E20 F, genomic survey sequence.
ACCESSION   AZ343730
VERSION     AZ343730.1  GI:10422288
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0077  row: E  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0077E20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
                ||||||||||||| |||||
Db         19 GAAAAAAAAAAAAGAAAAA 1


RESULT 2301
AL048772
LOCUS       AL048772                 21 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp566N143_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566N143, mRNA sequence.
ACCESSION   AL048772
VERSION     AL048772.1  GI:4727843
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566N143"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
                || |||||||||||||||
Db          3 TTAAAAAAAAAAAAAAAAA 21


RESULT 2302
BX548564/c
LOCUS       BX548564                 21 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX548564 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse101g03_p1c, mRNA sequence.
ACCESSION   BX548564
VERSION     BX548564.1  GI:33298798
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse101g03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||||||| |||
Db         21 AAAAAAAAAAAAAAAAGAAA 3


RESULT 2303
CF296213/c
LOCUS       CF296213                 21 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--06-H19, mRNA sequence.
ACCESSION   CF296213
VERSION     CF296213.1  GI:33665246
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
```

of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--06-H19"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||| ||||||||
Db 21 AAAAAAAAAACAAAAAAAA 3

RESULT 2304
AZ308846/c
LOCUS AZ308846 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0012H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0012H15 F, genomic survey sequence.
ACCESSION AZ308846
VERSION AZ308846.1 GI:10349246
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: H column: 15
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||| ||||||
Db 21 AAAAAAAAAAAACAAAAAA 3

RESULT 2305
AZ317208/c
LOCUS AZ317208 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0035J02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0035J02 R, genomic survey sequence.
ACCESSION AZ317208
VERSION AZ317208.1 GI:10365804
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: J column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035J02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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  Query Match              0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||| |||||||||||||
Db         21 AAAAAGAAAAAAAAAAAA 3
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RESULT 2306
AZ486776/c
LOCUS       AZ486776                21 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0315M10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0315M10 F, genomic survey sequence.
ACCESSION   AZ486776
VERSION     AZ486776.1  GI:10653882
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0315  row: M  column: 10
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0315M10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
```

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```
  Query Match              0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||| |||||||||||||
Db         21 AAAAATAAAAAAAAAAAA 3
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RESULT 2307
AZ822825
LOCUS       AZ822825                21 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0096I20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0096I20 F, genomic survey sequence.
ACCESSION   AZ822825
VERSION     AZ822825.1  GI:12992733
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0096  row: I  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0096I20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||  |||||||||
Db          1 AAAAAAAAACAAAAAAAAA 19
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RESULT 2308
AZ853429
LOCUS       AZ853429                 21 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0156D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0156D09 R, genomic survey sequence.
ACCESSION   AZ853429
VERSION     AZ853429.1  GI:13041543
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0156  row: D  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0156D09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

```
  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||| ||||
Db          1 AAAAAAAAAAAAAACAAAA 19
```

```
RESULT 2309
AZ627840/c
LOCUS       AZ627840                 21 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0474B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0474B05 F, genomic survey sequence.
ACCESSION   AZ627840
VERSION     AZ627840.1  GI:11750126
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0474  row: B  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0474B05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||| ||||||||||||||
Db         21 AAAACAAAAAAAAAAAAA 3
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RESULT 2310
CF319625/c
LOCUS CF319625 21 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--10-D06, mRNA sequence.
ACCESSION CF319625
VERSION CF319625.1 GI:33691386
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--10-D06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||| ||
Db         21 TTTTTTTTTTTTTTTTATA 3
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RESULT 2311
AZ341108/c
LOCUS AZ341108 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0073O14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0073O14 F, genomic survey sequence.
ACCESSION AZ341108
VERSION AZ341108.1 GI:10417030
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: O column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0073O14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2162 CTCCTTTTTTTTTTTTTT 2180
              | ||||||||||||||||||
Db         19 CCCCTTTTTTTTTTTTTT 1
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RESULT 2312
TA303G05P
LOCUS       TA303G05P                 22 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 303g05, forward sequence,
            genomic survey sequence.
ACCESSION   AL497383
VERSION     AL497383.1  GI:11865504
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="303g05"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 22;
  Best Local Similarity   94.7%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||| ||||||
Db          1 AAAAAAAAAAAAGAAAAAA 19


RESULT 2313
CF318882/c
LOCUS       CF318882                  22 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-C23.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-C23, mRNA sequence.
ACCESSION   CF318882
VERSION     CF318882.1  GI:33690643
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--09-C23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 22;
  Best Local Similarity   94.7%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAA 2800
              ||| ||||||||||||||||
Db         19 ATTCAAAAAAAAAAAAAA 1


RESULT 2314
AZ307896
LOCUS       AZ307896                  22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0010N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0010N18 F, genomic survey sequence.
ACCESSION   AZ307896
VERSION     AZ307896.1  GI:10347346
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0010  row: N  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0010N18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 22;
Best Local Similarity 94.7%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              ||||| ||||||||||||||
Db          4 CTTTTGTTTTTTTTTTTT 22
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RESULT 2315
AZ317017
LOCUS AZ317017 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0035P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0035P09 F, genomic survey sequence.
ACCESSION AZ317017
VERSION AZ317017.1 GI:10365400
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: P column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035P09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 22;
Best Local Similarity 94.7%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2162 CTCCTTTTTTTTTTTTTTT 2180
              | ||||||||||||||||||
Db          4 CCCCTTTTTTTTTTTTTTT 22
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RESULT 2316
AZ486853/c
LOCUS AZ486853 23 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0315M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315M14 R, genomic survey sequence.
ACCESSION AZ486853
VERSION AZ486853.1 GI:10654033
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: M column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
source 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315M14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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  Query Match              0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
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Db         23 AAAAAAAAAAAAGAAAAAA 5
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RESULT 2317
AZ645254/c
LOCUS       AZ645254                 23 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0510O05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0510O05 R, genomic survey sequence.
ACCESSION   AZ645254
VERSION     AZ645254.1  GI:11774572
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0510  row: O  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0510O05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

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  Query Match              0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         23 AAAAAAAAAAAAGAAAAAA 5
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RESULT 2318
AZ382013
LOCUS       AZ382013                 23 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0138M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0138M14 R, genomic survey sequence.
ACCESSION   AZ382013
VERSION     AZ382013.1  GI:10495713
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0138  row: M  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0138M14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||| ||||||||||
Db          1 AAAAAAAATAAAAAAAAAA 19


RESULT 2319
AZ627841/c
LOCUS       AZ627841                 23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0474E01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0474E01 F, genomic survey sequence.
ACCESSION   AZ627841
VERSION     AZ627841.1  GI:11750127
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0474  row: E  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0474E01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db         23 AAAAAAAAAAATAAAAAAA 5


RESULT 2320
TA55C06P
LOCUS       TA55C06P                 23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 55c06, forward sequence,
            genomic survey sequence.
ACCESSION   AL455778
VERSION     AL455778.1  GI:11856729
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="55c06"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||| ||||||||
Db          1 AAAAAAAAAATAAAAAAAA 19
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RESULT 2321
AW335179
LOCUS       AW335179                 23 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S44B4 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION   AW335179
VERSION     AW335179.1  GI:6831798
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
  ORGANISM  Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Pneumocystis carinii"
                     /mol_type="mRNA"
                     /db_xref="taxon:4754"
                     /lab_host="E. coli"
                     /clone_lib="AGS-1"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (3x10e9) from a single rat (99-1-6,
                     sacrificed on 3/17/99)  at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT priming, standard
                     conditions described by  vendor, Stratagene. Further
                     details see www.uky.edu/Project/Pneumocystis/"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTCAA 19


RESULT 2322
CF334146/c
LOCUS       CF334146                 23 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-F05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-F05, mRNA sequence.
ACCESSION   CF334146
VERSION     CF334146.1  GI:33816628
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--03-F05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
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Db         19 TGGAAAAAAAAAAAAAAAA 1


RESULT 2323
AZ627850
LOCUS       AZ627850                 24 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0474N20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0474N20 F, genomic survey sequence.
ACCESSION   AZ627850
VERSION     AZ627850.1  GI:11750136
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0474  row: N  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0474N20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 24;
Best Local Similarity 94.7%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db          1 AAAAAAAAAAAATAAAAAA 19
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RESULT 2324
CF331867
LOCUS CF331867 24 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--08-C13.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-C13, mRNA sequence.
ACCESSION CF331867
VERSION CF331867.1 GI:33811957
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-C13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 24;
Best Local Similarity 94.7%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2172 TTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTACT 19
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RESULT 2325
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LOCUS CF331868 24 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--08-C13.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-C13, mRNA sequence.
ACCESSION CF331868
VERSION CF331868.1 GI:33811959
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--08-C13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 24;
Best Local Similarity 94.7%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2172 TTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||| |||
Db         24 TTTTTTTTTTTTTTTTACT 6
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RESULT 2326
CF327904
LOCUS CF327904 24 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-J06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-J06, mRNA sequence.
ACCESSION CF327904
VERSION CF327904.1 GI:33804058
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 24;
  Best Local Similarity   94.7%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTAAAT 19


RESULT 2327
CF327904/c
LOCUS       CF327904                 24 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-J06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-J06, mRNA sequence.
ACCESSION   CF327904
VERSION     CF327904.1  GI:33804058
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--02-J06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 24;
  Best Local Similarity   94.7%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAA 2800
              ||| |||||||||||||||
Db         19 ATTTAAAAAAAAAAAAAAA 1


RESULT 2328
TA155F12Q/c
LOCUS       TA155F12Q                24 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 155f12, reverse sequence,
            genomic survey sequence.
ACCESSION   AL472698
VERSION     AL472698.1  GI:11838089
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nhl@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="155f12"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 24;
  Best Local Similarity   94.7%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2180
              | |||||||||||||||||
Db         19 CCCCTTTTTTTTTTTTTTT 1


RESULT 2329
TA388E06P
LOCUS       TA388E06P                25 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 388e06, forward sequence,
            genomic survey sequence.
ACCESSION   AL498782
VERSION     AL498782.1  GI:11874504
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nhl@sanger.ac.uk
```

```
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="388e06"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| |
Db          1 AAAAAAAAAAAAAAAAAGA 19


RESULT 2330
AV737092
LOCUS       AV737092                 25 bp    mRNA    linear   EST 17-OCT-2000
DEFINITION  AV737092 CB Homo sapiens cDNA clone CBFBIB11 5', mRNA sequence.
ACCESSION   AV737092
VERSION     AV737092.1  GI:10854673
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
  TITLE     Homo sapiens CB library cDNA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CBFBIB11"
                     /tissue_type="cord blood"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="CB"
                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is
                     cloned randomly with the EcoRI digestion"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||| |||||||||||||
Db          6 AAAACAAAAAAAAAAAAA 24


RESULT 2331
AU012885/c
LOCUS       AU012885                 25 bp    mRNA    linear   EST 03-AUG-1998
DEFINITION  AU012885 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc07426, mRNA sequence.
ACCESSION   AU012885
VERSION     AU012885.1  GI:3357794
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Schizosaccharomyces pombe"
                     /mol_type="mRNA"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc07426"
                     /sex="h minus"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTAACTTTGA 2194
              ||||||||||||| ||||||
Db         25 TTTTTTTTTTAGCTTTGA 7


RESULT 2332
BX554728/c
LOCUS       BX554728                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX554728 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse17b03_p1c, mRNA sequence.
ACCESSION   BX554728
VERSION     BX554728.1  GI:33436050
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
```

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   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse17b03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 26;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  |
Db         26 AAAAAAAAAAAAAAAAACA 8


RESULT 2333
BQ585188/c
LOCUS       BQ585188                 26 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S014222-024-001-E10-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-001-E10 5-PRIME, mRNA sequence.
ACCESSION   BQ585188
VERSION     BQ585188.1  GI:26114770
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 26   Std Error: 0.00
            Plate: 1  row: E  column: 10
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:181514"
                     /db_xref="taxon:161934"
                     /clone="024-001-E10"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 26;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2801
              || |||||||||||||||
Db         26 TTAAAAAAAAAAAAAAAA 8


RESULT 2334
TA319G03Q
LOCUS       TA319G03Q                26 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 319g03, reverse sequence,
            genomic survey sequence.
ACCESSION   AL492820
VERSION     AL492820.1  GI:11867590
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="319g03"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 26;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTT 2180
              | ||||||||||||||||||
Db          8 CCCCTTTTTTTTTTTTTT 26
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RESULT 2335
BX568027
LOCUS       BX568027                 29 bp    mRNA    linear   EST 14-OCT-2003
DEFINITION  BX568027 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse91d12_q1c, mRNA sequence.
ACCESSION   BX568027
VERSION     BX568027.1  GI:33434924
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse91d12_q1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 29;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  |
Db          1 AAAAAAAAAAAAAAAAACA 19


RESULT 2336
AU268044
LOCUS       AU268044                 31 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA
            sequence.
ACCESSION   AU268044
VERSION     AU268044.1  GI:20526842
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSH836"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 31;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||  |||||||||||||
Db          1 AAAAACAAAAAAAAAAAAA 19


RESULT 2337
AZ579477
LOCUS       AZ579477                 31 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0367A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0367A08 F, genomic survey sequence.
ACCESSION   AZ579477
VERSION     AZ579477.1  GI:11693906
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0367  row: A  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0367A08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
```

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 31;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||| ||
Db          3 GAAAAAAAAAAAAAAAAGAA 21
```

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RESULT 2338
AL941390/c
LOCUS       AL941390                  32 bp    DNA     linear   GSS 24-OCT-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-257B04-014921,
            genomic survey sequence.
ACCESSION   AL941390
VERSION     AL941390.1  GI:24397988
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 32)
  AUTHORS   Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion close to or within gene At5g42900. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-257B04-014921"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
```

```
  Query Match             0.6%;  Score 17.4;  DB 1;  Length 32;
  Best Local Similarity   94.7%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  |
Db         32 AAAAAAAAAAAAAAAAAGA 14
```

```
RESULT 2339
TA369C05P
LOCUS       TA369C05P                 37 bp    DNA     linear   GSS 15-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 369c05, forward sequence,
            genomic survey sequence.
ACCESSION   AL496346
VERSION     AL496346.1  GI:11872269
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="369c05"
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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 37;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||| |||||||||
Db          2 AAAAAAAAAGAAAAAAAA 20
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```
RESULT 2340
CF642215
LOCUS       CF642215                  39 bp    mRNA    linear   EST 02-OCT-2003
DEFINITION  D49_A04 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
```

```
            sequence.
ACCESSION   CF642215
VERSION     CF642215.1  GI:37409389
KEYWORDS    EST.
SOURCE      Ustilago maydis
  ORGANISM  Ustilago maydis
            Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
            Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Nugent,K.G., Choffe,K. and Saville,B.J.
  TITLE     Gene Expression during Ustilago maydis Diploid Filamentous Growth:
            EST Library Creation and Analyses
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Barry J. Saville
            Saville Lab
            University of Toronto
            3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
            Tel: 905 569 4702
            Fax: 905 828 3792
            Email: bsaville@utm.utoronto.ca
            Plate: UTM-UM-D126/7-049-UTM  row: 04  column: A
            Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGGG 3')
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Ustilago maydis"
                     /mol_type="mRNA"
                     /strain="FBD12"
                     /db_xref="taxon:5270"
                     /cell_type="Mycelia"
                     /dev_stage="Filamentous diploid"
                     /clone_lib="Filamentous Forced Diploid"
                     /note="Vector: pSport; mRNA was extracted from diploid
                     mycelia. A cDNA library was constructed and
                     unidirectionally cloned into pSPORT plasmid, with the use
                     of the Superscript II cDNA Library Construction Kit."

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 39;
  Best Local Similarity   94.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||  |
Db          1 AAAAAAAAAAAAAAAAAGA 19


RESULT 2341
AZ345485
LOCUS       AZ345485                 22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080C02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080C02 F, genomic survey sequence.
ACCESSION   AZ345485
VERSION     AZ345485.1  GI:10424722
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: C  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080C02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTT 2184
              | ||||||||||||  ||||||
Db          1 TTCTTTTTTTTTTAATTTTTT 22


RESULT 2342
AZ471736/c
LOCUS       AZ471736                 22 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0286I12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0286I12 R, genomic survey sequence.
ACCESSION   AZ471736
VERSION     AZ471736.1  GI:10629957
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
```

```
           Insert Length: 10000   Std Error: 0.00
           Plate: 0286  row: I  column: 12
           Seq primer: CACACAGGAAACAGCTATGACC
           Class: plasmid ends
           High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0286I12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 22;
  Best Local Similarity   86.4%;  Pred. No. 1.8e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTT 2175
                ||||||||  |  ||||||||||
Db         22 ATTTTTTTATGGTTTTTTTTT 1


RESULT 2343
CF311534/c
LOCUS       CF311534                23 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-M14.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-M14, mRNA sequence.
ACCESSION   CF311534
VERSION     CF311534.1  GI:33683295
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--06-M14"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2803
                | | | ||||||||||||||||
Db         22 AGTCACAAAAAAAAAAAAAAA 1


RESULT 2344
AU267617
LOCUS       AU267617                23 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU267617 VS Dictyostelium discoideum cDNA clone VSH555 5', mRNA
            sequence.
ACCESSION   AU267617
VERSION     AU267617.1  GI:20526415
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSH555"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAA 2798
                ||||||||  |  ||||||||||
Db          2 TTAGAATTTAGTAAAAAAAAAA 23


RESULT 2345
CF290998/c
LOCUS       CF290998                23 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E03.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-E03, mRNA sequence.
ACCESSION   CF290998
```

```
VERSION     CF290998.1  GI:33660031
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-E03"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||||||  || |
Db         23 TTTTTTTTTTTTTTTTGGCTGT 2


RESULT 2346
BI094838
LOCUS       BI094838                 24 bp    mRNA    linear   EST 14-DEC-2001
DEFINITION  EST-CD34N-038 cDNA library of human CD 34+ stem/progenitor cells
            Homo sapiens cDNA 3', mRNA sequence.
ACCESSION   BI094838
VERSION     BI094838.1  GI:17737215
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Zhou,G., Chen,J., Lee,S., Terry,C., Rowley,J.D. and Wang,S.M.
  TITLE     The pattern of gene expression in human hematopoietic CD34+
            stem/progenitor cells
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wang SM
            Hem/Onc
            University of Chicago Medical Center
            5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
            Tel: 773-702-6788
            Fax: 773-702-3002
            Email: swang1@midway.uchicago.edu
            This EST fragment was amplified from cDNA Library of human CD 34+
            stem/progenitor cells with GLGI technique (Generation of Longer
            cDNA fragments from SAGE tags for Gene Identification, Proc. Natl.
            Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till
            the first CATG site of the target cDNA sequence.
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="Bone marrow"
                     /cell_type="CD34+ stem/progenitor cells"
                     /clone_lib="cDNA library of human CD 34+ stem/progenitor
                     cells"
                     /note="3'ESTs converted from the SAGE tag sequences using
                     GLGI method"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   86.4%;  Pred. No. 2.2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||  || |
Db          1 TTTTTTTTTTTTTTTCGTTCA 22


RESULT 2347
CF328136
LOCUS       CF328136                 24 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-O07.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-O07, mRNA sequence.
ACCESSION   CF328136
VERSION     CF328136.1  GI:33804522
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--02-O07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   86.4%;  Pred. No. 2.2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2800
              ||| ||  ||||||||||||||
Db          3 AGAGTTCGAAAAAAAAAAAAAA 24


RESULT 2348
CF328136/c
LOCUS       CF328136                 24 bp    mRNA    linear   EST 18-AUG-2003
```

```
DEFINITION  NACL--02-O07.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-O07, mRNA sequence.
ACCESSION   CF328136
VERSION     CF328136.1  GI:33804522
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--02-O07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   86.4%;  Pred. No. 2.2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||||||  |||| |
Db         24 TTTTTTTTTTTTTTCGAACTCT 3


RESULT 2349
AZ349008
LOCUS       AZ349008                 24 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0085O13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0085O13 R, genomic survey sequence.
ACCESSION   AZ349008
VERSION     AZ349008.1  GI:10428245
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0085  row: O  column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0085O13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 24;
  Best Local Similarity   86.4%;  Pred. No. 2.2e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTTTTTTT 2179
              |||  || ||||||||||||||
Db          3 TTTGTTCGTTTTTTTTTTTTT 24


RESULT 2350
AV740046
LOCUS       AV740046                 25 bp    mRNA    linear   EST 17-OCT-2000
DEFINITION  AV740046 CB Homo sapiens cDNA clone CBFAWF04 5', mRNA sequence.
ACCESSION   AV740046
VERSION     AV740046.1  GI:10857627
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
  TITLE     Homo sapiens CB library cDNA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES             Location/Qualifiers
     scource         1. .25
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CBFAWF04"
                     /tissue_type="cord blood"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="CB"
                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is
                     cloned randomly with the EcoRI digestion"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2802
              |||  |  ||||||||||||||||
Db          3 GAAGGGGNAAAAAAAAAAAAAAA 25


RESULT 2351
AW247153
LOCUS       AW247153                 25 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819969.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819969 3',
            mRNA sequence.
ACCESSION   AW247153
VERSION     AW247153.1  GI:6590146
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819969.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 7 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 25 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM2  row: P  column: 18
            High quality sequence stop: 7.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819969"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||  ||||  |  |||||
Db          2 TTTTTTTTTGTTTTGTGTTTTA 23


RESULT 2352
CF296608/c
LOCUS       CF296608                 25 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-A20.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--07-A20, mRNA sequence.
ACCESSION   CF296608
VERSION     CF296608.1  GI:33665641
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--07-A20"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAA 2796
              |||||||  |  ||||||||||||
Db         22 TGTTAGATTAAAAAAAAAAAAA 1


RESULT 2353
BZ593276/c
LOCUS       BZ593276                 26 bp    DNA     linear   GSS 07-JAN-2003
DEFINITION  SALK_068322.21.25.n Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_068322.21.25.n, genomic
            survey sequence.
ACCESSION   BZ593276
VERSION     BZ593276.1  GI:27533795
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_068322.21.25.n"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 26;
  Best Local Similarity   86.4%;  Pred. No. 2.5e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAA 2802
              ||  ||||||  ||||||||||
Db         26 AAAAGAAAAAGAAAAAAAAAAA 5


RESULT 2354
BQ590128
LOCUS       BQ590128                 17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012843-024-019-E19-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-E19 3-PRIME, mRNA sequence.
ACCESSION   BQ590128
VERSION     BQ590128.1  GI:26119711
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 19  row: E  column: 19
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189986"
                     /db_xref="taxon:161934"
                     /clone="024-019-E19"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTA 17


RESULT 2355
BQ590687
LOCUS       BQ590687                 17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013717-024-018-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
ACCESSION   BQ590687
VERSION     BQ590687.1  GI:26120270
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 18  row: B  column: 24
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189432"
                     /db_xref="taxon:161934"
                     /clone="024-018-B24"
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/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 17
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RESULT 2356
BQ590687/c
LOCUS BQ590687 17 bp mRNA linear EST 06-DEC-2002
DEFINITION S013717-024-018-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
ACCESSION BQ590687
VERSION BQ590687.1 GI:26120270
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 18 row: B column: 24
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189432"
/db_xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db         17 TTTTTTTTTTTTTTTTT 1
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RESULT 2357
BQ591177
LOCUS BQ591177 17 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-B22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-B22 3-PRIME, mRNA sequence.
ACCESSION BQ591177
VERSION BQ591177.1 GI:26120760
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
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Seq primer: T7; GTAATACGACTCACTATAGGGC.
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/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2358
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LOCUS       BQ591177                 17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-B22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-B22 3-PRIME, mRNA sequence.
ACCESSION   BQ591177
VERSION     BQ591177.1  GI:26120760
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
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            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /tissue_type="storage root"
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                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
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Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2359
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LOCUS       CF290854                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-A21, mRNA sequence.
ACCESSION   CF290854
VERSION     CF290854.1  GI:33659887
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2360
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LOCUS       CF290854                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-A21, mRNA sequence.
ACCESSION   CF290854
VERSION     CF290854.1  GI:33659887
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Qy       2786 AAAAAAAAAAAAAAAAA 2802
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Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2361
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LOCUS       CF294668                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--04-E17, mRNA sequence.
ACCESSION   CF294668
VERSION     CF294668.1  GI:33663701
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TTTTTTTTTTTTTTTTA 17


RESULT 2362
CF295988
LOCUS       CF295988                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--06-C17, mRNA sequence.
ACCESSION   CF295988
VERSION     CF295988.1  GI:33665021
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Db          1 TTTTTTTTTTTTTTTTA 17


RESULT 2363
CF298589
LOCUS       CF298589                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A18, mRNA sequence.
ACCESSION   CF298589
VERSION     CF298589.1  GI:33670350
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
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RESULT 2364
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LOCUS       CF298589                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A18, mRNA sequence.
ACCESSION   CF298589
VERSION     CF298589.1  GI:33670350
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
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Db         17 AAAAAAAAAAAAAAAA 1


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DEFINITION  7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-P11, mRNA sequence.
ACCESSION   CF302447
VERSION     CF302447.1  GI:33674208
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         17 GAAAAAAAAAAAAAAA 1


RESULT 2366
CF310219
LOCUS       CF310219                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--04-M02, mRNA sequence.
ACCESSION   CF310219
VERSION     CF310219.1  GI:33681980
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                     then used for PCR. mRNA was prepared from ABA-responsive
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                     line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
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RESULT 2367
CF310219/c
LOCUS       CF310219                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--04-M02, mRNA sequence.
ACCESSION   CF310219
VERSION     CF310219.1  GI:33681980
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--04-M02"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 1


RESULT 2368
CF313013/c
LOCUS       CF313013                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-P19, mRNA sequence.
ACCESSION   CF313013
VERSION     CF313013.1  GI:33684774
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--08-P19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 1


RESULT 2369
CF334566
LOCUS       CF334566                  17 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-O13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-O13, mRNA sequence.
ACCESSION   CF334566
VERSION     CF334566.1  GI:33817460
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 2370
CF334566/c
LOCUS       CF334566                17 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-O13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-O13, mRNA sequence.
ACCESSION   CF334566
VERSION     CF334566.1  GI:33817460
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--03-O13"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 1


RESULT 2371
CF336950
LOCUS       CF336950                17 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.
ACCESSION   CF336950
VERSION     CF336950.1  GI:33822280
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--07-D04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTA 17


RESULT 2372
CF301057
LOCUS       CF301057                18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-M05, mRNA sequence.
ACCESSION   CF301057
VERSION     CF301057.1  GI:33672818
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2373
CF301151/c
LOCUS       CF301151                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-O05.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-O05, mRNA sequence.
ACCESSION   CF301151
VERSION     CF301151.1  GI:33672912
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-O05"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2374
CF320418/c
LOCUS       CF320418                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-E22.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--11-E22, mRNA sequence.
ACCESSION   CF320418
VERSION     CF320418.1  GI:33692179
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
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                     /db_xref="taxon:4530"
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
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Db         18 AAAAAAAAAAAAAAAAA 2

RESULT 2375
CF298591
LOCUS       CF298591                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A20, mRNA sequence.
ACCESSION   CF298591
VERSION     CF298591.1  GI:33670352
KEYWORDS    EST.
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SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTAA 17


RESULT 2376
CF300456/c
LOCUS       CF300456                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-N23, mRNA sequence.
ACCESSION   CF300456
VERSION     CF300456.1  GI:33672217
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 2377
CF302409
LOCUS       CF302409                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-N19, mRNA sequence.
ACCESSION   CF302409
VERSION     CF302409.1  GI:33674170
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-N19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTA 17


RESULT 2378
CF320046
LOCUS       CF320046                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-M11.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-M11, mRNA sequence.
ACCESSION   CF320046
VERSION     CF320046.1  GI:33691807
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KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-M11"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTA 17


RESULT 2379
AZ450180
LOCUS       AZ450180                 19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0248K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0248K13 R, genomic survey sequence.
ACCESSION   AZ450180
VERSION     AZ450180.1  GI:10604710
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0248  row: K  column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0248K13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
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Db          3 AAAAAAAAAAAAAAAAA 19


RESULT 2380
AZ853220/c
LOCUS       AZ853220                 19 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0156J15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0156J15 F, genomic survey sequence.
ACCESSION   AZ853220
VERSION     AZ853220.1  GI:13041116
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
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           Plate: 0156  row: J  column: 15
           Seq primer: CGTTGTAAAACGACGGCCAGT
           Class: plasmid ends
           High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0156J15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db         19 TTTTTTTTTTTTTTTTT 3


RESULT 2381
CF278272
LOCUS       CF278272                  19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--04-C01, mRNA sequence.
ACCESSION   CF278272
VERSION     CF278272.1  GI:33655658
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTAA 17


RESULT 2382
CF298207
LOCUS       CF298207                  20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-H23, mRNA sequence.
ACCESSION   CF298207
VERSION     CF298207.1  GI:33669968
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 17


RESULT 2383
AZ818055/c
LOCUS       AZ818055                  20 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0087B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
```

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            clone UUGC2M0087B23 R, genomic survey sequence.
ACCESSION   AZ818055
VERSION     AZ818055.1  GI:12987963
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0087  row: B  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0087B23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db         20 TTTTTTTTTTTTTTTT 4


RESULT 2384
CF319428
LOCUS       CF319428                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-O20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-O20, mRNA sequence.
ACCESSION   CF319428
VERSION     CF319428.1  GI:33691189
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--09-O20"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 CTTTTTTTTTTTTTTT 17


RESULT 2385
AZ943299/c
LOCUS       AZ943299                 21 bp    DNA     linear   GSS 26-APR-2001
DEFINITION  2M0203K21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0203K21 R, genomic survey sequence.
ACCESSION   AZ943299
VERSION     AZ943299.1  GI:13807290
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
```

```
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0203  row: K  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0203K21"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAA 5


RESULT 2386
CF333393/c
LOCUS       CF333393                 21 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-E09.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--02-E09, mRNA sequence.
ACCESSION   CF333393
VERSION     CF333393.1  GI:33815062
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--02-E09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2387
BQ591193
LOCUS       BQ591193                 22 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-D14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-D14 3-PRIME, mRNA sequence.
ACCESSION   BQ591193
VERSION     BQ591193.1  GI:26120776
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 22   Std Error: 0.00
            Plate: 17  row: D  column: 14
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188927"
                     /db_xref="taxon:161934"
                     /clone="024-017-D14"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
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Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2172 TTTTTTTTTTTTTTTAA 2188
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Db          1 TTTTTTTTTTTTTTTAA 17
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RESULT 2388
CF297521/c
LOCUS CF297521 22 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--08-H01.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--08-H01, mRNA sequence.
ACCESSION CF297521
VERSION CF297521.1 GI:33666554
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--08-H01"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAAAAA 2799
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Db         17 TTGAAAAAAAAAAAAAA 1
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RESULT 2389
TA211D06P
LOCUS TA211D06P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 211d06, forward sequence, genomic survey sequence.
ACCESSION AL478564
VERSION AL478564.1 GI:11844523
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="211d06"

Query Match 0.6%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17
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RESULT 2390
TA211D06P/c
LOCUS TA211D06P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 211d06, forward sequence, genomic survey sequence.
ACCESSION AL478564
VERSION AL478564.1 GI:11844523
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

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FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="211d06"

  Query Match              0.6%;  Score 17;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2391
CF291486
LOCUS       CF291486                 23 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-O21, mRNA sequence.
ACCESSION   CF291486
VERSION     CF291486.1  GI:33660519
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-O21"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match              0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2392
CF291486/c
LOCUS       CF291486                 23 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-O21, mRNA sequence.
ACCESSION   CF291486
VERSION     CF291486.1  GI:33660519
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-O21"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match              0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2393
AZ435597
LOCUS       AZ435597                 23 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0222P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0222P09 R, genomic survey sequence.
ACCESSION   AZ435597
VERSION     AZ435597.1  GI:10559610
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0222  row: P  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
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Class: plasmid ends
High quality sequence stop: 23.

FEATURES Location/Qualifiers
source 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0222P09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAA 2802
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Db          1 AAAAAAAAAAAAAAAAA 17
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RESULT 2394
AZ435597/c
LOCUS AZ435597 23 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0222P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0222P09 R, genomic survey sequence.
ACCESSION AZ435597
VERSION AZ435597.1 GI:10559610
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 row: P column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES Location/Qualifiers
source 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0222P09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTT 2182
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Db         17 TTTTTTTTTTTTTTTTT 1
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RESULT 2395
AZ862224
LOCUS AZ862224 23 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0169N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0169N18 F, genomic survey sequence.
ACCESSION AZ862224
VERSION AZ862224.1 GI:13059330
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0169 row: N column: 18
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

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FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0169N18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 17


RESULT 2396
AZ862224/c
LOCUS       AZ862224                 23 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0169N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0169N18 F, genomic survey sequence.
ACCESSION   AZ862224
VERSION     AZ862224.1  GI:13059330
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0169  row: N  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0169N18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db         17 TTTTTTTTTTTTTTTTT 1


RESULT 2397
CF292725
LOCUS       CF292725                 24 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-K12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--01-K12, mRNA sequence.
ACCESSION   CF292725
VERSION     CF292725.1  GI:33661758
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--01-K12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
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                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 17;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTA 17


RESULT 2398
CF315032/c
LOCUS       CF315032                  25 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--03-M19.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--03-M19, mRNA sequence.
ACCESSION   CF315032
VERSION     CF315032.1  GI:33686793
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--03-M19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAAAAA 2801
              ||  |||   ||||||||||||||||
Db         25 TTTCAATCTCAAAAAAAAAAAAAAA 1


RESULT 2399
T57657/c
LOCUS       T57657                    25 bp    mRNA    linear   EST 08-FEB-1995
DEFINITION  yb59h02.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone
            IMAGE:75507 3' similar to similar to gb:M17589 TYROSINE
            3-MONOOXYGENASE ISOZYMES (HUMAN), mRNA sequence.
ACCESSION   T57657
VERSION     T57657.1  GI:659518
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
            Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
            and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
   PUBMED   8889549
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence starts: 1
            High qality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -21m13
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:505236"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:75507"
                     /sex="female"
                     /dev_stage="49 year old"
                     /lab_host="SOLR cells (kanamycin resistant)"
                     /clone_lib="Stratagene ovary (#937217)"
                     /note="Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI;
                     Site_2: XhoI; Cloned unidirectionally.  Primer: Oligo dT.
                     Total ovary tissue, normal, caucasian. Average insert
                     size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5'
                     GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTT 3'"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 2400
CF319953/c
LOCUS       CF319953                  25 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-K11.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-K11, mRNA sequence.
ACCESSION   CF319953
VERSION     CF319953.1  GI:33691714
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 25)
```

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  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-K11"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              | ||   || ||||||||||||||||
Db         25 AAAACCCAACAAAAAAAAAAAAAAA 1


RESULT 2401
AI560179/c
LOCUS       AI560179                 25 bp    mRNA    linear   EST 24-MAR-1999
DEFINITION  tq59h01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2213137 3'
            similar to SW:NU5M_ASCSU P24884 NADH-UBIQUINONE OXIDOREDUCTASE
            CHAIN 5 ;contains element MER30 repetitive element ;, mRNA
            sequence.
ACCESSION   AI560179
VERSION     AI560179.1  GI:4510520
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2213137"
                     /tissue_type="well-differentiated endometrial
                     adenocarcinoma, 7 pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut1"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Life Technologies catalog #:
                     11538-014"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||| || | |||||| |||| ||||
Db         25 TTTATCGCTTTTTTTCTTTGTTTT 1


RESULT 2402
BG929133
LOCUS       BG929133                 25 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC34-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BG929133
VERSION     BG929133.1  GI:14323656
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  MEDLINE   21482651
   PUBMED   11597177
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="cartilage"
                     /lab_host="E.coli DH10 B"
                     /clone_lib="HNC (Human Normal Cartilage)"
                     /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                     Directional"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTT 2180
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Db          1 TTTTTTTTCTTTATTGTGTTTTTTT 25


RESULT 2403
```

```
AZ343444/c
LOCUS       AZ343444                 25 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0076O01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0076O01 R, genomic survey sequence.
ACCESSION   AZ343444
VERSION     AZ343444.1  GI:10421687
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0076  row: O  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0076O01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
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Db         25 TTTTTTTTTTTTTTTAA 9


RESULT 2404
AZ658622
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LOCUS       AZ658622                 25 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0535F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0535F04 R, genomic survey sequence.
ACCESSION   AZ658622
VERSION     AZ658622.1  GI:11795768
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0535  row: F  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0535F04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1781 TGAACCCCATTCTTTCCTTCTCTGA 1805
              |||  |||||||||| || | ||||
Db          1 TGACTCCCATTCTTTGCTGCACTGA 25


RESULT 2405
BZ767540
LOCUS       BZ767540                 25 bp    DNA     linear   GSS 13-MAR-2003
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```
DEFINITION  SALK_139012.18.15.n Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_139012.18.15.n, genomic
            survey sequence.
ACCESSION   BZ767540
VERSION     BZ767540.1  GI:28940093
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_139012.18.15.n"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||| ||| ||||| |||  ||||
Db          1 TTTTTATTTATTTTTGTTTGTCTTT 25


RESULT 2406
TA324F07P/c
LOCUS       TA324F07P                25 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 324f07, forward sequence,
            genomic survey sequence.
ACCESSION   AL493403
VERSION     AL493403.1  GI:11867768
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="324f07"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 2407
BX552372
LOCUS       BX552372                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX552372 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse123b02_p1c, mRNA sequence.
ACCESSION   BX552372
VERSION     BX552372.1  GI:33376646
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse123b02_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
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                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              |||   |  ||||||||||||||||
Db          2 TCTAGATAGTTTTTTTTTTTTTTT 26


RESULT 2408
BX553653
LOCUS       BX553653                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX553653 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse12h01_p1c, mRNA sequence.
ACCESSION   BX553653
VERSION     BX553653.1  GI:33377798
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse12h01_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              |||   |  ||||||||||||||||
Db          2 TCTAAATAGTTTTTTTTTTTTTTT 26


RESULT 2409
BX553888
LOCUS       BX553888                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX553888 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse131b10_p1c, mRNA sequence.
ACCESSION   BX553888
VERSION     BX553888.1  GI:33378008
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse131b10_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              |||   |  ||||||||||||||||
Db          2 TCTAGATAGTTTTTTTTTTTTTTT 26


RESULT 2410
BX557791
LOCUS       BX557791                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX557791 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse34g02_p1c, mRNA sequence.
ACCESSION   BX557791
VERSION     BX557791.1  GI:33428966
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
```

```
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse34g02_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              |||    |  ||||||||||||||||
Db          2 TCTAGATAGTTTTTTTTTTTTTTT 26


RESULT 2411
BX560008
LOCUS       BX560008                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX560008 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse47c08_p1c, mRNA sequence.
ACCESSION   BX560008
VERSION     BX560008.1  GI:33368000
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse47c08_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db         10 TTTTTTTTTTTTTTTTT 26


RESULT 2412
BX560008/c
LOCUS       BX560008                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX560008 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse47c08_p1c, mRNA sequence.
ACCESSION   BX560008
VERSION     BX560008.1  GI:33368000
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse47c08_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAA 10
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RESULT 2413
BX566514
LOCUS       BX566514                 26 bp    mRNA    linear   EST 14-OCT-2003
DEFINITION  BX566514 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse82f08_p1c, mRNA sequence.
ACCESSION   BX566514
VERSION     BX566514.1  GI:33433497
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse82f08_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              |||   |  ||||||||||||||||
Db          2 TCTAGATAGTTTTTTTTTTTTTTT 26


RESULT 2414
BX567795
LOCUS       BX567795                 26 bp    mRNA    linear   EST 14-OCT-2003
DEFINITION  BX567795 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse8b03_p1c, mRNA sequence.
ACCESSION   BX567795
VERSION     BX567795.1  GI:33434709
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse8b03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              |||   |  ||||||||||||||||
Db          2 TCTAGATAGTTTTTTTTTTTTTTT 26


RESULT 2415
AZ818035
LOCUS       AZ818035                 26 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0087O15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0087O15 R, genomic survey sequence.
ACCESSION   AZ818035
VERSION     AZ818035.1  GI:12987943
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0087  row: O  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
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     source          1. .26
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0087O15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 17


RESULT 2416
AZ818035/c
LOCUS       AZ818035                 26 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0087O15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0087O15 R, genomic survey sequence.
ACCESSION   AZ818035
VERSION     AZ818035.1  GI:12987943
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0087  row: O  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0087O15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db         17 TTTTTTTTTTTTTTTTT 1


RESULT 2417
BX555323/c
LOCUS       BX555323                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555323 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse1g09_p1c, mRNA sequence.
ACCESSION   BX555323
VERSION     BX555323.1  GI:33379323
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse1g09_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2418
BI094728
LOCUS       BI094728                 27 bp    mRNA    linear   EST 14-DEC-2001
DEFINITION  EST-CD34N-059 cDNA library of human CD 34+ stem/progenitor cells
            Homo sapiens cDNA 3', mRNA sequence.
ACCESSION   BI094728
VERSION     BI094728.1  GI:17737109
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Zhou,G., Chen,J., Lee,S., Terry,C., Rowley,J.D. and Wang,S.M.
  TITLE     The pattern of gene expression in human hematopoietic CD34+
            stem/progenitor cells
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wang SM
            Hem/Onc
            University of Chicago Medical Center
            5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
            Tel: 773-702-6788
            Fax: 773-702-3002
            Email: swang1@midway.uchicago.edu
            This EST fragment was amplified from cDNA Library of human CD 34+
            stem/progenitor cells with GLGI technique (Generation of Longer
            cDNA fragments from SAGE tags for Gene Identification, Proc. Natl.
            Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till
            the first CATG site of the targeted cDNA sequence.
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="Bone marrow"
                     /cell_type="CD34+ stem/progenitor cells"
                     /clone_lib="cDNA library of human CD 34+ stem/progenitor
                     cells"
                     /note="3'ESTs converted from the SAGE tag sequences using
                     GLGI method"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 2419
BX550767/c
LOCUS       BX550767                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX550767 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse114f12_p1c, mRNA sequence.
ACCESSION   BX550767
VERSION     BX550767.1  GI:33374306
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse114f12_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2420
BX550946/c
LOCUS       BX550946                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX550946 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse115f11_p1c, mRNA sequence.
ACCESSION   BX550946
VERSION     BX550946.1  GI:33374735
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
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  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
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                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse115f11_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2421
BX551145/c
LOCUS       BX551145                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX551145 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse116h03_p1c, mRNA sequence.
ACCESSION   BX551145
VERSION     BX551145.1  GI:33375002
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
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                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse116h03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2422
BX551153/c
LOCUS       BX551153                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX551153 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse116h08_p1c, mRNA sequence.
ACCESSION   BX551153
VERSION     BX551153.1  GI:33375010
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
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                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
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Db         27 AAAAAAAAAAAAAAAA 11


RESULT 2423
BX551505/c
LOCUS       BX551505                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX551505 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse119a03_p1c, mRNA sequence.
ACCESSION   BX551505
VERSION     BX551505.1  GI:33375704
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
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                     /db_xref="taxon:37546"
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                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         27 AAAAAAAAAAAAAAAA 11


RESULT 2424
BX551552/c
LOCUS       BX551552                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX551552 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse119c07_p1c, mRNA sequence.
ACCESSION   BX551552
VERSION     BX551552.1  GI:33375771
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse119c07_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         27 AAAAAAAAAAAAAAAA 11


RESULT 2425
BX551708/c
LOCUS       BX551708                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX551708 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse11c02_p1c, mRNA sequence.
ACCESSION   BX551708
VERSION     BX551708.1  GI:33376038
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
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            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /clone="Tse11c02_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2426
BX551731/c
LOCUS       BX551731                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX551731 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse11d03_p1c, mRNA sequence.
ACCESSION   BX551731
VERSION     BX551731.1  GI:33376060
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse11d03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2427
BX551875/c
LOCUS       BX551875                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX551875 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse120c06_p1c, mRNA sequence.
ACCESSION   BX551875
VERSION     BX551875.1  GI:33376196
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /mol_type="mRNA"
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                     /clone="Tse120c06_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2428
BX551974/c
LOCUS       BX551974                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX551974 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse120h02_p1c, mRNA sequence.
ACCESSION   BX551974
VERSION     BX551974.1  GI:33376288
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
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  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse120h02_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2429
BX552003/c
LOCUS       BX552003                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX552003 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse121a07_p1c, mRNA sequence.
ACCESSION   BX552003
VERSION     BX552003.1  GI:33376315
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /mol_type="mRNA"
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                     /clone="Tse121a07_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2430
BX552041/c
LOCUS       BX552041                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX552041 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse121c04_p1c, mRNA sequence.
ACCESSION   BX552041
VERSION     BX552041.1  GI:33376347
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse121c04_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
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                gut"
                /note="country: Zimbabwe; EST from adult gut infected with
                T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2431
BX553159/c
LOCUS       BX553159                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX553159 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse127g01_p1c, mRNA sequence.
ACCESSION   BX553159
VERSION     BX553159.1  GI:33377351
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /sub_species="morsitans"
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                     /clone="Tse127g01_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2432
BX553354/c
LOCUS       BX553354                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX553354 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse128h11_p1c, mRNA sequence.
ACCESSION   BX553354
VERSION     BX553354.1  GI:33377529
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
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                     /clone="Tse128h11_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2433
BX553476/c
LOCUS       BX553476                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX553476 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse129f12_p1c, mRNA sequence.
ACCESSION   BX553476
VERSION     BX553476.1  GI:33377634
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
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   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
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                     /db_xref="taxon:37546"
                     /clone="Tse129f12_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2434
BX553666/c
LOCUS       BX553666                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX553666 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse12h08_p1c, mRNA sequence.
ACCESSION   BX553666
VERSION     BX553666.1  GI:33377811
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse12h08_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2435
BX553766/c
LOCUS       BX553766                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX553766 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse130e04_p1c, mRNA sequence.
ACCESSION   BX553766
VERSION     BX553766.1  GI:33377899
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
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                     /clone="Tse130e04_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11
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RESULT 2436
BX554327/c
LOCUS       BX554327                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX554327 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse14g09_p1c, mRNA sequence.
ACCESSION   BX554327
VERSION     BX554327.1  GI:33378417
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
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                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse14g09_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2437
BX554598/c
LOCUS       BX554598                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX554598 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse16c09_p1c, mRNA sequence.
ACCESSION   BX554598
VERSION     BX554598.1  GI:33378671
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse16c09_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2438
BX555101/c
LOCUS       BX555101                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555101 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse19d11_p1c, mRNA sequence.
ACCESSION   BX555101
VERSION     BX555101.1  GI:33379126
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
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          the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse19d11_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2439
BX555155/c
LOCUS       BX555155                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555155 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse19g11_p1c, mRNA sequence.
ACCESSION   BX555155
VERSION     BX555155.1  GI:33379174
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /mol_type="mRNA"
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                     /db_xref="taxon:37546"
                     /clone="Tse19g11_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2440
BX555158/c
LOCUS       BX555158                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555158 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse19h01_p1c, mRNA sequence.
ACCESSION   BX555158
VERSION     BX555158.1  GI:33379177
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
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                     /db_xref="taxon:37546"
                     /clone="Tse19h01_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2441
BX555385/c
LOCUS       BX555385                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555385 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse20b09_p1c, mRNA sequence.
ACCESSION   BX555385
VERSION     BX555385.1  GI:33379380
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse20b09_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2442
BX555500/c
LOCUS       BX555500                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555500 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse21a01_p1c, mRNA sequence.
ACCESSION   BX555500
VERSION     BX555500.1  GI:33379491
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /mol_type="mRNA"
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                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2443
BX555567/c
LOCUS       BX555567                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555567 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse21d12_p1c, mRNA sequence.
ACCESSION   BX555567
VERSION     BX555567.1  GI:33379550
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
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                     /clone="Tse21d12_p1c"
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                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
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                    T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2444
BX555594/c
LOCUS       BX555594                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555594 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse21f02_p1c, mRNA sequence.
ACCESSION   BX555594
VERSION     BX555594.1  GI:33379576
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse21f02_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2445
BX555829/c
LOCUS       BX555829                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555829 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse23b06_p1c, mRNA sequence.
ACCESSION   BX555829
VERSION     BX555829.1  GI:33379800
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /clone="Tse23b06_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2446
BX555864/c
LOCUS       BX555864                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555864 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse23d05_p1c, mRNA sequence.
ACCESSION   BX555864
VERSION     BX555864.1  GI:33379834
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
```

```
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
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            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES              Location/Qualifiers
     source           1. .27
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                      /clone="Tse23d05_p1c"
                      /tissue_type="adult infected gut"
                      /clone_lib="Glossina morsitans morsitans adult infected
                      gut"
                      /note="country: Zimbabwe; EST from adult gut infected with
                      T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2447
BX555901/c
LOCUS       BX555901                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555901 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse23f02_p1c, mRNA sequence.
ACCESSION   BX555901
VERSION     BX555901.1  GI:33379871
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES              Location/Qualifiers
     source           1. .27
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                      /clone="Tse23f02_p1c"
                      /tissue_type="adult infected gut"
                      /clone_lib="Glossina morsitans morsitans adult infected
                      gut"
                      /note="country: Zimbabwe; EST from adult gut infected with
                      T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2448
BX555930/c
LOCUS       BX555930                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555930 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse23g07_p1c, mRNA sequence.
ACCESSION   BX555930
VERSION     BX555930.1  GI:33379899
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES              Location/Qualifiers
     source           1. .27
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                      /db_xref="taxon:37546"
                      /clone="Tse23g07_p1c"
                      /tissue_type="adult infected gut"
                      /clone_lib="Glossina morsitans morsitans adult infected
                      gut"
                      /note="country: Zimbabwe; EST from adult gut infected with
                      T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2449
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BX556112/c
LOCUS       BX556112                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX556112 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse25a07_p1c, mRNA sequence.
ACCESSION   BX556112
VERSION     BX556112.1  GI:33380051
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
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                     /clone="Tse25a07_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2450
BX556156/c
LOCUS       BX556156                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX556156 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse25c09_p1c, mRNA sequence.
ACCESSION   BX556156
VERSION     BX556156.1  GI:33380093
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
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                     /clone="Tse25c09_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2451
BX556515/c
LOCUS       BX556515                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX556515 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse27f09_p1c, mRNA sequence.
ACCESSION   BX556515
VERSION     BX556515.1  GI:33427775
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
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                     /clone="Tse27f09_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2452
BX557271/c
LOCUS       BX557271                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX557271 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse31c08_p1c, mRNA sequence.
ACCESSION   BX557271
VERSION     BX557271.1  GI:33428470
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
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                     /db_xref="taxon:37546"
                     /clone="Tse31c08_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2453
BX557363/c
LOCUS       BX557363                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX557363 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse31g12_p1c, mRNA sequence.
ACCESSION   BX557363
VERSION     BX557363.1  GI:33428552
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
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                     /db_xref="taxon:37546"
                     /clone="Tse31g12_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2454
BX557794/c
LOCUS       BX557794                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX557794 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse34g04_p1c, mRNA sequence.
ACCESSION   BX557794
VERSION     BX557794.1  GI:33428969
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
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REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
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            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse34g04_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2455
BX558430/c
LOCUS       BX558430                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX558430 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse38e12_p1c, mRNA sequence.
ACCESSION   BX558430
VERSION     BX558430.1  GI:33365138
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse38e12_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2456
BX559230/c
LOCUS       BX559230                27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX559230 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse42d01_p1c, mRNA sequence.
ACCESSION   BX559230
VERSION     BX559230.1  GI:33366559
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse42d01_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"
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```
  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2457
BX559542/c
LOCUS       BX559542                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX559542 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse44c03_p1c, mRNA sequence.
ACCESSION   BX559542
VERSION     BX559542.1  GI:33367130
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse44c03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2458
BX560210/c
LOCUS       BX560210                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX560210 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse48f09_p1c, mRNA sequence.
ACCESSION   BX560210
VERSION     BX560210.1  GI:33368352
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse48f09_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2459
BX560901/c
LOCUS       BX560901                 27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX560901 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse52f10_p1c, mRNA sequence.
ACCESSION   BX560901
VERSION     BX560901.1  GI:33370020
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
```

```
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES                Location/Qualifiers
     source             1. .27
                        /organism="Glossina morsitans morsitans"
                        /mol_type="mRNA"
                        /sub_species="morsitans"
                        /db_xref="taxon:37546"
                        /clone="Tse52f10_p1c"
                        /tissue_type="adult infected gut"
                        /clone_lib="Glossina morsitans morsitans adult infected
                        gut"
                        /note="country: Zimbabwe; EST from adult gut infected with
                        T.brucei"

  Query Match              0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2460
BX562177/c
LOCUS       BX562177                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX562177 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse5b09_p1c, mRNA sequence.
ACCESSION   BX562177
VERSION     BX562177.1  GI:33372299
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES                Location/Qualifiers
     source             1. .27
                        /organism="Glossina morsitans morsitans"
                        /mol_type="mRNA"
                        /sub_species="morsitans"
                        /db_xref="taxon:37546"
                        /clone="Tse5b09_p1c"
                        /tissue_type="adult infected gut"
                        /clone_lib="Glossina morsitans morsitans adult infected
                        gut"
                        /note="country: Zimbabwe; EST from adult gut infected with
                        T.brucei"

  Query Match              0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2461
BX564083/c
LOCUS       BX564083                  27 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX564083 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse6f02_p1c, mRNA sequence.
ACCESSION   BX564083
VERSION     BX564083.1  GI:33431280
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES                Location/Qualifiers
     source             1. .27
                        /organism="Glossina morsitans morsitans"
                        /mol_type="mRNA"
                        /sub_species="morsitans"
                        /db_xref="taxon:37546"
                        /clone="Tse6f02_p1c"
                        /tissue_type="adult infected gut"
                        /clone_lib="Glossina morsitans morsitans adult infected
                        gut"
                        /note="country: Zimbabwe; EST from adult gut infected with
                        T.brucei"

  Query Match              0.6%;  Score 17;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 2462
AL587605/c
LOCUS       AL587605                  28 bp    mRNA    linear   EST 02-MAR-2001
```

```
DEFINITION  AL587605 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS059F11, mRNA sequence.
ACCESSION   AL587605
VERSION     AL587605.1  GI:13192639
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS059F11"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"

  Query Match             0.6%;  Score 17;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||| |
Db         23 AAAAAAAAAAAAAAAAN 6


RESULT 2463
AI207866/c
LOCUS       AI207866                 31 bp    mRNA    linear   EST 19-OCT-1998
DEFINITION  an06c06.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone
            IMAGE:1684810 3' similar to SW:YM14_PARTE P15615 HYPOTHETICAL 47.2
            KD PROTEIN ;contains MER22.t3 MER28 repetitive element ;, mRNA
            sequence.
ACCESSION   AI207866
VERSION     AI207866.1  GI:3769808
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1684810"
                     /sex="male"
                     /tissue_type="schizophrenic brain S-11 frontal lobe"
                     /dev_stage="34 years old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="Stratagene schizo brain S11"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI;  Library
                     constructed from S-11 frontal lobe, male, 34 years old,
                     50% caucasian, 50% Aleutian.  Schizophrenic suicide.
                     Random primed into EcoRI site of ZAP II Vector.  Mass
                     excised. Custom library. Avg insert length 1.4kb.
                     Material obtained by Johnston N., Torrey, E.F., Yolken R.,
                     and the Stanley Neuropathology Consortium - Analysis of
                     RNAs from the Brains of Individuals with Psychiatric
                     Diseases (Unpublished) Stanley Neurovirology Laboratory,
                     Johns Hopkins School of Medicine, Baltimore MD."

  Query Match             0.6%;  Score 17;  DB 1;  Length 31;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2803
              |||   |||||||||||| || ||||
Db         29 AGAGAAGAAAAAAAAAAGAAGAAAA 5


RESULT 2464
AZ451251/c
LOCUS       AZ451251                 32 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0250I05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0250I05 R, genomic survey sequence.
ACCESSION   AZ451251
VERSION     AZ451251.1  GI:10606869
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0250  row: I  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 32.
```

```
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0250I05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 17;  DB 1;  Length 32;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
                | ||   |||| ||||||||||||
Db         26 AAAAAACAAAACAAAAAAAAAAAAA 2


RESULT 2465
BJ036312/c
LOCUS       BJ036312                35 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  BJ036312 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL035k09 5', mRNA sequence.
ACCESSION   BJ036312
VERSION     BJ036312.1  GI:17396897
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL035k09"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"

  Query Match             0.6%;  Score 17;  DB 1;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
                |||||||||||||||||
Db         31 AAAAAAAAAAAAAAAAA 15


RESULT 2466
AZ351309
LOCUS       AZ351309                35 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0089K13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0089K13 F, genomic survey sequence.
ACCESSION   AZ351309
VERSION     AZ351309.1  GI:10430546
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0089  row: K  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 35.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0089K13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
```

adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          2 AAAAAAAAAAAAAAAAA 18
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RESULT 2467
TA115E07P
LOCUS TA115E07P 37 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 115e07, forward sequence, genomic survey sequence.
ACCESSION AL462838
VERSION AL462838.1 GI:11832519
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 37)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .37
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="115e07"

Query Match 0.6%; Score 17; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 17
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RESULT 2468
CF299570/c
LOCUS CF299570 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-K09, mRNA sequence.
ACCESSION CF299570
VERSION CF299570.1 GI:33671331
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-K09"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              | | ||||||||||||||||||
Db         20 TAGTAAAAAAAAAAAAAAAA 1
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RESULT 2469
CF301101
LOCUS CF301101 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-N04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-N04, mRNA sequence.
ACCESSION CF301101
VERSION CF301101.1 GI:33672862
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-N04"
/tissue_type="leaf"
/dev_stage="7 days after germination"

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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              |||||||||||||||| || |
Db          1 TTTTTTTTTTTTTTTCTTCT 20


RESULT 2470
AZ343730
LOCUS       AZ343730                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0077E20 F, genomic survey sequence.
ACCESSION   AZ343730
VERSION     AZ343730.1  GI:10422288
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0077  row: E  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0077E20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||| |||||||||||| |
Db          1 TTTTTCTTTTTTTTTTTCT 20


RESULT 2471
AW333777
LOCUS       AW333777                 20 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S25H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION   AW333777
VERSION     AW333777.1  GI:6830134
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
  ORGANISM  Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Pneumocystis carinii"
                     /mol_type="mRNA"
                     /db_xref="taxon:4754"
                     /lab_host="E. coli"
                     /clone_lib="AGS-1"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (3x10e9) from a single rat (99-1-6,
                     sacrificed on 3/17/99)  at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT priming, standard
                     conditions described by  vendor, Stratagene. Further
                     details see www.uky.edu/Project/Pneumocystis/"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||| | |||
Db          1 TTTTTTTTTTTTTTATATTA 20


RESULT 2472
CF282165/c
LOCUS       CF282165                 20 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-I22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-I22, mRNA sequence.
ACCESSION   CF282165
VERSION     CF282165.1  GI:33659552
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
```

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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--09-I22"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2800
              | ||| ||||||||||||||
Db         20 ATTTGCAAAAAAAAAAAAAA 1


RESULT 2473
CF298018
LOCUS       CF298018                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-D19, mRNA sequence.
ACCESSION   CF298018
VERSION     CF298018.1  GI:33669779
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--01-D19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTGATT 20


RESULT 2474
CF298018/c
LOCUS       CF298018                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-D19, mRNA sequence.
ACCESSION   CF298018
VERSION     CF298018.1  GI:33669779
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--01-D19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2800
              |||  ||||||||||||||
Db         20 AATCAAAAAAAAAAAAAAAA 1


RESULT 2475
CF300961
LOCUS       CF300961                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-K03, mRNA sequence.
ACCESSION   CF300961
VERSION     CF300961.1  GI:33672722
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-K03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||  |||
Db          1 TTTTTTTTTTTTTTTCCTTT 20


RESULT 2476
CF300961/c
LOCUS       CF300961                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-K03, mRNA sequence.
ACCESSION   CF300961
VERSION     CF300961.1  GI:33672722
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-K03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2800
              ||  ||||||||||||||||
Db         20 AAAGGAAAAAAAAAAAAAAA 1


RESULT 2477
CF330490/c
LOCUS       CF330490                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-D16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-D16, mRNA sequence.
ACCESSION   CF330490
VERSION     CF330490.1  GI:33809214
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-D16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2801
              |||  ||||||||||||||||
Db         20 ATTCCAAAAAAAAAAAAAAA 1


RESULT 2478
AZ633741/c
LOCUS       AZ633741                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0489G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0489G12 F, genomic survey sequence.
ACCESSION   AZ633741
VERSION     AZ633741.1  GI:11755931
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0489  row: G  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0489G12"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              |||  ||||||||||||||||
Db         20 TTTGGTTTTTTTTTTTTTT 1


RESULT 2479
CF293087/c
LOCUS       CF293087                 21 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--02-C07.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--02-C07, mRNA sequence.
ACCESSION   CF293087
VERSION     CF293087.1  GI:33662120
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="30DGS--02-C07"
                      /tissue_type="leaf"
                      /dev_stage="30 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              |||  ||||||||||||||||
Db         20 TTGTCAAAAAAAAAAAAAAA 1


RESULT 2480
AW246884
LOCUS       AW246884                 22 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822626.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822626 3',
            mRNA sequence.
ACCESSION   AW246884
VERSION     AW246884.1  GI:6589877
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822626.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 20
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 22 contiguous distinct
            peaks following vector sequence.
            Plate: LLCM9  row: O  column: 11
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            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822626"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 22;
  Best Local Similarity   90.0%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2181
              ||| ||||||||||||||| |
Db          1 CTCTTTTTTTTTTTTTTCT 20


RESULT 2481
AW246884/c
LOCUS       AW246884                 22 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822626.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822626 3',
            mRNA sequence.
ACCESSION   AW246884
VERSION     AW246884.1  GI:6589877
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822626.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 20
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 22 contiguous distinct
            peaks following vector sequence.
            Plate: LLCM9  row: O  column: 11
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822626"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 22;
  Best Local Similarity   90.0%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||| |
Db         21 GAGAAAAAAAAAAAAAAAGA 2


RESULT 2482
AZ845735
LOCUS       AZ845735                 22 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0145J07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0145J07 R, genomic survey sequence.
ACCESSION   AZ845735
VERSION     AZ845735.1  GI:13015643
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0145  row: J  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0145J07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
```

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2173 TTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||||  ||||
Db          1 TTTTTTTTTTTTTTGGCTTT 20
```

RESULT 2483
TA330H07Q/c
LOCUS TA330H07Q 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 330h07, reverse sequence, genomic survey sequence.
ACCESSION AL492002
VERSION AL492002.1 GI:11868302
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="330h07"

Query Match 0.6%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2315 ATTTGTTGCTGCTTGTCACC 2334
              ||||||||||  ||||||||
Db         20 ATTTGTTGCTAGTTGTCACC 1
```

RESULT 2484
AL048695
LOCUS AL048695 23 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp566D063_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566D063, mRNA sequence.
ACCESSION AL048695
VERSION AL048695.1 GI:4727766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 23)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES Location/Qualifiers
source 1. .23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566D063"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||| |||
Db          4 TCAAAAAAAAAAAAAAGAAA 23
```

RESULT 2485
CF302134
LOCUS CF302134 23 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-F21, mRNA sequence.
ACCESSION CF302134
VERSION CF302134.1 GI:33673895
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-F21"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||  |||
Db          1 TTTTTTTTTTTTTTTCTACT 20
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RESULT 2486
AZ382429
LOCUS AZ382429 23 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0139E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0139E11 R, genomic survey sequence.
ACCESSION AZ382429
VERSION AZ382429.1 GI:10496129
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: E column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0139E11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
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Db          2 GAAAAAAAAAACCAAAAAAA 21
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RESULT 2487
CF334146
LOCUS CF334146 23 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-F05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-F05, mRNA sequence.
ACCESSION CF334146
VERSION CF334146.1 GI:33816628
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-F05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
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Db          1 TTTTTTTTTTTTTTTTCCAC 20
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RESULT 2488
CF290997
LOCUS CF290997 23 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-E03.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-E03, mRNA sequence.
ACCESSION CF290997
VERSION CF290997.1 GI:33660030
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-E03"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTGGCT 20


RESULT 2489
CF308058
LOCUS       CF308058                23 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-L15.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-L15, mRNA sequence.
ACCESSION   CF308058
VERSION     CF308058.1  GI:33679819
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||  ||||
Db          1 TTTTTTTTTTTTTTACTAAC 20


RESULT 2490
CF302406
LOCUS       CF302406                24 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-N18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-N18, mRNA sequence.
ACCESSION   CF302406
VERSION     CF302406.1  GI:33674167
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTT 2192
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Db          1 TTTTTTTTTTTTTTAAATAT 20


RESULT 2491
AZ827015
LOCUS       AZ827015                24 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0103J11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0103J11 F, genomic survey sequence.
ACCESSION   AZ827015
VERSION     AZ827015.1  GI:12996923
KEYWORDS    GSS.
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SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0103  row: J  column: 11
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0103J11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||| |||||| |||||
Db          5 TTTTTTTGTTTTTGTTTTT 24


RESULT 2492
BZ765670/c
LOCUS       BZ765670                 25 bp    DNA     linear   GSS 13-MAR-2003
DEFINITION  SALK_133356.14.20.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_133356.14.20.x, genomic
            survey sequence.
ACCESSION   BZ765670
VERSION     BZ765670.1  GI:28938223
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_133356.14.20.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||| ||||
Db         24 GAAAAAAAAAATAAACAAAA 5


RESULT 2493
AZ404619/c
LOCUS       AZ404619                 25 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0173L20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0173L20 F, genomic survey sequence.
ACCESSION   AZ404619
VERSION     AZ404619.1  GI:10528632
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
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            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0173  row: L  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0173L20"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db         22 TAGCCATTCAAATATCAAAT 3


RESULT 2494
CF300303/c
LOCUS       CF300303                  27 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-K11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-K11, mRNA sequence.
ACCESSION   CF300303
VERSION     CF300303.1  GI:33672064
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="7LEAF--04-K11"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 27;
  Best Local Similarity   90.0%;  Pred. No. 2.8e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2800
              ||  |  ||||||||||||||||
Db         20 AAGTAAAAAAAAAAAAAAAA 1


RESULT 2495
AI971979
LOCUS       AI971979                  28 bp    mRNA    linear   EST 27-OCT-1999
DEFINITION  wv30h06.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531099 3'
            similar to TR:O63545 O63545 NADH DEHYDROGENASE SUBUNIT 5 ;contains
            TAR1.b1 TAR1 repetitive element ;, mRNA sequence.
ACCESSION   AI971979
VERSION     AI971979.1  GI:5768805
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
            Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .28
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2531099"
                      /tissue_type="fibrotheoma"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NCI_CGAP_Ov18"
                      /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGCGACATTTTTTTTTTTTTTTTT 3'];
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia),  digested with Not I and cloned into the Not
                      I and Eco RI sites  of the modified pT7T3 vector. Library
                      went through one round of normalization, and was
                      constructed by Bento Soares and M. Fatima Bonaldo.  "

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 28;
```

```
  Best Local Similarity   90.0%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||| |||| |||||
Db          3 GAAAAAAAACAAAACAAAAA 22


RESULT 2496
AL953605/c
LOCUS       AL953605                  30 bp    DNA     linear   GSS 30-NOV-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-352E12-016361,
            genomic survey sequence.
ACCESSION   AL953605
VERSION     AL953605.1  GI:24410227
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 30)
  AUTHORS   Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone F2K11. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-352E12-016361"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              |||||||| ||||| |||||
Db         30 TGAAAAAACAAAAATAAAAA 11


RESULT 2497
AU265130
LOCUS       AU265130                  34 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU265130 VS Dictyostelium discoideum cDNA clone VSF372 5', mRNA
            sequence.
ACCESSION   AU265130
VERSION     AU265130.1  GI:20523928
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSF372"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 34;
  Best Local Similarity   72.4%;  Pred. No. 2.7e+03;
  Matches   21;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAAAAA 2804
              || |  ||  ||||||||||||   ||||
Db          1 GTAAATATAAAAAAAAAAAAAATTNAAAA 29


RESULT 2498
BF239380
LOCUS       BF239380                  35 bp    mRNA    linear   EST 14-NOV-2000
DEFINITION  601906237F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134224 5',
            mRNA sequence.
ACCESSION   BF239380
VERSION     BF239380.1  GI:11153302
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1036  row: i  column: 09
            High quality sequence stop: 3.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Homo sapiens"
```

```
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4134224"
                     /tissue_type="from chronic myelogenous leukemia"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_54"
                     /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); Double-stranded cDNA was prepared from
                     cell line RNA.  5' and 3' adaptors were used in cloning as
                     follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.75 kb (range 0.9-4.0 kb).  15/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 35;
  Best Local Similarity   90.0%;  Pred. No. 2.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2801
              || ||||||||| |||||||
Db          6 ATAGAAAAAAAAGAAAAAAA 25


RESULT 2499
CF290998
LOCUS       CF290998                 23 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E03.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-E03, mRNA sequence.
ACCESSION   CF290998
VERSION     CF290998.1  GI:33660031
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-E03"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 23;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAA 2803
              || |  ||||||||||||||||
Db          1 AACAGCCAAAAAAAAAAAAAAA 23


RESULT 2500
AW249550
LOCUS       AW249550                 23 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821204.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821204 3',
            mRNA sequence.
ACCESSION   AW249550
VERSION     AW249550.1  GI:6592543
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821204.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 23 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM6  row: D  column: 5
            High quality sequence stop: 9.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821204"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 23;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAACTTTGAAAGTT 2199
              |||||||||||||  | ||| ||
Db          1 TTTTTTTTTTAACAATTAAATTT 23


RESULT 2501
AZ330773
LOCUS       AZ330773                 23 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0056O08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
```

```
            clone UUGC1M0056O08 F, genomic survey sequence.
ACCESSION   AZ330773
VERSION     AZ330773.1  GI:10392809
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0056  row: O  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0056O08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 23;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAA 2800
                ||   || ||||||||||||||
Db          1 TATTTTTCAAAAAAAAAAAAAAA 23


RESULT 2502
CF292725/c
LOCUS       CF292725                 24 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-K12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--01-K12, mRNA sequence.
ACCESSION   CF292725
VERSION     CF292725.1  GI:33661758
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--01-K12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAAA 2804
                ||||    ||||||||||||||||
Db         24 ATTGTCCTAAAAAAAAAAAAAAA 2


RESULT 2503
CF291636
LOCUS       CF291636                 24 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-C09.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-C09, mRNA sequence.
ACCESSION   CF291636
VERSION     CF291636.1  GI:33660669
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
```

```
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-C09"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGACGC 73
              ||||||| ||||||||| |  ||
Db          1 GCGGCGGCGGCGGCGGCGGCGGC 23


RESULT 2504
AZ399663
LOCUS       AZ399663                 24 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0165C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0165C10 R, genomic survey sequence.
ACCESSION   AZ399663
VERSION     AZ399663.1  GI:10514737
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0165  row: C  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0165C10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTT 2183
              | |  |||| ||||||||||||
Db          1 TTTAATTTTGTTTTTTTTTTTT 23


RESULT 2505
AZ782507
LOCUS       AZ782507                 24 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0022L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0022L22 R, genomic survey sequence.
ACCESSION   AZ782507
VERSION     AZ782507.1  GI:12916299
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0022  row: L  column: 22
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0022L22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
```

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2186
              | |||||||||| || ||| ||
Db          2 CGTTTTTTTTTTGTTGTTTGTT 24
```

RESULT 2506
CF296608
LOCUS CF296608 25 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--07-A20.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--07-A20, mRNA sequence.
ACCESSION CF296608
VERSION CF296608.1 GI:33665641
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .25
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--07-A20"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.8e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2169 TTTTTTTTTTTTTTTTTAACTT 2191
              |||||||||||||  | |||| |
Db          1 TTTTTTTTTTTTTAATCTAACAT 23
```

RESULT 2507
AI682835/c
LOCUS AI682835 25 bp mRNA linear EST 17-DEC-1999
DEFINITION wc66h10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323651 3' similar to TR:O14187 O14187 PROBABLE PRE-MRNA SPLICING FACTOR C4F8.12C. ;contains TAR1.t3 MSR1 repetitive element ;, mRNA sequence.
ACCESSION AI682835
VERSION AI682835.1 GI:4893017
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1245 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2323651"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.8e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        252 TCCCCCACCTCTCCTCCGCCGGG 274
              |||||| | | ||| ||||||||
Db         25 TCCCCCCCTTGTCCCCCGCCGGG 3
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RESULT 2508
AI745099/c
LOCUS AI745099 25 bp mRNA linear EST 21-JUN-1999
DEFINITION tr21a09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218936 3' similar to TR:Q34096 Q34096 MURF2 PROTEIN. ;contains element L1 L1 repetitive element ;, mRNA sequence.
ACCESSION AI745099
VERSION AI745099.1 GI:5113387
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2218936"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ov23"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.8e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTT 2177
              ||||||||||| | | ||| ||||
Db         23 TTTTTTTCTCATCTGTTTCTTTT 1


RESULT 2509
AZ510128/c
LOCUS       AZ510128                 25 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0354L23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0354L23 F, genomic survey sequence.
ACCESSION   AZ510128
VERSION     AZ510128.1  GI:10691444
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0354  row: L  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0354L23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.8e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAA 2188
              || | |  ||||||||||||||||
Db         23 TTGTATGGTTTTTTTTTTTTAA 1


RESULT 2510
BH856226
LOCUS       BH856226                 25 bp    DNA     linear   GSS 08-JUL-2002
DEFINITION  SALK_083159.52.35.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_083159.52.35.x, genomic
            survey sequence.
ACCESSION   BH856226
VERSION     BH856226.1  GI:21705816
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_083159.52.35.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
```

be found at http://signal.salk.edu/tdna_protocols.html"

Query Match 0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.8e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       1976 TTGAAAAAAAGAAAAGTGTGTAT 1998
              || ||| ||||||||| ||| ||
Db          2 TTAAAAGAAAGAAAAGAGTGAAT 24
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RESULT 2511
AZ495352/c
LOCUS AZ495352 27 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0331E14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0331E14 F, genomic survey sequence.
ACCESSION AZ495352
VERSION AZ495352.1 GI:10670743
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0331 row: E column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
FEATURES Location/Qualifiers
source 1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0331E14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.6; DB 1; Length 27;
Best Local Similarity 82.6%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
              | ||  |||||||| ||||||||
Db         23 AAAAAGGAAAAAAAGAAAAAAAA 1
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RESULT 2512
BQ591183/c
LOCUS BQ591183 27 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-L16-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-L16 3-PRIME, mRNA sequence.
ACCESSION BQ591183
VERSION BQ591183.1 GI:26120766
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 27)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 27 Std Error: 0.00
Plate: 17 row: L column: 16
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .27
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188934"
/db_xref="taxon:161934"
/clone="024-017-L16"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16.6; DB 1; Length 27;
Best Local Similarity 82.6%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
              | ||   ||||||||||||||||
Db         23 AAAACATAAAAAAAAAAAAAAAA 1
```

```
RESULT 2513
CF335736/c
LOCUS       CF335736                  33 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--05-I12.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--05-I12, mRNA sequence.
ACCESSION   CF335736
VERSION     CF335736.1  GI:33819839
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--05-I12"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 33;
  Best Local Similarity   82.6%;  Pred. No. 2.7e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
                | ||   ||||||||||||||||
Db         23 ACAAACCAAAAAAAAAAAAAAAA 1


RESULT 2514
CF298591/c
LOCUS       CF298591                  18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A20, mRNA sequence.
ACCESSION   CF298591
VERSION     CF298591.1  GI:33670352
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-A20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              || |||||||||||||||
Db         18 TTTAAAAAAAAAAAAAAA 1


RESULT 2515
CF300456
LOCUS       CF300456                  18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-N23, mRNA sequence.
ACCESSION   CF300456
VERSION     CF300456.1  GI:33672217
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-N23"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||| |
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Db          1 TTTTTTTTTTTTTTTCT 18


RESULT 2516
CF320046/c
LOCUS       CF320046                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-M11.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-M11, mRNA sequence.
ACCESSION   CF320046
VERSION     CF320046.1  GI:33691807
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-M11"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||
Db         18 ATAAAAAAAAAAAAAAA 1


RESULT 2517
AL048754
LOCUS       AL048754                 18 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp566L173_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566L173, mRNA sequence.
ACCESSION   AL048754
VERSION     AL048754.1  GI:4727825
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566L173"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="X1-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2801
              | |||||||||||||||
Db          1 TCAAAAAAAAAAAAAAA 18


RESULT 2518
AL048754/c
LOCUS       AL048754                 18 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp566L173_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566L173, mRNA sequence.
ACCESSION   AL048754
VERSION     AL048754.1  GI:4727825
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566L173"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="X1-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||| |
Db         18 TTTTTTTTTTTTTTTGA 1


RESULT 2519
BM658677
LOCUS       BM658677                 18 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
            sequence.
ACCESSION   BM658677
VERSION     BM658677.1  GI:18958948
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Porcine ESTs
  JOURNAL   Unpublished (2002)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone_lib="CSEQFXL37 pig adrenal"
                     /note="Organ: adrenal gland; Vector: pBluescript SK+;
                     Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
                     GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     non-normalized library, sequenced 3' with M13R primer."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||||| |||||||||
Db          1 TTTTTTTTCTTTTTTTT 18


RESULT 2520
BM658677/c
LOCUS       BM658677                 18 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
            sequence.
ACCESSION   BM658677
VERSION     BM658677.1  GI:18958948
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Porcine ESTs
  JOURNAL   Unpublished (2002)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone_lib="CSEQFXL37 pig adrenal"
                     /note="Organ: adrenal gland; Vector: pBluescript SK+;
                     Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
                     GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     non-normalized library, sequenced 3' with M13R primer."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||| ||||||||
Db         18 AAAAAAAAAGAAAAAAA 1


RESULT 2521
CF309376
LOCUS       CF309376                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-I19, mRNA sequence.
ACCESSION   CF309376
VERSION     CF309376.1  GI:33681137
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--03-I19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
              |||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTACT 18


RESULT 2522
CF329285
LOCUS       CF329285                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-I22, mRNA sequence.
ACCESSION   CF329285
VERSION     CF329285.1  GI:33806806
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-I22"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTCTA 18


RESULT 2523
CF329285/c
LOCUS       CF329285                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-I22, mRNA sequence.
ACCESSION   CF329285
VERSION     CF329285.1  GI:33806806
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-I22"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2800
              | ||||||||||||||||
Db         18 TAGAAAAAAAAAAAAAA 1


RESULT 2524
CF329484
LOCUS       CF329484                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION   CF329484
VERSION     CF329484.1  GI:33807207
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
              |||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTACT 18


RESULT 2525
CF329485/c
LOCUS       CF329485                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION   CF329485
VERSION     CF329485.1  GI:33807209
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-N06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
              ||||||||||||||| |||
Db         18 TTTTTTTTTTTTTTTACT 1


RESULT 2526
CF309636
LOCUS       CF309636                19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-O08.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-O08, mRNA sequence.
ACCESSION   CF309636
VERSION     CF309636.1  GI:33681397
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--03-O08"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAA 2188
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTGAA 18


RESULT 2527
CF334610/c
LOCUS       CF334610                19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-P13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-P13, mRNA sequence.
ACCESSION   CF334610
VERSION     CF334610.1  GI:33817556
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--03-P13"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              || |||||||||||||||
Db         18 AATAAAAAAAAAAAAAAA 1


RESULT 2528
AZ360314/c
LOCUS       AZ360314                19 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0103G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0103G03 R, genomic survey sequence.
ACCESSION   AZ360314
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VERSION     AZ360314.1  GI:10474014
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0103  row: G  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0103G03"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||||| |||||||
Db         19 TTTTTTTTTCTTTTTTT 2


RESULT 2529
CF278272/c
LOCUS       CF278272                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--04-C01, mRNA sequence.
ACCESSION   CF278272
VERSION     CF278272.1  GI:33655658
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--04-C01"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              || |||||||||||||||
Db         18 TTTAAAAAAAAAAAAAAA 1


RESULT 2530
CF295672
LOCUS       CF295672                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-L12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-L12, mRNA sequence.
ACCESSION   CF295672
VERSION     CF295672.1  GI:33664705
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /db_xref="taxon:4530"
                     /clone="30DGS--05-L12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTAACAT 18


RESULT 2531
CF298472
LOCUS       CF298472                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-O01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-O01, mRNA sequence.
ACCESSION   CF298472
VERSION     CF298472.1  GI:33670233
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--01-O01"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTATA 18


RESULT 2532
CF308042/c
LOCUS       CF308042                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-L07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-L07, mRNA sequence.
ACCESSION   CF308042
VERSION     CF308042.1  GI:33679803
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--01-L07"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2801
              || |||||||||||||||
Db         18 TGTAAAAAAAAAAAAAA 1


RESULT 2533
CF319596
LOCUS       CF319596                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-C14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.
ACCESSION   CF319596
VERSION     CF319596.1  GI:33691357
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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     source          1. .19
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-C14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAA 2188
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTGAA 18


RESULT 2534
CF319596/c
LOCUS       CF319596                  19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-C14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.
ACCESSION   CF319596
VERSION     CF319596.1  GI:33691357
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-C14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              || |||||||||||||||
Db         18 TTCAAAAAAAAAAAAAAA 1


RESULT 2535
CF326845
LOCUS       CF326845                  19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-B12.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-B12, mRNA sequence.
ACCESSION   CF326845
VERSION     CF326845.1  GI:33801944
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--01-B12"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              | |||||||||||||||||
Db          2 TAGAAAAAAAAAAAAAAA 19


RESULT 2536
CF326845/c
LOCUS       CF326845                  19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-B12.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-B12, mRNA sequence.
ACCESSION   CF326845
VERSION     CF326845.1  GI:33801944
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
```

```
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="NACL--01-B12"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||||| ||
Db         19 TTTTTTTTTTTTTTTCTA 2


RESULT 2537
AZ465954
LOCUS       AZ465954                 19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0276E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0276E16 F, genomic survey sequence.
ACCESSION   AZ465954
VERSION     AZ465954.1  GI:10624079
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0276  row: E  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0276E16"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTT 2179
              | |||||||||||||||
Db          2 CCCCTTTTTTTTTTTTT 19


RESULT 2538
AZ766990/c
LOCUS       AZ766990                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0564H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0564H19 R, genomic survey sequence.
ACCESSION   AZ766990
VERSION     AZ766990.1  GI:12884624
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0564  row: H  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0564H19"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
```

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2163 TCCTTTTTTTTTTTTTT 2180
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Db         18 TCCATTTTTTTTTTTTT 1
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RESULT 2539
CF319428/c
LOCUS CF319428 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--09-O20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-O20, mRNA sequence.
ACCESSION CF319428
VERSION CF319428.1 GI:33691189
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-O20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAAAAAAA 2801
              | |||||||||||||||
Db         19 TCAAAAAAAAAAAAAAA 2
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RESULT 2540
CF317946
LOCUS CF317946 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-N06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--07-N06, mRNA sequence.
ACCESSION CF317946
VERSION CF317946.1 GI:33689707
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HD--07-N06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         52 CGGCGGGGGCGGCGGCAG 69
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Db          1 CGGCGGCGGCGGCGGCAG 18
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RESULT 2541
AZ368518/c
LOCUS AZ368518 20 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0118G09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0118G09 R, genomic survey sequence.
ACCESSION AZ368518
VERSION AZ368518.1 GI:10482218
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

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            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0118  row: G  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0118G09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAA 2188
              ||||| ||||||||||||
Db         20 TTTTTGTTTTTTTTTTAA 3


RESULT 2542
CF319625
LOCUS       CF319625                21 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-D06, mRNA sequence.
ACCESSION   CF319625
VERSION     CF319625.1  GI:33691386
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||
Db          4 ATAAAAAAAAAAAAAAAA 21


RESULT 2543
CF293087
LOCUS       CF293087                21 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--02-C07.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--02-C07, mRNA sequence.
ACCESSION   CF293087
VERSION     CF293087.1  GI:33662120
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--02-C07"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2172 TTTTTTTTTTTTTTTAAC 2189
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Db          1 TTTTTTTTTTTTTTGAC 18
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RESULT 2544
CF319122/c
LOCUS CF319122 21 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--09-I07.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-I07, mRNA sequence.
ACCESSION CF319122
VERSION CF319122.1 GI:33690883
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-I07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAA 2802
              ||||||||||||| ||||
Db         18 GAAAAAAAAAAAATAAAA 1
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RESULT 2545
CF318882
LOCUS CF318882 22 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--09-C23.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-C23, mRNA sequence.
ACCESSION CF318882
VERSION CF318882.1 GI:33690643
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-C23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2171 TTTTTTTTTTTTTTTAA 2188
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTGAA 18
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RESULT 2546
AZ307896/c
LOCUS AZ307896 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0010N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0010N18 F, genomic survey sequence.
ACCESSION AZ307896
VERSION AZ307896.1 GI:10347346
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

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            Plate: 0010  row: N  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES              Location/Qualifiers
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                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0010N18"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 22;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||||||||||| ||||
Db         22 AAAAAAAAAAAAACAAAA 5


RESULT 2547
BQ591193/c
LOCUS       BQ591193                 22 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-D14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-D14 3-PRIME, mRNA sequence.
ACCESSION   BQ591193
VERSION     BQ591193.1  GI:26120776
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 22   Std Error: 0.00
            Plate: 17  row: D  column: 14
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:188927"
                      /db_xref="taxon:161934"
                      /clone="024-017-D14"
                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-storage root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 22;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAA 2799
              ||| ||||||||||||||
Db         18 ATTAAAAAAAAAAAAAAA 1


RESULT 2548
AZ330773/c
LOCUS       AZ330773                 23 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0056O08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0056O08 F, genomic survey sequence.
ACCESSION   AZ330773
VERSION     AZ330773.1  GI:10392809
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0056  row: O  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0056O08"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2171 TTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||| ||
Db         23 TTTTTTTTTTTTTTTGAA 6
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RESULT 2549
BX560037
LOCUS BX560037 23 bp mRNA linear EST 10-OCT-2003
DEFINITION BX560037 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse47e08_p1c, mRNA sequence.
ACCESSION BX560037
VERSION BX560037.1 GI:33368052
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 23)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.
FEATURES Location/Qualifiers
source 1. .23
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse47e08_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.6%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2171 TTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTCTAA 18
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RESULT 2550
AZ308447
LOCUS AZ308447 23 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0011J24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0011J24 F, genomic survey sequence.
ACCESSION AZ308447
VERSION AZ308447.1 GI:10348452
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: J column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
source 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0011J24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
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Db          1 AAAAAAAAAAAAAAAGAA 18
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RESULT 2551
AZ308447/c
LOCUS AZ308447 23 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0011J24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0011J24 F, genomic survey sequence.
ACCESSION AZ308447
VERSION AZ308447.1 GI:10348452
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: J column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
 source 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0011J24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2180
              | ||||||||||||||||
Db         18 TTCTTTTTTTTTTTTTT 1
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RESULT 2552
AZ662734/c
LOCUS AZ662734 23 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0542D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0542D04 F, genomic survey sequence.
ACCESSION AZ662734
VERSION AZ662734.1 GI:11799880
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: D column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
 source 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542D04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||| ||||
Db         23 TTTTTTTTTTTTTATTTA 6
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RESULT 2553
AZ984045
LOCUS AZ984045 23 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0265I23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0265I23 F, genomic survey sequence.
ACCESSION AZ984045
VERSION AZ984045.1 GI:13855272
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0265 row: I column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
source 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0265I23"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2171 TTTTTTTTTTTTTTTAA 2188
              ||| ||||||||||||||
Db          1 TTTATTTTTTTTTTTAA 18
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RESULT 2554
CF302406/c
LOCUS CF302406 24 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-N18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-N18, mRNA sequence.
ACCESSION CF302406
VERSION CF302406.1 GI:33674167
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-N18"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 24;
Best Local Similarity 94.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2782 ATTGAAAAAAAAAAAAAA 2799
              ||| ||||||||||||||
Db         18 ATTTAAAAAAAAAAAAAA 1
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RESULT 2555
AZ399663/c
LOCUS AZ399663 24 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0165C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0165C10 R, genomic survey sequence.
ACCESSION AZ399663
VERSION AZ399663.1 GI:10514737
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)

```
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0165  row: C  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES              Location/Qualifiers
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                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0165C10"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||||||||||  ||||
Db         23 AAAAAAAAAAAAACAAAA 6


RESULT 2556
CF295238
LOCUS       CF295238                 24 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-B07.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-B07, mRNA sequence.
ACCESSION   CF295238
VERSION     CF295238.1  GI:33664271
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .24
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="30DGS--05-B07"
                      /tissue_type="leaf"
                      /dev_stage="30 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTT 2179
              | ||||||||||||||||
Db          7 CCCCTTTTTTTTTTTTTT 24


RESULT 2557
AZ665864
LOCUS       AZ665864                 24 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0547I04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0547I04 R, genomic survey sequence.
ACCESSION   AZ665864
VERSION     AZ665864.1  GI:11803010
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0547  row: I  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES              Location/Qualifiers
     source           1. .24
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
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                     /db_xref="taxon:10090"
                     /clone="UUGC1M0547I04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        105 CGCTTGGGGGCTGGGGGG 122
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Db          1 CGCTTGGGGGCCGGGGGG 18


RESULT 2558
AZ329925
LOCUS       AZ329925                  25 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0054N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0054N14 R, genomic survey sequence.
ACCESSION   AZ329925
VERSION     AZ329925.1  GI:10391126
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0054  row: N  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0054N14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||| ||||||||||||||
Db          8 GAAGAAAAAAAAAAAAAA 25


RESULT 2559
AZ515233
LOCUS       AZ515233                  25 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0054N14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0054N14 F, genomic survey sequence.
ACCESSION   AZ515233
VERSION     AZ515233.1  GI:10696549
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0054  row: N  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0054N14"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAA 2802
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Db          8 GAAGAAAAAAAAAAAAA 25
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RESULT 2560
AZ997733/c
LOCUS AZ997733 25 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0284E22F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0284E22 F, genomic survey sequence.
ACCESSION AZ997733
VERSION AZ997733.1 GI:13868960
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0284 row: E column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
FEATURES Location/Qualifiers
source 1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0284E22"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2162 CTCCTTTTTTTTTTTTT 2179
              | |||||||||||||||
Db         18 CCCCTTTTTTTTTTTTT 1
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RESULT 2561
BM658913/c
LOCUS BM658913 26 bp mRNA linear EST 27-FEB-2002
DEFINITION LQG602768282.R1 CSEQFXL36 fetal brain Sus scrofa cDNA, mRNA sequence.
ACCESSION BM658913
VERSION BM658913.1 GI:18959184
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Adelson,D.L. and Gill,C.A.
TITLE Porcine ESTs
JOURNAL Unpublished (2002)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
FEATURES Location/Qualifiers
source 1. .26
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/dev_stage="fetal"
/clone_lib="CSEQFXL36 fetal brain"
/note="Organ: brain; Vector: pBluescript SK+; Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert (5'-NNN. . .NNNinsert) GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG. non-normalized library, sequenced 3' with M13R primer."

Query Match 0.6%; Score 16.4; DB 1; Length 26;
Best Local Similarity 94.4%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||||| ||
Db         26 AAAAAAAAAAAAAAAGAA 9


RESULT 2562
AU265518/c
LOCUS       AU265518                  26 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU265518 VS Dictyostelium discoideum cDNA clone VSF623 5', mRNA
            sequence.
ACCESSION   AU265518
VERSION     AU265518.1  GI:20524316
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSF623"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 26;
  Best Local Similarity   94.4%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||| |
Db         26 AAAAAAAAAAAAAAAAGA 9


RESULT 2563
BX563414/c
LOCUS       BX563414                  26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX563414 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse66e05_p1c, mRNA sequence.
ACCESSION   BX563414
VERSION     BX563414.1  GI:33430654
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse66e05_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 26;
  Best Local Similarity   76.9%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||  ||||||||||||||
Db         26 AAAAAAAAAAACCAAAAAAAAAAAAA 1


RESULT 2564
AU265398
LOCUS       AU265398                  27 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU265398 VS Dictyostelium discoideum cDNA clone VSF546 5', mRNA
            sequence.
ACCESSION   AU265398
VERSION     AU265398.1  GI:20524196
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSF546"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 27;
  Best Local Similarity   76.9%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2804
              | | ||  |||| || ||||||||||
```

```
Db          2 AAATTTTTAAAATAATAAAAAAAAAA 27


RESULT 2565
CF318113
LOCUS       CF318113                  27 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-B07.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--08-B07, mRNA sequence.
ACCESSION   CF318113
VERSION     CF318113.1  GI:33689874
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--08-B07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 27;
  Best Local Similarity   76.9%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   |||  ||||||||||||||
Db          1 AAAAAAAAAACCAAAAAAAAAAAAAA 26


RESULT 2566
AW250467
LOCUS       AW250467                  27 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822354.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822354 3',
            mRNA sequence.
ACCESSION   AW250467
VERSION     AW250467.1  GI:6593460
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822354.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 27
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 27 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM9  row: D  column: 3
            High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822354"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 27;
  Best Local Similarity   76.9%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAACTT 2191
              |||||||||  ||  ||  |  ||  ||||
Db          2 TTTTTTTTTCTTCTTATATTCTACTT 27


RESULT 2567
AZ827060/c
LOCUS       AZ827060                  29 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0103F17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0103F17 F, genomic survey sequence.
ACCESSION   AZ827060
VERSION     AZ827060.1  GI:12996968
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
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           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000   Std Error: 0.00
           Plate: 0103  row: F  column: 17
           Seq primer: CGTTGTAAAACGACGGCCAGT
           Class: plasmid ends
           High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0103F17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 29;
  Best Local Similarity   76.9%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||| ||| |||||||
Db         29 AAAAACAAAAAAAACAAACAAAAAAA 4


RESULT 2568
AU269375
LOCUS       AU269375                 29 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU269375 VS Dictyostelium discoideum cDNA clone VSI875 5', mRNA
            sequence.
ACCESSION   AU269375
VERSION     AU269375.1  GI:20528173
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSI875"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 29;
  Best Local Similarity   76.9%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | || | || ||||||  ||||||||
Db          2 ATAAATAAATAAAAAAGTAAAAAAAA 27


RESULT 2569
AU264794
LOCUS       AU264794                 31 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU264794 VS Dictyostelium discoideum cDNA clone VSF157 5', mRNA
            sequence.
ACCESSION   AU264794
VERSION     AU264794.1  GI:20523592
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSF157"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 31;
  Best Local Similarity   76.9%;  Pred. No. 2.9e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | || | || ||||||  ||||||||
Db          4 ATAAATAAATAAAAAAGTAAAAAAAA 29


RESULT 2570
BX556940/c
LOCUS       BX556940                 32 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX556940 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse2d03_p1c, mRNA sequence.
ACCESSION   BX556940
VERSION     BX556940.1  GI:33428171
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse2d03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 32;
  Best Local Similarity   76.9%;  Pred. No. 2.8e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   |||||  ||||||||||||
Db         26 AAAAAAAAAAAAGGAAAAAAAAAAAA 1


RESULT 2571
R38731/c
LOCUS       R38731                    33 bp    mRNA    linear   EST 04-MAY-1995
DEFINITION  yd03g06.s1 Soares infant brain 1NIB Homo sapiens cDNA clone
            IMAGE:24658 3' similar to gb:A18658 INSULIN RECEPTOR PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION   R38731
VERSION     R38731.1  GI:796187
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 2331
            High quality sequence starts: 1 High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL This clone is available royalty-free
            through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)
            for further information. Trace considered overall poor quality
            Insert Length: 2331   Std Error: 0.00
            Seq primer: -21m13
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:397005"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:24658"
                     /sex="female"
                     /dev_stage="73 days post natal"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares infant brain 1NIB"
                     /note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                     I; Site_2: Hind III; 1st strand cDNA was primed with a Not
                     I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTT 3'];
                     double-stranded cDNA was ligated to Hind III adaptors
                     (Pharmacia), digested with Not I and directionally cloned
                     into the Not I and Hind III sites of the Lafmid BA vector.
                     Library went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 33;
  Best Local Similarity   76.9%;  Pred. No. 2.7e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              ||||   || ||||| ||| ||||||
Db         28 AGAAAAAAAGAAAAAGAAAGAAAAAA 3


RESULT 2572
CF319784
LOCUS       CF319784                  34 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-G18.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-G18, mRNA sequence.
ACCESSION   CF319784
VERSION     CF319784.1  GI:33691545
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-G18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
```

cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.4; DB 1; Length 34;
Best Local Similarity 94.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||||| ||
Db          1 AAAAAAAAAAAAAAAGAA 18
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RESULT 2573
AZ339890
LOCUS AZ339890 39 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0071L05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0071L05 R, genomic survey sequence.
ACCESSION AZ339890
VERSION AZ339890.1 GI:10414608
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 39)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: L column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 39.
FEATURES Location/Qualifiers
source 1. .39
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0071L05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 39;
Best Local Similarity 76.9%; Pred. No. 2.3e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||| ||||||| |||
Db          2 AAAAAACAAAAAAACAAAAAAACAAA 27
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RESULT 2574
AZ326980/c
LOCUS AZ326980 40 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0050A12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0050A12 F, genomic survey sequence.
ACCESSION AZ326980
VERSION AZ326980.1 GI:10385271
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 40)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0050 row: A column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 40.
FEATURES Location/Qualifiers
source 1. .40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0050A12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 40;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAA 2803
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Db         39 AAAAAAAAAACAAAAAAA 22
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RESULT 2575
CF330439/c
LOCUS CF330439 21 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-C12, mRNA sequence.
ACCESSION CF330439
VERSION CF330439.1 GI:33809110
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-C12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAAAAAAAAA 2804
              ||  | ||||||||||||||||
Db         21 TGTTATAAAAAAAAAAAAAA 1
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RESULT 2576
CF319122
LOCUS CF319122 21 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--09-I07.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-I07, mRNA sequence.
ACCESSION CF319122
VERSION CF319122.1 GI:33690883
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-I07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||| ||||||||||||  ||
Db          1 TTTTATTTTTTTTTTTTCGTT 21
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RESULT 2577
AZ316019/c
LOCUS AZ316019 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0033C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0033C05 R, genomic survey sequence.
ACCESSION AZ316019
VERSION AZ316019.1 GI:10363426
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: C column: 05
Seq primer: CACACAGGAAACAGCTATGACC

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          Class: plasmid ends
          High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0033C05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTT 2181
              | |  ||||||||||||||||
Db         21 TGTGGTTTTTTTTTTTTTTT 1


RESULT 2578
AZ345540
LOCUS       AZ345540                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080P05 F, genomic survey sequence.
ACCESSION   AZ345540
VERSION     AZ345540.1  GI:10424777
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: P  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080P05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTT 2185
              |||||| ||||||| || |||
Db          1 CTTTTTCTTTTTTTCTTCTTT 21


RESULT 2579
AZ346717
LOCUS       AZ346717                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0082O02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0082O02 F, genomic survey sequence.
ACCESSION   AZ346717
VERSION     AZ346717.1  GI:10425954
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0082  row: O  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
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FEATURES             Location/Qualifiers
     source          1. .21
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0082O02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTT 2185
              |||| ||| ||| ||||||||
Db          1 CTTTCTTTCTTTCTTTTTTT 21


RESULT 2580
AZ625662/c
LOCUS       AZ625662                 21 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0465C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0465C23 F, genomic survey sequence.
ACCESSION   AZ625662
VERSION     AZ625662.1  GI:11747852
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0465  row: C  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0465C23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              | | | ||||||||||||||||
Db         21 TATATATTTTTTTTTTTTTA 1


RESULT 2581
AZ316361/c
LOCUS       AZ316361                 22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0034I16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0034I16 F, genomic survey sequence.
ACCESSION   AZ316361
VERSION     AZ316361.1  GI:10364110
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0034  row: I  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034I16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||   ||||||||||||||||
Db         22 TTTAAATTTTTTTTTTTTTT 2
```

RESULT 2582
AU267170
LOCUS AU267170 23 bp mRNA linear EST 10-MAY-2002
DEFINITION AU267170 VS Dictyostelium discoideum cDNA clone VSH269 5', mRNA sequence.
ACCESSION AU267170
VERSION AU267170.1 GI:20525968
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 23)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .23
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH269"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.6%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2779 AGAATTGAAAAAAAAAAAAAA 2799
              | ||| |||| ||||||||||
Db          3 ACAATAGAAATAAAAAAAAAA 23
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RESULT 2583
AZ468097
LOCUS AZ468097 23 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0279K22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0279K22 R, genomic survey sequence.
ACCESSION AZ468097
VERSION AZ468097.1 GI:10626222
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0279 row: K column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
source 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0279K22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.7e+03;

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  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||| ||| ||||||
Db          3 TTTTTTGTTTGTTTGTTTTT 23


RESULT 2584
CF337747/c
LOCUS       CF337747                 24 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--08-F05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--08-F05, mRNA sequence.
ACCESSION   CF337747
VERSION     CF337747.1  GI:33823871
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--08-F05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              ||  | ||||||||||||||||
Db         21 ATATACAAAAAAAAAAAAAAA 1


RESULT 2585
CF328535
LOCUS       CF328535                 24 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-H21.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-H21, mRNA sequence.
ACCESSION   CF328535
VERSION     CF328535.1  GI:33805314
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-H21"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTT 2185
              |||| ||||| ||||| ||||
Db          1 CTTTCTTTTTCTTTTTCTTT 21


RESULT 2586
AZ308225
LOCUS       AZ308225                 24 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0011E06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0011E06 F, genomic survey sequence.
ACCESSION   AZ308225
VERSION     AZ308225.1  GI:10348004
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0011  row: E  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
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/clone="UUGC1M0011E06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||| ||| ||| |||||
Db          3 TTTTTTTGTTTGTTTGTTTTT 23
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RESULT 2587
AI445764
LOCUS AI445764 25 bp mRNA linear EST 13-APR-1999
DEFINITION tj09g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141058 3' similar to SW:YM04_PARTE P15605 HYPOTHETICAL 18.8 KD PROTEIN ;contains element L1 repetitive element ;, mRNA sequence.
ACCESSION AI445764
VERSION AI445764.1 GI:4290493
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 715 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2141058"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2781 AATTGAAAAAAAAAAAAAAAA 2801
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Db          1 AAATAAAAAAAACAAAAAAAA 21
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RESULT 2588
CF308158/c
LOCUS CF308158 25 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--01-N19.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--01-N19, mRNA sequence.
ACCESSION CF308158
VERSION CF308158.1 GI:33679919
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .25
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--01-N19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1970 TTTACCTTGAAAAAAAGAAAA 1990
              |||| ||| ||||||| ||||
Db         23 TTTATCTTAAAAAAAAAAAAA 3
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RESULT 2589
AV740046/c
LOCUS AV740046 25 bp mRNA linear EST 17-OCT-2000
DEFINITION AV740046 CB Homo sapiens cDNA clone CBFAWF04 5', mRNA sequence.

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ACCESSION   AV740046
VERSION     AV740046.1  GI:10857627
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
  TITLE     Homo sapiens CB library cDNA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CBFAWF04"
                     /tissue_type="cord blood"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="CB"
                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is
                     cloned randomly with the EcoRI digestion"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||   |||
Db         25 TTTTTTTTTTTTTTTNCCCCTT 4


RESULT 2590
AV739265/c
LOCUS       AV739265                 27 bp    mRNA    linear   EST 17-OCT-2000
DEFINITION  AV739265 CB Homo sapiens cDNA clone CBFAWE01 5', mRNA sequence.
ACCESSION   AV739265
VERSION     AV739265.1  GI:10856846
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
  TITLE     Homo sapiens CB library cDNA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CBFAWE01"
                     /tissue_type="cord blood"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="CB"
                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is
                     cloned randomly with the EcoRI digestion"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 27;
  Best Local Similarity   78.3%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCATTCT 1793
              ||||||||||||    ||| ||||
Db         24 TTTTTTTTTTTTNCNCCCCTTCT 2


RESULT 2591
BQ590166
LOCUS       BQ590166                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-K18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-K18 3-PRIME, mRNA sequence.
ACCESSION   BQ590166
VERSION     BQ590166.1  GI:26119749
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 19  row: K  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189955"
                     /db_xref="taxon:161934"
                     /clone="024-019-K18"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
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  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2592
BQ590166/c
LOCUS       BQ590166                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-K18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-K18 3-PRIME, mRNA sequence.
ACCESSION   BQ590166
VERSION     BQ590166.1  GI:26119749
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 19  row: K  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189955"
                     /db_xref="taxon:161934"
                     /clone="024-019-K18"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2593
BQ590507
LOCUS       BQ590507                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION   BQ590507
VERSION     BQ590507.1  GI:26120090
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 19  row: M  column: 04
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
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                     /db_xref="GABI:189608"
                     /db_xref="taxon:161934"
                     /clone="024-019-M04"
                     /tissue_type="storage root"
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                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTA 16


RESULT 2594
BQ592600
LOCUS       BQ592600                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013686-024-028-F08-SP6R MPIZ-ADIS-024-developing root Beta
            vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
ACCESSION   BQ592600
VERSION     BQ592600.1  GI:26122183
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 28  row: F  column: 08
            Seq primer: SP6r; ATTTAGGTGACACTATAGAAGA.
FEATURES             Location/Qualifiers
     source          1. .16
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:194262"
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                     /clone="024-028-F08"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2595
BQ592600/c
LOCUS       BQ592600                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013686-024-028-F08-SP6R MPIZ-ADIS-024-developing root Beta
            vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
ACCESSION   BQ592600
VERSION     BQ592600.1  GI:26122183
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 28  row: F  column: 08
            Seq primer: SP6r; ATTTAGGTGACACTATAGAAGA.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:194262"
                     /db_xref="taxon:161934"
                     /clone="024-028-F08"
                     /tissue_type="developing root"
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                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 2596
BQ592965
LOCUS       BQ592965                  16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013324-024-028-A01-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION   BQ592965
VERSION     BQ592965.1  GI:26122548
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 28  row: A  column: 01
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     line)"
                     /db_xref="GABI:193895"
                     /db_xref="taxon:161934"
                     /clone="024-028-A01"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2597
BQ592965/c
LOCUS       BQ592965                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013324-024-028-A01-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION   BQ592965
VERSION     BQ592965.1  GI:26122548
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 28  row: A  column: 01
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:193895"
                     /db_xref="taxon:161934"
                     /clone="024-028-A01"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
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Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2598
BQ595369
LOCUS       BQ595369                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013317-024-022-P02-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION   BQ595369
VERSION     BQ595369.1  GI:26124952
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 22  row: P  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:191489"
                     /db_xref="taxon:161934"
                     /clone="024-022-P02"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
```

Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2172 TTTTTTTTTTTTTTTA 2187
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Db          1 TTTTTTTTTTTTTTTA 16
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RESULT 2599
BQ595717
LOCUS BQ595717 16 bp mRNA linear EST 06-DEC-2002
DEFINITION E012692-024-022-H07-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-H07 5-PRIME, mRNA sequence.
ACCESSION BQ595717
VERSION BQ595717.1 GI:26125300
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: H column: 07
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:191134"
/db_xref="taxon:161934"
/clone="024-022-H07"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16
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RESULT 2600
BQ595717/c
LOCUS BQ595717 16 bp mRNA linear EST 06-DEC-2002
DEFINITION E012692-024-022-H07-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-H07 5-PRIME, mRNA sequence.
ACCESSION BQ595717
VERSION BQ595717.1 GI:26125300
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: H column: 07
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .16
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:191134"
/db_xref="taxon:161934"
/clone="024-022-H07"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTT 2181
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Db         16 TTTTTTTTTTTTTTTT 1
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RESULT 2601
CF279325
LOCUS CF279325 16 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-J09, mRNA sequence.
ACCESSION CF279325
VERSION CF279325.1 GI:33656711
KEYWORDS EST.

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SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--05-J09"
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2602
CF279325/c
LOCUS       CF279325                 16 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--05-J09, mRNA sequence.
ACCESSION   CF279325
VERSION     CF279325.1  GI:33656711
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--05-J09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2603
CF296130
LOCUS       CF296130                 16 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--06-F22, mRNA sequence.
ACCESSION   CF296130
VERSION     CF296130.1  GI:33665163
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--06-F22"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTA 16


RESULT 2604
CF311057
LOCUS       CF311057                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.
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ACCESSION   CF311057
VERSION     CF311057.1  GI:33682818
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2605
CF311057/c
LOCUS       CF311057                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.
ACCESSION   CF311057
VERSION     CF311057.1  GI:33682818
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2606
CF314013
LOCUS       CF314013                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--02-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--02-G01, mRNA sequence.
ACCESSION   CF314013
VERSION     CF314013.1  GI:33685774
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2172 TTTTTTTTTTTTTTTA 2187
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Db          1 TTTTTTTTTTTTTTTA 16


RESULT 2607
CF314377
LOCUS       CF314377                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--02-O01.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--02-O01, mRNA sequence.
ACCESSION   CF314377
VERSION     CF314377.1  GI:33686138
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2608
CF314377/c
LOCUS       CF314377                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--02-O01.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--02-O01, mRNA sequence.
ACCESSION   CF314377
VERSION     CF314377.1  GI:33686138
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2609
CF315789
LOCUS       CF315789                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-N10.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--04-N10, mRNA sequence.
ACCESSION   CF315789
VERSION     CF315789.1  GI:33687550
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2181
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Db 1 TTTTTTTTTTTTTTTT 16

RESULT 2610
CF315789/c
LOCUS CF315789 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--04-N10.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--04-N10, mRNA sequence.
ACCESSION CF315789
VERSION CF315789.1 GI:33687550
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
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Qy 2786 AAAAAAAAAAAAAAAA 2801
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Db 16 AAAAAAAAAAAAAAAA 1

RESULT 2611
CF316056
LOCUS CF316056 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--05-D07.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.
ACCESSION CF316056
VERSION CF316056.1 GI:33687817
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/clone="HD--05-D07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2181
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Db 1 TTTTTTTTTTTTTTTT 16

RESULT 2612
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LOCUS CF316056 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--05-D07.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.
ACCESSION CF316056
VERSION CF316056.1 GI:33687817
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16

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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
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Qy       2786 AAAAAAAAAAAAAAAA 2801
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Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2613
CF317718
LOCUS       CF317718                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-I05.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-I05, mRNA sequence.
ACCESSION   CF317718
VERSION     CF317718.1  GI:33689479
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 16


RESULT 2614
CF317718/c
LOCUS       CF317718                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-I05.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-I05, mRNA sequence.
ACCESSION   CF317718
VERSION     CF317718.1  GI:33689479
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
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                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
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Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2615
CF320356
LOCUS       CF320356                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-D14.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.
ACCESSION   CF320356
VERSION     CF320356.1  GI:33692117
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
```

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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
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Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2616
CF320356/c
LOCUS       CF320356                16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-D14.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.
ACCESSION   CF320356
VERSION     CF320356.1  GI:33692117
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
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              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2617
CF327722
LOCUS       CF327722                16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-F06, mRNA sequence.
ACCESSION   CF327722
VERSION     CF327722.1  GI:33803695
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
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Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2618
CF327722/c
LOCUS       CF327722                16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-F06, mRNA sequence.
ACCESSION   CF327722
VERSION     CF327722.1  GI:33803695
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
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Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2619
CF329320
LOCUS       CF329320                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-J17, mRNA sequence.
ACCESSION   CF329320
VERSION     CF329320.1  GI:33806877
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTA 16


RESULT 2620
CF333386
LOCUS       CF333386                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.
ACCESSION   CF333386
VERSION     CF333386.1  GI:33815044
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--02-E05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2621
CF333386/c
LOCUS       CF333386                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.
ACCESSION   CF333386
VERSION     CF333386.1  GI:33815044
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KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--02-E05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 2622
BQ590128/c
LOCUS       BQ590128                 17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012843-024-019-E19-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-E19 3-PRIME, mRNA sequence.
ACCESSION   BQ590128
VERSION     BQ590128.1  GI:26119711
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 19  row: E  column: 19
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189986"
                     /db_xref="taxon:161934"
                     /clone="024-019-E19"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2623
CF294668/c
LOCUS       CF294668                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--04-E17, mRNA sequence.
ACCESSION   CF294668
VERSION     CF294668.1  GI:33663701
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--04-E17"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
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  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2624
CF295988/c
LOCUS       CF295988                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--06-C17, mRNA sequence.
ACCESSION   CF295988
VERSION     CF295988.1  GI:33665021
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--06-C17"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2625
CF302447
LOCUS       CF302447                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-P11, mRNA sequence.
ACCESSION   CF302447
VERSION     CF302447.1  GI:33674208
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-P11"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2626
CF313013
LOCUS       CF313013                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-P19, mRNA sequence.
ACCESSION   CF313013
VERSION     CF313013.1  GI:33684774
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--08-P19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16
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RESULT 2627
CF336950/c
LOCUS CF336950 17 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.
ACCESSION CF336950
VERSION CF336950.1 GI:33822280
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-D04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1
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RESULT 2628
BQ591181
LOCUS BQ591181 17 bp mRNA linear EST 06-DEC-2002
DEFINITION E012715-024-017-H16-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-H16 3-PRIME, mRNA sequence.
ACCESSION BQ591181
VERSION BQ591181.1 GI:26120764
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: H column: 16
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188932"
/db_xref="taxon:161934"
/clone="024-017-H16"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2172 TTTTTTTTTTTTTTTA 2187
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Db          1 TTTTTTTTTTTTTTTA 16
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RESULT 2629
CF295807
LOCUS CF295807 17 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--05-O12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--05-O12, mRNA sequence.
ACCESSION CF295807
VERSION CF295807.1 GI:33664840
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

```
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="30DGS--05-O12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2630
CF295807/c
LOCUS       CF295807                  17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-O12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-O12, mRNA sequence.
ACCESSION   CF295807
VERSION     CF295807.1  GI:33664840
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--05-O12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2631
CF299639
LOCUS       CF299639                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L20, mRNA sequence.
ACCESSION   CF299639
VERSION     CF299639.1  GI:33671400
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-L20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2632
CF299639/c
LOCUS       CF299639                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L20, mRNA sequence.
ACCESSION   CF299639
VERSION     CF299639.1  GI:33671400
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-L20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2633
CF299997/c
LOCUS       CF299997                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-D19, mRNA sequence.
ACCESSION   CF299997
VERSION     CF299997.1  GI:33671758
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-D19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 2634
CF311499
LOCUS       CF311499                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION   CF311499
VERSION     CF311499.1  GI:33683260
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--06-L20"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTA 16


RESULT 2635
CF319075
LOCUS       CF319075                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-H06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence.
ACCESSION   CF319075
VERSION     CF319075.1  GI:33690836
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--09-H06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTA 16


RESULT 2636
CF302409/c
LOCUS       CF302409                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-N19, mRNA sequence.
ACCESSION   CF302409
VERSION     CF302409.1  GI:33674170
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-N19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2637
CF301359/c
LOCUS       CF301359                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-D05, mRNA sequence.
ACCESSION   CF301359
VERSION     CF301359.1  GI:33673120
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 2638
CF308042
LOCUS       CF308042                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-L07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-L07, mRNA sequence.
ACCESSION   CF308042
VERSION     CF308042.1  GI:33679803
KEYWORDS    EST.
SOURCE      Oryza sativa
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  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
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                     /db_xref="taxon:4530"
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTA 16


RESULT 2639
CF298134
LOCUS       CF298134                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-G09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-G09, mRNA sequence.
ACCESSION   CF298134
VERSION     CF298134.1  GI:33669895
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db          4 GAAAAAAAAAAAAAAA 19


RESULT 2640
CF311668
LOCUS       CF311668                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-A05.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-A05, mRNA sequence.
ACCESSION   CF311668
VERSION     CF311668.1  GI:33683429
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="ABF--07-A05"
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2641
CF311668/c
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LOCUS       CF311668                19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-A05.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-A05, mRNA sequence.
ACCESSION   CF311668
VERSION     CF311668.1  GI:33683429
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 2642
CF327587
LOCUS       CF327587                19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-C04, mRNA sequence.
ACCESSION   CF327587
VERSION     CF327587.1  GI:33803426
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--02-C04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         1 TTTTTTTTTTTTTTTT 16


RESULT 2643
CF327587/c
LOCUS       CF327587                19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-C04, mRNA sequence.
ACCESSION   CF327587
VERSION     CF327587.1  GI:33803426
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--02-C04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1
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RESULT 2644
AZ764517
LOCUS       AZ764517                19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0560L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0560L07 R, genomic survey sequence.
ACCESSION   AZ764517
VERSION     AZ764517.1  GI:12879561
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0560  row: L  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0560L07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16
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RESULT 2645
AZ764517/c
LOCUS       AZ764517                19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0560L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0560L07 R, genomic survey sequence.
ACCESSION   AZ764517
VERSION     AZ764517.1  GI:12879561
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0560  row: L  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0560L07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1
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RESULT 2646
AZ316019
LOCUS       AZ316019                21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0033C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0033C05 R, genomic survey sequence.
ACCESSION   AZ316019
VERSION     AZ316019.1  GI:10363426
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0033  row: C  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0033C05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
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Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2647
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CF309614
LOCUS       CF309614                21 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-N20.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-N20, mRNA sequence.
ACCESSION   CF309614
VERSION     CF309614.1  GI:33681375
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--03-N20"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          3 CTTTTTTTTTTTTTTT 18


RESULT 2648
CF310806/c
LOCUS       CF310806                22 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-K20.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--05-K20, mRNA sequence.
ACCESSION   CF310806
VERSION     CF310806.1  GI:33682567
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
```

```
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 16;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 2649
AZ316361
LOCUS       AZ316361                 22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0034I16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0034I16 F, genomic survey sequence.
ACCESSION   AZ316361
VERSION     AZ316361.1  GI:10364110
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0034  row: I  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0034I16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
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Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2650
AZ307559
LOCUS       AZ307559                 22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0009O20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0009O20 F, genomic survey sequence.
ACCESSION   AZ307559
VERSION     AZ307559.1  GI:10346680
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0009  row: O  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0009O20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
```

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 16;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAA 2188
              ||||||||||||||||
Db          6 TTTTTTTTTTTTTTAA 21
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RESULT 2651
AZ310057
LOCUS       AZ310057                 22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0018A15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0018A15 R, genomic survey sequence.
ACCESSION   AZ310057
VERSION     AZ310057.1  GI:10351664
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0018  row: A  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0018A15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
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  Query Match             0.6%;  Score 16;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16
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RESULT 2652
AZ310057/c
LOCUS       AZ310057                 22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0018A15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0018A15 R, genomic survey sequence.
ACCESSION   AZ310057
VERSION     AZ310057.1  GI:10351664
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0018  row: A  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0018A15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
```

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 16 AAAAAAAAAAAAAAAA 1

RESULT 2653
AZ375417/c
LOCUS AZ375417 22 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0128E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0128E13 R, genomic survey sequence.
ACCESSION AZ375417
VERSION AZ375417.1 GI:10489117
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0128 row: E column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0128E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTT 2179
||||||||||||||||
Db 22 CCTTTTTTTTTTTTTT 7

RESULT 2654
TA367G08P
LOCUS TA367G08P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 367g08, forward sequence, genomic survey sequence.
ACCESSION AL493527
VERSION AL493527.1 GI:11870537
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="367g08"

Query Match 0.6%; Score 16; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2173 TTTTTTTTTTTTTTAA 2188
||||||||||||||||
Db 1 TTTTTTTTTTTTTTAA 16

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RESULT 2655
CF290997/c
LOCUS       CF290997                 23 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-E03, mRNA sequence.
ACCESSION   CF290997
VERSION     CF290997.1  GI:33660030
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-E03"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2656
CF280704/c
LOCUS       CF280704                 23 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-H17.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--07-H17, mRNA sequence.
ACCESSION   CF280704
VERSION     CF280704.1  GI:33658090
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--07-H17"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAA 2188
              ||||||||||||||||
Db         23 TTTTTTTTTTTTTTAA 8


RESULT 2657
TA367D08P
LOCUS       TA367D08P                23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 367d08, forward sequence,
            genomic survey sequence.
ACCESSION   AL493509
VERSION     AL493509.1  GI:11870519
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="367d08"

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2173 TTTTTTTTTTTTTTAA 2188
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTAA 16


RESULT 2658
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LOCUS       AZ768927                 24 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0569H07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0569H07 F, genomic survey sequence.
ACCESSION   AZ768927
VERSION     AZ768927.1  GI:12888530
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0569  row: H  column: 07
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0569H07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 3e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2658 GTGAGTGTGCAGTACAGTGTGTGT 2681
              |||||||||| ||||   | |||||
Db         24 GTGAGTGTGTAGTAGTATATGTGT 1


RESULT 2659
AW249476/c
LOCUS       AW249476                 25 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821131.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821131 3',
            mRNA sequence.
ACCESSION   AW249476
VERSION     AW249476.1  GI:6592469
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821131.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 25
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 25 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM6  row: A  column: 4
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821131"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||| ||| ||||||||||
Db         25 AAAAAAAAAAGAAATAAAAAAAAA 2


RESULT 2660
AZ442170
LOCUS       AZ442170                 25 bp    DNA     linear   GSS 03-OCT-2000
```

```
DEFINITION  1M0234H18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0234H18 R, genomic survey sequence.
ACCESSION   AZ442170
VERSION     AZ442170.1  GI:10566183
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0234  row: H  column: 18
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0234H18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||   |||||  ||||||||||||
Db          1 AAAAAAAAAATTAAAAAAAAAAAA 24


RESULT 2661
AZ476141/c
LOCUS       AZ476141                 25 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0294M10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0294M10 R, genomic survey sequence.
ACCESSION   AZ476141
VERSION     AZ476141.1  GI:10634266
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0294  row: M  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0294M10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||   || |||||||  ||||||||
Db         24 AAAAAAACAAAAAAACAAAAAAAA 1


RESULT 2662
AW247153/c
LOCUS       AW247153                 25 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819969.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819969 3',
            mRNA sequence.
```

```
ACCESSION   AW247153
VERSION     AW247153.1  GI:6590146
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819969.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 7 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 25 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM2  row: P  column: 18
            High quality sequence stop: 7.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819969"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              |||  || | |||| |||||||||
Db         25 AATAAAACACAAAACAAAAAAAAA 2

RESULT 2663
TA324F07P
LOCUS       TA324F07P                25 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 324f07, forward sequence,
            genomic survey sequence.
ACCESSION   AL493403
VERSION     AL493403.1  GI:11867768
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="324f07"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16

RESULT 2664
AZ437459/c
LOCUS       AZ437459                 26 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0225B15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0225B15 R, genomic survey sequence.
ACCESSION   AZ437459
VERSION     AZ437459.1  GI:10561472
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0225  row: B  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus musculus"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0225B15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 79.2%; Pred. No. 3.1e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   |||||| |||| |||||||
Db         26 AAAAAAAAAAAGAAAAGAAAAAAA 3
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RESULT 2665
AU265818
LOCUS AU265818 26 bp mRNA linear EST 10-MAY-2002
DEFINITION AU265818 VS Dictyostelium discoideum cDNA clone VSF805 5', mRNA sequence.
ACCESSION AU265818
VERSION AU265818.1 GI:20524616
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 26)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .26
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSF805"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 79.2%; Pred. No. 3.1e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              || | || |||||| ||||||||
Db          1 AAATAAATAAAAAAGTAAAAAAAA 24
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RESULT 2666
AU268466
LOCUS AU268466 26 bp mRNA linear EST 10-MAY-2002
DEFINITION AU268466 VS Dictyostelium discoideum cDNA clone VSI294 5', mRNA sequence.
ACCESSION AU268466
VERSION AU268466.1 GI:20527264
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 26)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .26
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSI294"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 79.2%; Pred. No. 3.1e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              || | || |||||| ||||||||
Db          1 AAATAAATAAAAAAGTAAAAAAAA 24
```

RESULT 2667
BX552372/c
LOCUS BX552372 26 bp mRNA linear EST 10-OCT-2003
DEFINITION BX552372 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse123b02_plc, mRNA sequence.
ACCESSION BX552372
VERSION BX552372.1 GI:33376646
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 26)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198

```
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse123b02_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11


RESULT 2668
BX553653/c
LOCUS       BX553653                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX553653 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse12h01_p1c, mRNA sequence.
ACCESSION   BX553653
VERSION     BX553653.1  GI:33377798
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse12h01_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11


RESULT 2669
BX553888/c
LOCUS       BX553888                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX553888 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse131b10_p1c, mRNA sequence.
ACCESSION   BX553888
VERSION     BX553888.1  GI:33378008
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse131b10_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11
```

```
RESULT 2670
BX557791/c
LOCUS       BX557791                 26 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX557791 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse34g02_p1c, mRNA sequence.
ACCESSION   BX557791
VERSION     BX557791.1  GI:33428966
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse34g02_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11


RESULT 2671
BX566514/c
LOCUS       BX566514                 26 bp    mRNA    linear   EST 14-OCT-2003
DEFINITION  BX566514 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse82f08_p1c, mRNA sequence.
ACCESSION   BX566514
VERSION     BX566514.1  GI:33433497
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse82f08_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11


RESULT 2672
BX567795/c
LOCUS       BX567795                 26 bp    mRNA    linear   EST 14-OCT-2003
DEFINITION  BX567795 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse8b03_p1c, mRNA sequence.
ACCESSION   BX567795
VERSION     BX567795.1  GI:33434709
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
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FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse8b03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11


RESULT 2673
AU267251
LOCUS       AU267251                  27 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU267251 VS Dictyostelium discoideum cDNA clone VSH318 5', mRNA
            sequence.
ACCESSION   AU267251
VERSION     AU267251.1  GI:20526049
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSH318"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.6%;  Score 16;  DB 1;  Length 27;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              || | || ||||||  ||||||||
Db          2 AAATAAATAAAAAAGTAAAAAAAA 25


RESULT 2674
CF329137
LOCUS       CF329137                  19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-F15.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-F15, mRNA sequence.
ACCESSION   CF329137
VERSION     CF329137.1  GI:33806511
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-F15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||| | ||||||||||||||
Db          1 AAAGATAAAAAAAAAAAAA 19


RESULT 2675
AZ345499/c
LOCUS       AZ345499                  19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080F06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080F06 F, genomic survey sequence.
ACCESSION   AZ345499
VERSION     AZ345499.1  GI:10424736
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: F  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
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            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080F06"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  | |||||
Db         19 AAAAAAAAAAAGAGAAAAA 1


RESULT 2676
AZ447251/c
LOCUS       AZ447251                 19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0244J19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0244J19 F, genomic survey sequence.
ACCESSION   AZ447251
VERSION     AZ447251.1  GI:10599050
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0244  row: J  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0244J19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
              ||  ||||||||||||||||
Db         19 TTATAAAAAAAAAAAAAAA 1


RESULT 2677
AZ786336/c
LOCUS       AZ786336                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0031H17 R, genomic survey sequence.
ACCESSION   AZ786336
VERSION     AZ786336.1  GI:12923992
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0031  row: H  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
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FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0031H17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  | |||||
Db         19 AAAAAAAAAAAGAGAAAAA 1


RESULT 2678
CF298472/c
LOCUS       CF298472                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-O01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-O01, mRNA sequence.
ACCESSION   CF298472
VERSION     CF298472.1  GI:33670233
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAA 2800
              ||  ||||||||||||||||
Db         19 ATATAAAAAAAAAAAAAAA 1


RESULT 2679
CF298134/c
LOCUS       CF298134                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-G09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-G09, mRNA sequence.
ACCESSION   CF298134
VERSION     CF298134.1  GI:33669895
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--01-G09"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
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Db         19 TTTTTTTTTTTTTTTCCTT 1


RESULT 2680
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LOCUS       CF300236                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-I24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-I24, mRNA sequence.
ACCESSION   CF300236
VERSION     CF300236.1  GI:33671997
KEYWORDS    EST.
SOURCE      Oryza sativa
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  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
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                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTGATT 19


RESULT 2681
CF300236/c
LOCUS       CF300236                19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-I24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-I24, mRNA sequence.
ACCESSION   CF300236
VERSION     CF300236.1  GI:33671997
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /clone="7LEAF--04-I24"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              |||  ||||||||||||||||
Db         19 AATCAAAAAAAAAAAAAAA 1


RESULT 2682
CF309858/c
LOCUS       CF309858                19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-D16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--04-D16, mRNA sequence.
ACCESSION   CF309858
VERSION     CF309858.1  GI:33681619
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--04-D16"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              | | ||||||||||||||||
Db         19 TATGTTTTTTTTTTTTTTA 1


RESULT 2683
AZ509929
LOCUS       AZ509929                19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0354A07 F, genomic survey sequence.
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ACCESSION   AZ509929
VERSION     AZ509929.1  GI:10691245
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0354  row: A  column: 07
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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                     /db_xref="taxon:10090"
                     /clone="UUGC1M0354A07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db          1 AAAAAAAAAAAAAAAATTAA 19


RESULT 2684
AZ509929/c
LOCUS       AZ509929                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0354A07 F, genomic survey sequence.
ACCESSION   AZ509929
VERSION     AZ509929.1  GI:10691245
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0354  row: A  column: 07
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /clone="UUGC1M0354A07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
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Db         19 TTAATTTTTTTTTTTTTTT 1


RESULT 2685
AZ611602
LOCUS       AZ611602                 19 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0438G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0438G03 F, genomic survey sequence.
ACCESSION   AZ611602
VERSION     AZ611602.1  GI:11733792
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KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0438  row: G  column: 03
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /clone="UUGC1M0438G03"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
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Db          1 TTTTTGGTTTTTTTTTTT 19


RESULT 2686
AZ611602/c
LOCUS       AZ611602                 19 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0438G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0438G03 F, genomic survey sequence.
ACCESSION   AZ611602
VERSION     AZ611602.1  GI:11733792
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0438  row: G  column: 03
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0438G03"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
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Db         19 AAAAAAAAAAAACCAAAAA 1


RESULT 2687
AW333777/c
LOCUS       AW333777                 20 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S25H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION   AW333777
VERSION     AW333777.1  GI:6830134
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
  ORGANISM  Pneumocystis carinii
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            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Pneumocystis carinii"
                     /mol_type="mRNA"
                     /db_xref="taxon:4754"
                     /lab_host="E. coli"
                     /clone_lib="AGS-1"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (3x10e9) from a single rat (99-1-6,
                     sacrificed on 3/17/99)  at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT priming, standard
                     conditions described by  vendor, Stratagene. Further
                     details see www.uky.edu/Project/Pneumocystis/"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              |||  ||||||||||||||
Db         19 AATATAAAAAAAAAAAAAA 1


RESULT 2688
CF330490
LOCUS       CF330490                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-D16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-D16, mRNA sequence.
ACCESSION   CF330490
VERSION     CF330490.1  GI:33809214
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-D16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAA 2188
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Db          1 TTTTTTTTTTTTTTTGGAA 19


RESULT 2689
AZ633741
LOCUS       AZ633741                 20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0489G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0489G12 F, genomic survey sequence.
ACCESSION   AZ633741
VERSION     AZ633741.1  GI:11755931
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0489  row: G  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0489G12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
```

adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2804
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Db          1 AAAAAAAAAAAAAAACCAA 19
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RESULT 2690
AZ368518
LOCUS AZ368518 20 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0118G09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0118G09 R, genomic survey sequence.
ACCESSION AZ368518
VERSION AZ368518.1 GI:10482218
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0118 row: G column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0118G09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2782 ATTGAAAAAAAAAAAAAAA 2800
              ||| |||||||||| |||||
Db          2 ATTAAAAAAAAAACAAAAA 20
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RESULT 2691
CF336815/c
LOCUS CF336815 20 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--07-A04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-A04, mRNA sequence.
ACCESSION CF336815
VERSION CF336815.1 GI:33822012
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-A04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||  ||||||||||||||||
Db         19 GAGCAAAAAAAAAAAAAAA 1
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RESULT 2692
CF340627
LOCUS CF340627 20 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--08-K02.g1 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--08-K02, mRNA sequence.
ACCESSION CF340627
VERSION CF340627.1 GI:33829609
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

```
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="RCL1--08-K02"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli SOLR"
                     /clone_lib="Regenerated callus lambda phage cDNA library
                     (RCL1)"
                     /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
                     XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
                     end with SstI and 3' end with XhoI site. Callus was
                     induced on 2N6 media for 30 days and cultured for 36hrs on
                     regenerated media"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTT 2173
              ||||||| ||||||||||
Db          2 TTTTTTTCCCTTTTTTT 20


RESULT 2693
AW248782/c
LOCUS       AW248782                 21 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821017.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821017 3',
            mRNA sequence.
ACCESSION   AW248782
VERSION     AW248782.1  GI:6591775
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821017.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 21
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 21 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: L  column: 10
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821017"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||  |||||||||
Db         20 AAAAAAAATTAAAAAAAAA 2


RESULT 2694
AZ597932/c
LOCUS       AZ597932                 21 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0412D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0412D23 F, genomic survey sequence.
ACCESSION   AZ597932
VERSION     AZ597932.1  GI:11720122
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0412  row: D  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
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                     /db_xref="taxon:10090"
                     /clone="UUGC1M0412D23"
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                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||| |||||| ||||
Db         21 AAAAAAAGAAAAAAGAAAA 3


RESULT 2695
AZ647578/c
LOCUS       AZ647578                  21 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0514I17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0514I17 F, genomic survey sequence.
ACCESSION   AZ647578
VERSION     AZ647578.1  GI:11779183
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0514  row: I  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0514I17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||| |||||| ||||
Db         21 AAAAAAAGAAAAAGAAAAA 3


RESULT 2696
AZ442146/c
LOCUS       AZ442146                  22 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0234B16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0234B16 R, genomic survey sequence.
ACCESSION   AZ442146
VERSION     AZ442146.1  GI:10566159
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0234  row: B  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0234B16"
```

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                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||  |||||||||
Db         22 AAAAAAAACCAAAAAAAAA 4


RESULT 2697
AZ345485/c
LOCUS       AZ345485                 22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080C02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080C02 F, genomic survey sequence.
ACCESSION   AZ345485
VERSION     AZ345485.1  GI:10424722
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: C  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080C02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||  ||||||||||||
Db         22 AAAAAATTAAAAAAAAAAA 4


RESULT 2698
AZ355624/c
LOCUS       AZ355624                 22 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0095E22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0095E22 F, genomic survey sequence.
ACCESSION   AZ355624
VERSION     AZ355624.1  GI:10468133
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0095  row: E  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0095E22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGAAAG 2197
              ||||||||||  || |||||
Db         22 TTTTTTTTAATTTAGAAAG 4


RESULT 2699
AZ447220
LOCUS       AZ447220                 23 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0244E15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0244E15 F, genomic survey sequence.
ACCESSION   AZ447220
VERSION     AZ447220.1  GI:10598989
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0244  row: E  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0244E15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||  |||  |||||||||
Db          2 AAAAATAAATAAAAAAAAA 20


RESULT 2700
BX560037/c
LOCUS       BX560037                 23 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX560037 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse47e08_p1c, mRNA sequence.
ACCESSION   BX560037
VERSION     BX560037.1  GI:33368052
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse47e08_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.6%; Score 15.8; DB 1; Length 23;
Best Local Similarity 89.5%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
              || | ||||||||||||||||
Db         19 TTTAGAAAAAAAAAAAAAA 1
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RESULT 2701
AZ514388/c
LOCUS AZ514388 24 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0361H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0361H04 F, genomic survey sequence.
ACCESSION AZ514388
VERSION AZ514388.1 GI:10695704
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: H column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES Location/Qualifiers
source 1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361H04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||| | |
Db         24 AAAAAAAAAAAAAAAGAGA 6
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RESULT 2702
AZ814559/c
LOCUS AZ814559 24 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0082P18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0082P18 F, genomic survey sequence.
ACCESSION AZ814559
VERSION AZ814559.1 GI:12984467
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: P column: 18
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES Location/Qualifiers
source 1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0082P18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||| |||| ||||||
Db         24 AAAAAAAGAAAAGAAAAAA 6


RESULT 2703
AZ827015/c
LOCUS       AZ827015                 24 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0103J11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0103J11 F, genomic survey sequence.
ACCESSION   AZ827015
VERSION     AZ827015.1  GI:12996923
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0103  row: J  column: 11
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0103J11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||| |||||| ||||||
Db         24 AAAAACAAAAAACAAAAAA 6


RESULT 2704
CF300715/c
LOCUS       CF300715                 24 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-E19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-E19, mRNA sequence.
ACCESSION   CF300715
VERSION     CF300715.1  GI:33672476
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-E19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTAACTTT 2192
              |||||||||||| || |||
Db         24 TTTTTTTTTTTTAAAATTT 6


RESULT 2705
CF300339
LOCUS       CF300339                 22 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-L05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-L05, mRNA sequence.
ACCESSION   CF300339
VERSION     CF300339.1  GI:33672100
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-L05"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||  ||  ||
Db          1 TTTTTTTTTTTTTTCCTAGTTT 22


RESULT 2706
CF300339/c
LOCUS       CF300339                 22 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-L05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-L05, mRNA sequence.
ACCESSION   CF300339
VERSION     CF300339.1  GI:33672100
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-L05"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2800
              | | | | ||||||||||||||||
Db         22 AAACTAGGAAAAAAAAAAAAAA 1


RESULT 2707
BH906256
LOCUS       BH906256                 22 bp    DNA     linear   GSS 04-SEP-2002
DEFINITION  SALK_109539.42.15.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_109539.42.15.x, genomic
            survey sequence.
ACCESSION   BH906256
VERSION     BH906256.1  GI:22719189
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_109539.42.15.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1119 CCTATGTCTGTGAAGCCGAATT 1140
              |||||   |||||||| |||||
Db          1 CCTATCATTGTGAAGCAGAATT 22


RESULT 2708
AW332764
LOCUS       AW332764                 23 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S12F12 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION   AW332764
VERSION     AW332764.1  GI:6829121
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
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  ORGANISM  Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Pneumocystis carinii"
                     /mol_type="mRNA"
                     /db_xref="taxon:4754"
                     /lab_host="E. coli"
                     /clone_lib="AGS-1"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (3x10e9) from a single rat (99-1-6,
                     sacrificed on 3/17/99)  at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT priming, standard
                     conditions described by  vendor, Stratagene. Further
                     details see www.uky.edu/Project/Pneumocystis/"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAA 2801
              ||||| || |||| | ||||||
Db          2 GAATTAAAGAAAAGATAAAAAA 23


RESULT 2709
AZ632757
LOCUS       AZ632757                 23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0487M05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0487M05 R, genomic survey sequence.
ACCESSION   AZ632757
VERSION     AZ632757.1  GI:11754947
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0487  row: M  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0487M05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTT 2182
              |||| ||||||  |||||| ||
Db          2 TCTCTTTTTTCCTTTTTGTT 23


RESULT 2710
AW247816/c
LOCUS       AW247816                 24 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820481.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820481 3',
            mRNA sequence.
ACCESSION   AW247816
VERSION     AW247816.1  GI:6590809
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820481.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 24 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
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            polyadenylated.
            Plate: LLCM4  row: F  column: 2
            High quality sequence stop: 10.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820481"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.2e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAA 2795
              ||  || ||  ||||||||||||
Db         22 TTTGTAAAAGTGAAAAAAAAAA 1


RESULT 2711
CNS00HLD
LOCUS       CNS00HLD                  24 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR35D24 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL073529
VERSION     AL073529.1  GI:4953410
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR35D24"
                     /clone_lib="RPCI-98"
                     /note="end : T7"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   76.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |:||| |||| : ||||||||
Db          3 TWTTTGTTTTVDNTTTTTTT 23


RESULT 2712
AU268810
LOCUS       AU268810                  25 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU268810 VS Dictyostelium discoideum cDNA clone VSI514 5', mRNA
            sequence.
ACCESSION   AU268810
VERSION     AU268810.1  GI:20527608
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSI514"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAAA 2804
              || ||||| || || |||||||
Db          1 TTTAAAAACAATAATAAAAAAA 22


RESULT 2713
AZ346849
LOCUS       AZ346849                  33 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0082I14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0082I14 F, genomic survey sequence.
ACCESSION   AZ346849
VERSION     AZ346849.1  GI:10426086
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
```

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            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0082  row: I  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0082I14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 33;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2800
              | |||| |||| |||| |||||
Db          8 AAAATTAAAAATAAAATAAAAA 29


RESULT 2714
BQ591181/c
LOCUS       BQ591181                 17 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-H16-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-H16 3-PRIME, mRNA sequence.
ACCESSION   BQ591181
VERSION     BQ591181.1  GI:26120764
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 17   Std Error: 0.00
            Plate: 17  row: H  column: 16
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188932"
                     /db_xref="taxon:161934"
                     /clone="024-017-H16"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         17 ATAAAAAAAAAAAAAAA 1


RESULT 2715
CF299997
LOCUS       CF299997                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-D19, mRNA sequence.
ACCESSION   CF299997
VERSION     CF299997.1  GI:33671758
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-D19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||||||||||||||  |
Db          1 TTTTTTTTTTTTTTCT 17


RESULT 2716
CF311499/c
LOCUS       CF311499                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION   CF311499
VERSION     CF311499.1  GI:33683260
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--06-L20"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              | |||||||||||||||
Db         17 GTAAAAAAAAAAAAAA 1


RESULT 2717
CF319075/c
LOCUS       CF319075                  17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-H06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence.
ACCESSION   CF319075
VERSION     CF319075.1  GI:33690836
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--09-H06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | |||||||||||||||
Db         17 ATAAAAAAAAAAAAAA 1


RESULT 2718
AW245664
LOCUS       AW245664                  17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3',
            mRNA sequence.
ACCESSION   AW245664
VERSION     AW245664.1  GI:6588657
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822994.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
```

project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence.
Plate: LLCM10 row: N column: 19.

FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822994"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTT 2179
||||| ||||||||||||
Db 1 TCCTGTTTTTTTTTTTT 17

RESULT 2719
AW248574
LOCUS AW248574 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821096.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821096 3', mRNA sequence.
ACCESSION AW248574
VERSION AW248574.1 GI:6591567
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821096.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 8 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM5 row: O column: 17
High quality sequence stop: 8.

FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821096"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2182
|||||||||| ||||||
Db 1 TTTTTTTTTGTTTTTT 17

RESULT 2720
AW248574/c
LOCUS AW248574 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821096.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821096 3', mRNA sequence.
ACCESSION AW248574
VERSION AW248574.1 GI:6591567
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821096.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 8 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM5 row: O column: 17
High quality sequence stop: 8.

FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:2821096"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2802
|||||| ||||||||||
Db 17 AAAAAACAAAAAAAAAA 1

RESULT 2721
BQ591588
LOCUS BQ591588 17 bp mRNA linear EST 06-DEC-2002
DEFINITION E012616-024-017-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-C15 5-PRIME, mRNA sequence.
ACCESSION BQ591588
VERSION BQ591588.1 GI:26121171
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: C column: 15
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188532"
/db_xref="taxon:161934"
/clone="024-017-C15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2182
|| ||||||||||||||
Db 1 TTATTTTTTTTTTTTT 17

RESULT 2722
BQ591588/c
LOCUS BQ591588 17 bp mRNA linear EST 06-DEC-2002
DEFINITION E012616-024-017-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-C15 5-PRIME, mRNA sequence.
ACCESSION BQ591588
VERSION BQ591588.1 GI:26121171
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: C column: 15
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188532"
/db_xref="taxon:161934"
/clone="024-017-C15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2802

```
              ||||||||||||||| ||
Db         17 AAAAAAAAAAAAAATAA 1


RESULT 2723
CF276637
LOCUS       CF276637                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--01-N18.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--01-N18, mRNA sequence.
ACCESSION   CF276637
VERSION     CF276637.1  GI:33654023
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--01-N18"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              ||||| ||||||||||
Db          1 AAAAACAAAAAAAAAAA 17


RESULT 2724
CF276637/c
LOCUS       CF276637                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--01-N18.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--01-N18, mRNA sequence.
ACCESSION   CF276637
VERSION     CF276637.1  GI:33654023
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--01-N18"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||||||||||| |||||
Db         17 TTTTTTTTTTGTTTTT 1


RESULT 2725
CF291802
LOCUS       CF291802                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION   CF291802
VERSION     CF291802.1  GI:33660835
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-G05"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              | ||||||||||||||||
Db          1 TGTTTTTTTTTTTTTT 17


RESULT 2726
CF291802/c
LOCUS       CF291802                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION   CF291802
VERSION     CF291802.1  GI:33660835
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-G05"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||||||||||| |
Db         17 AAAAAAAAAAAAAAAACA 1


RESULT 2727
CF297251
LOCUS       CF297251                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--07-P12, mRNA sequence.
ACCESSION   CF297251
VERSION     CF297251.1  GI:33666284
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--07-P12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              |||||||||||||||  |
Db          1 TTTTTTTTTTTTTTGA 17


RESULT 2728
CF297251/c
LOCUS       CF297251                 17 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--07-P12, mRNA sequence.
ACCESSION   CF297251
VERSION     CF297251.1  GI:33666284
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--07-P12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
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  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              | ||||||||||||||||
Db         17 TCAAAAAAAAAAAAAAA 1


RESULT 2729
CF298341/c
LOCUS       CF298341                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-K24, mRNA sequence.
ACCESSION   CF298341
VERSION     CF298341.1  GI:33670102
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db         17 GCAAAAAAAAAAAAAAA 1


RESULT 2730
CF299675
LOCUS       CF299675                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-M14.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-M14, mRNA sequence.
ACCESSION   CF299675
VERSION     CF299675.1  GI:33671436
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-M14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAA 2797
              |||| ||||||||||||
Db          1 AATTTAAAAAAAAAAAA 17


RESULT 2731
CF299675/c
LOCUS       CF299675                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-M14.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-M14, mRNA sequence.
ACCESSION   CF299675
VERSION     CF299675.1  GI:33671436
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-M14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
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  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTT 2191
              ||||||||||||||| ||
Db         17 TTTTTTTTTTTTAAATT 1


RESULT 2732
CF309376/c
LOCUS       CF309376                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-I19, mRNA sequence.
ACCESSION   CF309376
VERSION     CF309376.1  GI:33681137
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--03-I19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db         17 GTAAAAAAAAAAAAAA 1


RESULT 2733
CF329484/c
LOCUS       CF329484                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION   CF329484
VERSION     CF329484.1  GI:33807207
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-N06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db         17 GTAAAAAAAAAAAAAA 1


RESULT 2734
CF329485
LOCUS       CF329485                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION   CF329485
VERSION     CF329485.1  GI:33807209
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-N06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db          2 GTAAAAAAAAAAAAAAA 18
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RESULT 2735
CF329020
LOCUS CF329020 18 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-D03, mRNA sequence.
ACCESSION CF329020
VERSION CF329020.1 GI:33806277
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-D03"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2174 TTTTTTTTTTTTTAACT 2190
              ||||||||||||| |||
Db          1 TTTTTTTTTTTTTACT 17
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RESULT 2736
CF301222/c
LOCUS CF301222 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-P21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-P21, mRNA sequence.
ACCESSION CF301222
VERSION CF301222.1 GI:33672983
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-P21"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAAAAAA 2800
              || ||||||||||||||
Db         18 TGTAAAAAAAAAAAAA 2
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RESULT 2737
AZ589400
LOCUS AZ589400 21 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0398C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0398C23 F, genomic survey sequence.
ACCESSION AZ589400
VERSION AZ589400.1 GI:11711590
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0398 row: C column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0398C23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2162 CTCCTTTTTTTTTTTTT 2178
              | ||||||||||||||||
Db          5 CCCCTTTTTTTTTTTTT 21
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RESULT 2738
AZ843343/c
LOCUS AZ843343 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0142K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0142K10 F, genomic survey sequence.
ACCESSION AZ843343
VERSION AZ843343.1 GI:13013251
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: K column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0142K10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAA 2801
              || ||||||||||||||
Db         17 GAGAAAAAAAAAAAAAA 1
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RESULT 2739
CF297521
LOCUS CF297521 22 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--08-H01.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--08-H01, mRNA sequence.
ACCESSION CF297521
VERSION CF297521.1 GI:33666554
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--08-H01"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2172 TTTTTTTTTTTTTTAA 2188
              ||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTCAA 17
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RESULT 2740
AZ307559/c
LOCUS AZ307559 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0009O20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0009O20 F, genomic survey sequence.
ACCESSION AZ307559
VERSION AZ307559.1 GI:10346680
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: O column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0009O20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAAAAA 2799
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Db         22 TTTAAAAAAAAAAAAAA 6
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RESULT 2741
TA367G08P/c
LOCUS TA367G08P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 367g08, forward sequence, genomic survey sequence.
ACCESSION AL493527
VERSION AL493527.1 GI:11870537
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="367g08"

Query Match 0.5%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAAAAA 2799
              || |||||||||||||||
Db         17 TTTAAAAAAAAAAAAAA 1
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RESULT 2742
AZ470212/c
LOCUS AZ470212 22 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0284L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0284L09 F, genomic survey sequence.
ACCESSION AZ470212
VERSION AZ470212.1 GI:10628337
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0284  row: L  column: 09
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0284L09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              ||||||||||||| |||
Db         22 GAAAAAAAAAAAAGAAA 6


RESULT 2743
AL587602/c
LOCUS       AL587602                 23 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587602 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS059F08, mRNA sequence.
ACCESSION   AL587602
VERSION     AL587602.1  GI:13192636
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS059F08"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   88.9%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||| |||||||| |
Db         23 AAAAAAANAAAAAAAGA 6


RESULT 2744
AZ662734
LOCUS       AZ662734                 23 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0542D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0542D04 F, genomic survey sequence.
ACCESSION   AZ662734
VERSION     AZ662734.1  GI:11799880
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0542  row: D  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
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    source          1. .23
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0542D04"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   94.1%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||| ||||||||||||
Db          7 AAATAAAAAAAAAAAA 23


RESULT 2745
CF280704
LOCUS       CF280704                 23 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-H17.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--07-H17, mRNA sequence.
ACCESSION   CF280704
VERSION     CF280704.1  GI:33658090
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES            Location/Qualifiers
     source         1. .23
                    /organism="Oryza sativa"
                    /mol_type="mRNA"
                    /cultivar="Nackdong"
                    /db_xref="taxon:4530"
                    /clone="14ETL--07-H17"
                    /tissue_type="leaf"
                    /dev_stage="14 days after germination"
                    /lab_host="E.coli DH10B"
                    /clone_lib="Rice etiolated leaf plasmid cDNA library
                    (14ETL)"
                    /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                    with oligoribonucleotides and then used as templates for
                    RT-PCR."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   94.1%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2799
              || ||||||||||||||
Db          7 TTTAAAAAAAAAAAAA 23


RESULT 2746
TA367D08P/c
LOCUS       TA367D08P                23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 367d08, forward sequence,
            genomic survey sequence.
ACCESSION   AL493509
VERSION     AL493509.1  GI:11870519
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES            Location/Qualifiers
     source         1. .23
                    /organism="Trypanosoma brucei"
                    /mol_type="genomic DNA"
                    /strain="TREU927"
                    /db_xref="taxon:5691"
                    /clone="367d08"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   94.1%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2799
              || ||||||||||||||
Db         17 TTTAAAAAAAAAAAAA 1


RESULT 2747
AZ615086
LOCUS       AZ615086                 23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0444C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0444C14 F, genomic survey sequence.
ACCESSION   AZ615086
VERSION     AZ615086.1  GI:11737276
KEYWORDS    GSS.
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SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0444  row: C  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0444C14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   94.1%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTT 2178
              | ||||||||||||||||
Db          7 CCCCTTTTTTTTTTTTT 23


RESULT 2748
AZ819376/c
LOCUS       AZ819376                 23 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0089P23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0089P23 R, genomic survey sequence.
ACCESSION   AZ819376
VERSION     AZ819376.1  GI:12989284
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0089  row: P  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0089P23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   94.1%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTT 2178
              | ||||||||||||||||
Db         17 CCCCTTTTTTTTTTTTT 1


RESULT 2749
AZ343444
LOCUS       AZ343444                 25 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0076O01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0076O01 R, genomic survey sequence.
ACCESSION   AZ343444
VERSION     AZ343444.1  GI:10421687
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0076  row: O  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0076O01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              || |||||||||||||||
Db          9 TTAAAAAAAAAAAAAAA 25


RESULT 2750
AZ329925/c
LOCUS       AZ329925                 25 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0054N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0054N14 R, genomic survey sequence.
ACCESSION   AZ329925
VERSION     AZ329925.1  GI:10391126
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0054  row: N  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0054N14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||||||||||||| ||
Db         25 TTTTTTTTTTTTTCTT 9


RESULT 2751
AZ515233/c
LOCUS       AZ515233                 25 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0054N14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0054N14 F, genomic survey sequence.
ACCESSION   AZ515233
VERSION     AZ515233.1  GI:10696549
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0054  row: N  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0054N14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||| ||
Db         25 TTTTTTTTTTTTTTCTT 9


RESULT 2752
CF282165
LOCUS       CF282165                 20 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-I22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-I22, mRNA sequence.
ACCESSION   CF282165
VERSION     CF282165.1  GI:33659552
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--09-I22"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||| || |
Db          1 TTTTTTTTTTTTTTGCAAAT 20


RESULT 2753
CF336815
LOCUS       CF336815                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-A04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--07-A04, mRNA sequence.
ACCESSION   CF336815
VERSION     CF336815.1  GI:33822012
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--07-A04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
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                cDNA library (JMT)"
                /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                was reverse transcribed and then used for PCR. mRNA was
                pepared from Arabidopsis Jasmoinate Carboxyl
                methyltransferase overexpression line."

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||  | |
Db          1 TTTTTTTTTTTTTTTGCTCT 20


RESULT 2754
AZ316368/c
LOCUS       AZ316368                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0034L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0034L22 F, genomic survey sequence.
ACCESSION   AZ316368
VERSION     AZ316368.1  GI:10364124
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0034  row: L  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0034L22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||   ||||||||||||||||
Db         20 TTAAATTTTTTTTTTTTTTT 1


RESULT 2755
AZ843343
LOCUS       AZ843343                 21 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0142K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0142K10 F, genomic survey sequence.
ACCESSION   AZ843343
VERSION     AZ843343.1  GI:13013251
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0142  row: K  column: 10
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0142K10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
```

adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||| |  ||
Db          1 TTTTTTTTTTTTTTCTCCCT 20
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RESULT 2756
AZ339966
LOCUS AZ339966 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0071L11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0071L11 R, genomic survey sequence.
ACCESSION AZ339966
VERSION AZ339966.1 GI:10414760
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: L column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0071L11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              |||| |||||||| || |||
Db          1 TTTTCTTTTTTTTCTTCTTA 20
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RESULT 2757
AZ967472/c
LOCUS AZ967472 21 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0238L20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0238L20 F, genomic survey sequence.
ACCESSION AZ967472
VERSION AZ967472.1 GI:13838699
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0238 row: L column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0238L20"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        289 CCCCGCGCCACCCCTCTCCC 308
              ||||||||| |||| | |||
Db         20 CCCCGCGCCCCCCCCCCCCC 1
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RESULT 2758
D20705/c
LOCUS D20705 22 bp mRNA linear EST 30-JUL-1996
DEFINITION HUMGS01681 Human promyelocyte Homo sapiens cDNA clone pm2012 3', mRNA sequence.
ACCESSION D20705
VERSION D20705.1 GI:501801
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 22)
AUTHORS Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y., Yoshinari,H., Arimoto,J. and Matsubara,K.
TITLE Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed cDNA sequencing
JOURNAL Unpublished (1993)
COMMENT Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y., Yoshinari,H., Arimoto,J. and Matsubara,K.
Institute for Molecular and Cellular Biology
Osaka University
3-1 Yamada-oka,Suita,Osaka 565,Japan.
FEATURES Location/Qualifiers
source 1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="pm2012"
/clone_lib="Human promyelocyte"
/note="Female, adult, cell_line = HL60, cell_type = promyelocyte. "

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2469 TTAATATTAACTTTTAATGGT 2489
              || || || |||||||||| |
Db         22 TTTATTTTNACTTTTAATGAT 2
```

RESULT 2759
TA181E11P/c
LOCUS TA181E11P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 181e11, forward sequence, genomic survey sequence.
ACCESSION AL474328
VERSION AL474328.1 GI:11839616
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="181e11"

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1769 GCTTTTTTTTTTTGAACCCC 1788
              | |||||||||||  ||||
Db         21 GGTTTTTTTTTTGGCCCCC 2
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RESULT 2760
AU267211
LOCUS AU267211 23 bp mRNA linear EST 10-MAY-2002
DEFINITION AU267211 VS Dictyostelium discoideum cDNA clone VSH291 5', mRNA sequence.
ACCESSION AU267211
VERSION AU267211.1 GI:20526009
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 23)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .23
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH291"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.5%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2781 AATTGAAAAAAAAAAAAAAA 2800
              ||||| | | ||||||||||
Db          4 AATTGTATACAAAAAAAAAA 23
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```
RESULT 2761
AW245956
LOCUS       AW245956                 23 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2823002.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823002 3',
            mRNA sequence.
ACCESSION   AW245956
VERSION     AW245956.1  GI:6588949
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2823002.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washingtion Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 23 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM10  row: O  column: 3
            High quality sequence stop: 9.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2823002"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              |||| ||||| ||| |||||
Db          1 TTTTCTTTTTCTTTATTTTT 20


RESULT 2762
CF292525/c
LOCUS       CF292525                 23 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-G03.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--01-G03, mRNA sequence.
ACCESSION   CF292525
VERSION     CF292525.1  GI:33661558
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--01-G03"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAA 2799
              | | || ||||||||||||||
Db         20 GTAATGCAAAAAAAAAAAAA 1


RESULT 2763
CK277017
LOCUS       CK277017                 23 bp    mRNA    linear   EST 12-DEC-2003
DEFINITION  EST723095 potato abiotic stress cDNA library Solanum tuberosum cDNA
            clone POADX19 3' end, mRNA sequence.
ACCESSION   CK277017
VERSION     CK277017.1  GI:39833995
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
  TITLE     Generation of ESTs from abiotic stressed potato tissue
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: EST723094
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Clones can be requested from TIGR via potato@tigr.org
            Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
```

/clone="POADX19"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

Query Match 0.5%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2169 TTTTTTTTTTTTTTTTTTAA 2188
              ||| ||| ||||||| ||||
Db          2 TTTATTTCTTTTTTTCTTAA 21
```

RESULT 2764
CF328535/c
LOCUS CF328535 24 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-H21.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--03-H21, mRNA sequence.
ACCESSION CF328535
VERSION CF328535.1 GI:33805314
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-H21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.2; DB 1; Length 24;
Best Local Similarity 85.0%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||| ||||| ||
Db         22 GAAAAGAAAAAGAAAAAGAA 3
```

RESULT 2765
CF300715
LOCUS CF300715 24 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-E19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-E19, mRNA sequence.
ACCESSION CF300715
VERSION CF300715.1 GI:33672476
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-E19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.2; DB 1; Length 24;
Best Local Similarity 85.0%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2779 AGAATTGAAAAAAAAAAAAA 2798
              | ||||  ||||||||||||
Db          5 AAAATTTTAAAAAAAAAAAA 24
```

RESULT 2766
AW247816
LOCUS AW247816 24 bp mRNA linear EST 07-JAN-2000
DEFINITION 2820481.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820481 3', mRNA sequence.
ACCESSION AW247816
VERSION AW247816.1 GI:6590809
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820481.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 24 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM4  row: F  column: 2
            High quality sequence stop: 10.
FEATURES              Location/Qualifiers
     source           1. .24
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2820481"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_7"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 24;
  Best Local Similarity   85.0%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAACTTTGAAA 2196
              |||||||||| ||||| | |
Db          1 TTTTTTTTTTCACTTTACA 20


RESULT 2767
AZ953355/c
LOCUS       AZ953355                 27 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0218M01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0218M01 R, genomic survey sequence.
ACCESSION   AZ953355
VERSION     AZ953355.1  GI:13824582
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0218  row: M  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 27.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0218M01"
                      /sex="Female"
                      /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC2M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (female) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 27;
  Best Local Similarity   85.0%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||||||| |||| |||| |
Db         27 GAAAAAAAGAAAAGAAAAGA 8


RESULT 2768
AV741507/c
LOCUS       AV741507                 27 bp    mRNA    linear   EST 17-OCT-2000
DEFINITION  AV741507 CB Homo sapiens cDNA clone CBMAMC05 5', mRNA sequence.
ACCESSION   AV741507
VERSION     AV741507.1  GI:10859088
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
  TITLE     Homo sapiens CB library cDNA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
```

```
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CBMAMC05"
                     /tissue_type="cord blood"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="CB"
                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is
                     cloned randomly with the EcoRI digestion"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 27;
  Best Local Similarity   81.0%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||   | |
Db         27 TTTTTTTTTTTTTTTCCCCNT 7


RESULT 2769
BE230585
LOCUS       BE230585                 15 bp    mRNA    linear   EST 07-JUL-2000
DEFINITION  99AS799 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa
            (indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION   BE230585
VERSION     BE230585.1  GI:8956782
KEYWORDS    EST.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
            Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of ESTs from Rice Seedling
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Milyang23"
                     /db_xref="taxon:39946"
                     /clone="99AS799"
                     /dev_stage="5 days after pollination"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; Directional cDNA library inserted into lambda ZAPII
                     vector at 5'end with EcoRI and 3' end with Xho I site"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2770
BE230585/c
LOCUS       BE230585                 15 bp    mRNA    linear   EST 07-JUL-2000
DEFINITION  99AS799 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa
            (indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION   BE230585
VERSION     BE230585.1  GI:8956782
KEYWORDS    EST.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
            Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of ESTs from Rice Seedling
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Eun M.Y.
            Department of Cytogenetics
            National Inst. of Agri. Sci. and Tech, RDA
            Suwon, Kyunggido, Korea
            Tel: 82 331 290 0301
            Fax: 82 331 290 0307
            Email: myeun@sun20.asti.re.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Milyang23"
                     /db_xref="taxon:39946"
                     /clone="99AS799"
                     /dev_stage="5 days after pollination"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; Directional cDNA library inserted into lambda ZAPII
                     vector at 5'end with EcoRI and 3' end with Xho I site"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2771
BQ582543
LOCUS       BQ582543                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013300-024-007-B02-T7 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-007-B02 3-PRIME, mRNA sequence.
ACCESSION   BQ582543
VERSION     BQ582543.1  GI:26112120
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
```

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   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 7  row: B  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184162"
                     /db_xref="taxon:161934"
                     /clone="024-007-B02"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2772
BQ582543/c
LOCUS       BQ582543                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013300-024-007-B02-T7 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-007-B02 3-PRIME, mRNA sequence.
ACCESSION   BQ582543
VERSION     BQ582543.1  GI:26112120
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 7  row: B  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184162"
                     /db_xref="taxon:161934"
                     /clone="024-007-B02"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2773
BQ585820
LOCUS       BQ585820                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012533-024-014-H17-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-014-H17 5-PRIME, mRNA sequence.
ACCESSION   BQ585820
VERSION     BQ585820.1  GI:26115402
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 14  row: H  column: 17
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:187164"
                     /db_xref="taxon:161934"
                     /clone="024-014-H17"
                     /tissue_type="leaf"
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/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
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RESULT 2774
BQ585820/c
LOCUS BQ585820 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012533-024-014-H17-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-014-H17 5-PRIME, mRNA sequence.
ACCESSION BQ585820
VERSION BQ585820.1 GI:26115402
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 14 row: H column: 17
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:187164"
/db_xref="taxon:161934"
/clone="024-014-H17"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1
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RESULT 2775
BQ590410
LOCUS BQ590410 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012844-024-019-M08-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-019-M08 3-PRIME, mRNA sequence.
ACCESSION BQ590410
VERSION BQ590410.1 GI:26119993
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 19 row: M column: 08
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .15
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189710"
/db_xref="taxon:161934"
/clone="024-019-M08"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
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RESULT 2776
BQ590410/c
LOCUS       BQ590410                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-M08-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-M08 3-PRIME, mRNA sequence.
ACCESSION   BQ590410
VERSION     BQ590410.1  GI:26119993
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 19  row: M  column: 08
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189710"
                     /db_xref="taxon:161934"
                     /clone="024-019-M08"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2777
BQ590656
LOCUS       BQ590656                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S015086-024-018-L13-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-018-L13 5-PRIME, mRNA sequence.
ACCESSION   BQ590656
VERSION     BQ590656.1  GI:26120239
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 18  row: L  column: 13
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189464"
                     /db_xref="taxon:161934"
                     /clone="024-018-L13"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2778
BQ590656/c
LOCUS       BQ590656                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S015086-024-018-L13-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-018-L13 5-PRIME, mRNA sequence.
ACCESSION   BQ590656
VERSION     BQ590656.1  GI:26120239
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
```

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            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 18  row: L  column: 13
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .15
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189464"
                     /db_xref="taxon:161934"
                     /clone="024-018-L13"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2779
BQ591170
LOCUS       BQ591170                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-N18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-N18 3-PRIME, mRNA sequence.
ACCESSION   BQ591170
VERSION     BQ591170.1  GI:26120753
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 17  row: N  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
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                     /clone="024-017-N18"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2780
BQ591170/c
LOCUS       BQ591170                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-N18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-N18 3-PRIME, mRNA sequence.
ACCESSION   BQ591170
VERSION     BQ591170.1  GI:26120753
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 17  row: N  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188941"
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                     /db_xref="taxon:161934"
                     /clone="024-017-N18"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2781
BQ591178
LOCUS       BQ591178                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-F22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-F22 3-PRIME, mRNA sequence.
ACCESSION   BQ591178
VERSION     BQ591178.1  GI:26120761
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 17  row: F  column: 22
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188949"
                     /db_xref="taxon:161934"
                     /clone="024-017-F22"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2782
BQ591178/c
LOCUS       BQ591178                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-F22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-F22 3-PRIME, mRNA sequence.
ACCESSION   BQ591178
VERSION     BQ591178.1  GI:26120761
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 17  row: F  column: 22
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188949"
                     /db_xref="taxon:161934"
                     /clone="024-017-F22"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2786 AAAAAAAAAAAAAAA 2800
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 2783
BQ591223
LOCUS       BQ591223                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-H02-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-H02 3-PRIME, mRNA sequence.
ACCESSION   BQ591223
VERSION     BQ591223.1  GI:26120806
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 17  row: H  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188901"
                     /db_xref="taxon:161934"
                     /clone="024-017-H02"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2784
BQ591223/c
LOCUS       BQ591223                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-H02-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-H02 3-PRIME, mRNA sequence.
ACCESSION   BQ591223
VERSION     BQ591223.1  GI:26120806
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 17  row: H  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188901"
                     /db_xref="taxon:161934"
                     /clone="024-017-H02"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2785
BQ594689
LOCUS       BQ594689                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012404-024-024-M05-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-024-M05 3-PRIME, mRNA sequence.
ACCESSION   BQ594689
VERSION     BQ594689.1  GI:26124272
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
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            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 24  row: M  column: 05
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:192163"
                     /db_xref="taxon:161934"
                     /clone="024-024-M05"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2786
BQ594689/c
LOCUS       BQ594689                 15 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012404-024-024-M05-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-024-M05 3-PRIME, mRNA sequence.
ACCESSION   BQ594689
VERSION     BQ594689.1  GI:26124272
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 24  row: M  column: 05
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:192163"
                     /db_xref="taxon:161934"
                     /clone="024-024-M05"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2787
CF277319
LOCUS       CF277319                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--02-M23.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--02-M23, mRNA sequence.
ACCESSION   CF277319
VERSION     CF277319.1  GI:33654705
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--02-M23"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
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                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2788
CF277319/c
LOCUS       CF277319                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--02-M23.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--02-M23, mRNA sequence.
ACCESSION   CF277319
VERSION     CF277319.1  GI:33654705
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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Qy       2786 AAAAAAAAAAAAAAA 2800
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 2789
CF281923
LOCUS       CF281923                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-D04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-D04, mRNA sequence.
ACCESSION   CF281923
VERSION     CF281923.1  GI:33659310
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2790
CF281923/c
LOCUS       CF281923                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-D04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-D04, mRNA sequence.
ACCESSION   CF281923
VERSION     CF281923.1  GI:33659310
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


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CF290920
LOCUS       CF290920                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-C09.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-C09, mRNA sequence.
ACCESSION   CF290920
VERSION     CF290920.1  GI:33659953
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2792
CF290920/c
LOCUS       CF290920                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-C09.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-C09, mRNA sequence.
ACCESSION   CF290920
VERSION     CF290920.1  GI:33659953
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
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Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2793
CF291029
LOCUS       CF291029                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION   CF291029
VERSION     CF291029.1  GI:33660062
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /cultivar="Nackdong"
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                     /clone="14ROOT--01-E19"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2794
CF291029/c
LOCUS       CF291029                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION   CF291029
VERSION     CF291029.1  GI:33660062
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2795
CF291103
LOCUS       CF291103                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-G10, mRNA sequence.
ACCESSION   CF291103
VERSION     CF291103.1  GI:33660136
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2796
CF291103/c
LOCUS       CF291103                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
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ACCESSION   CF291103
VERSION     CF291103.1  GI:33660136
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2797
CF291717
LOCUS       CF291717                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-E04, mRNA sequence.
ACCESSION   CF291717
VERSION     CF291717.1  GI:33660750
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2798
CF291717/c
LOCUS       CF291717                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-E04, mRNA sequence.
ACCESSION   CF291717
VERSION     CF291717.1  GI:33660750
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
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                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
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                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2799
CF291798
LOCUS       CF291798                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G02, mRNA sequence.
ACCESSION   CF291798
VERSION     CF291798.1  GI:33660831
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2800
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DEFINITION  14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G02, mRNA sequence.
ACCESSION   CF291798
VERSION     CF291798.1  GI:33660831
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Db         15 AAAAAAAAAAAAAAA 1


RESULT 2801
CF292458
LOCUS       CF292458                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--01-E17, mRNA sequence.
ACCESSION   CF292458
VERSION     CF292458.1  GI:33661491
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Qy       2166 TTTTTTTTTTTTTTT 2180
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Db          1 TTTTTTTTTTTTTTT 15


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LOCUS       CF292458                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
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ACCESSION   CF292458
VERSION     CF292458.1  GI:33661491
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2803
CF292461
LOCUS       CF292461                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--01-E19, mRNA sequence.
ACCESSION   CF292461
VERSION     CF292461.1  GI:33661494
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Db          1 TTTTTTTTTTTTTTT 15


RESULT 2804
CF292461/c
LOCUS       CF292461                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--01-E19, mRNA sequence.
ACCESSION   CF292461
VERSION     CF292461.1  GI:33661494
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2805
CF295100
LOCUS       CF295100                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--04-O02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--04-O02, mRNA sequence.
ACCESSION   CF295100
VERSION     CF295100.1  GI:33664133
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
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Db          1 TTTTTTTTTTTTTTA 15


RESULT 2806
CF298148
LOCUS       CF298148                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-G17, mRNA sequence.
ACCESSION   CF298148
VERSION     CF298148.1  GI:33669909
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Db          1 TTTTTTTTTTTTTTT 15


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LOCUS       CF298148                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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ACCESSION   CF298148
VERSION     CF298148.1  GI:33669909
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  JOURNAL   Unpublished (2003)
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     RT-PCR."

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Db         15 AAAAAAAAAAAAAAA 1


RESULT 2808
CF298630
LOCUS       CF298630                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-B23, mRNA sequence.
ACCESSION   CF298630
VERSION     CF298630.1  GI:33670391
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
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            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Qy       2166 TTTTTTTTTTTTTTT 2180
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Db          1 TTTTTTTTTTTTTTT 15


RESULT 2809
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LOCUS       CF298630                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-B23, mRNA sequence.
ACCESSION   CF298630
VERSION     CF298630.1  GI:33670391
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         15 AAAAAAAAAAAAAAA 1


RESULT 2810
CF298733
LOCUS       CF298733                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-E20, mRNA sequence.
ACCESSION   CF298733
VERSION     CF298733.1  GI:33670494
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-E20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2811
CF298733/c
LOCUS       CF298733                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-E20, mRNA sequence.
ACCESSION   CF298733
VERSION     CF298733.1  GI:33670494
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="7LEAF--02-E20"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
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Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2812
CF298805
LOCUS       CF298805                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-G20, mRNA sequence.
ACCESSION   CF298805
VERSION     CF298805.1  GI:33670566
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="7LEAF--02-G20"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2813
CF298805/c
LOCUS       CF298805                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-G20, mRNA sequence.
ACCESSION   CF298805
VERSION     CF298805.1  GI:33670566
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
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            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="7LEAF--02-G20"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2814
CF298889
LOCUS       CF298889                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-J09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-J09, mRNA sequence.
ACCESSION   CF298889
VERSION     CF298889.1  GI:33670650
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2815
CF298889/c
LOCUS       CF298889                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-J09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-J09, mRNA sequence.
ACCESSION   CF298889
VERSION     CF298889.1  GI:33670650
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="leaf"
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          15 AAAAAAAAAAAAAAA 1


RESULT 2816
CF299602
LOCUS       CF299602                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
ACCESSION   CF299602
VERSION     CF299602.1  GI:33671363
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2817
CF299602/c
LOCUS       CF299602                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
ACCESSION   CF299602
VERSION     CF299602.1  GI:33671363
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2818
CF299608
LOCUS       CF299608                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L04, mRNA sequence.
ACCESSION   CF299608
VERSION     CF299608.1  GI:33671369
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2819
CF299608/c
LOCUS       CF299608                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L04, mRNA sequence.
ACCESSION   CF299608
VERSION     CF299608.1  GI:33671369
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2820
CF300121
LOCUS       CF300121                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-G12, mRNA sequence.
ACCESSION   CF300121
VERSION     CF300121.1  GI:33671882
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-G12"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2821
CF300121/c
LOCUS        CF300121                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION   7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
             sativa cDNA clone 7LEAF--04-G12, mRNA sequence.
ACCESSION    CF300121
VERSION      CF300121.1  GI:33671882
KEYWORDS     EST.
SOURCE       Oryza sativa
  ORGANISM   Oryza sativa
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1  (bases 1 to 15)
  AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE      Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL    Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, MyongJi University
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             Fax: 82 31 321 6355
             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-G12"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2822
CF300361
LOCUS        CF300361                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION   7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
             sativa cDNA clone 7LEAF--04-L16, mRNA sequence.
ACCESSION    CF300361
VERSION      CF300361.1  GI:33672122
KEYWORDS     EST.
SOURCE       Oryza sativa
  ORGANISM   Oryza sativa
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1  (bases 1 to 15)
  AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE      Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL    Unpublished (2003)
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             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-L16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2823
CF300361/c
LOCUS        CF300361                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION   7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
             sativa cDNA clone 7LEAF--04-L16, mRNA sequence.
ACCESSION    CF300361
VERSION      CF300361.1  GI:33672122
KEYWORDS     EST.
SOURCE       Oryza sativa
  ORGANISM   Oryza sativa
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1  (bases 1 to 15)
  AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE      Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL    Unpublished (2003)
COMMENT      Contact: Nahm B.H.
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          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, MyongJi University
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          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-L16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
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Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2824
CF300992
LOCUS       CF300992                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-K19, mRNA sequence.
ACCESSION   CF300992
VERSION     CF300992.1  GI:33672753
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-K19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2825
CF300992/c
LOCUS       CF300992                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-K19, mRNA sequence.
ACCESSION   CF300992
VERSION     CF300992.1  GI:33672753
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2826
CF302034
LOCUS       CF302034                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-C24, mRNA sequence.
ACCESSION   CF302034
VERSION     CF302034.1  GI:33673795
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2827
CF302034/c
LOCUS       CF302034                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-C24, mRNA sequence.
ACCESSION   CF302034
VERSION     CF302034.1  GI:33673795
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2828
CF302124
LOCUS       CF302124                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-F16, mRNA sequence.
ACCESSION   CF302124
VERSION     CF302124.1  GI:33673885
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2829
CF302124/c
LOCUS       CF302124                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-F16, mRNA sequence.
ACCESSION   CF302124
VERSION     CF302124.1  GI:33673885
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2830
CF302182
LOCUS       CF302182                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-H20, mRNA sequence.
ACCESSION   CF302182
VERSION     CF302182.1  GI:33673943
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2831
CF302182/c
LOCUS       CF302182                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-H20, mRNA sequence.
ACCESSION   CF302182
VERSION     CF302182.1  GI:33673943
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2832
CF307923
LOCUS       CF307923                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-I15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-I15, mRNA sequence.
ACCESSION   CF307923
VERSION     CF307923.1  GI:33679684
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

```
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--01-I15"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2833
CF307923/c
LOCUS       CF307923                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-I15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-I15, mRNA sequence.
ACCESSION   CF307923
VERSION     CF307923.1  GI:33679684
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2834
CF311159
LOCUS       CF311159                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-E11, mRNA sequence.
ACCESSION   CF311159
VERSION     CF311159.1  GI:33682920
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

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  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
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Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2835
CF311159/c
LOCUS       CF311159                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-E11, mRNA sequence.
ACCESSION   CF311159
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VERSION     CF311159.1  GI:33682920
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2836
CF311907
LOCUS       CF311907                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-G04, mRNA sequence.
ACCESSION   CF311907
VERSION     CF311907.1  GI:33683668
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="ABF--07-G04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2837
CF311907/c
LOCUS       CF311907                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-G04, mRNA sequence.
ACCESSION   CF311907
VERSION     CF311907.1  GI:33683668
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
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Db         15 AAAAAAAAAAAAAAA 1


RESULT 2838
CF313319
LOCUS       CF313319                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.
ACCESSION   CF313319
VERSION     CF313319.1  GI:33685080
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
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Db          1 TTTTTTTTTTTTTTT 15


RESULT 2839
CF313319/c
LOCUS       CF313319                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.
ACCESSION   CF313319
VERSION     CF313319.1  GI:33685080
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
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Db          15 AAAAAAAAAAAAAAA 1


RESULT 2840
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LOCUS       CF313320                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-G13.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.
ACCESSION   CF313320
VERSION     CF313320.1  GI:33685081
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
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Db          1 AAAAAAAAAAAAAAA 15
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RESULT 2841
CF313320/c
LOCUS CF313320 15 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--01-G13.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.
ACCESSION CF313320
VERSION CF313320.1 GI:33685081
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .15
/organism="Oryza sativa"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         15 TTTTTTTTTTTTTTT 1
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RESULT 2842
CF316251
LOCUS CF316251 15 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--05-H15.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.
ACCESSION CF316251
VERSION CF316251.1 GI:33688012
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:4530"
/clone="HD--05-H15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
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Db          1 AAAAAAAAAAAAAAA 15
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RESULT 2843
CF316251/c
LOCUS CF316251 15 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--05-H15.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.
ACCESSION CF316251
VERSION CF316251.1 GI:33688012
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/organism="Oryza sativa"

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                     /clone="HD--05-H15"
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
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Qy       2166 TTTTTTTTTTTTTTT 2180
             ||||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2844
CF318035
LOCUS       CF318035                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-P06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.
ACCESSION   CF318035
VERSION     CF318035.1  GI:33689796
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             ||||||||||||||||
Db         1 TTTTTTTTTTTTTTT 15


RESULT 2845
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LOCUS       CF318035                  15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-P06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.
ACCESSION   CF318035
VERSION     CF318035.1  GI:33689796
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2846
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LOCUS       CF327434                  15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-O18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-O18, mRNA sequence.
ACCESSION   CF327434
VERSION     CF327434.1  GI:33803127
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2847
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LOCUS       CF327434                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-O18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-O18, mRNA sequence.
ACCESSION   CF327434
VERSION     CF327434.1  GI:33803127
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2848
CF330195
LOCUS       CF330195                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-N03, mRNA sequence.
ACCESSION   CF330195
VERSION     CF330195.1  GI:33808618
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2849
CF330195/c
LOCUS       CF330195                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-N03, mRNA sequence.
ACCESSION   CF330195
VERSION     CF330195.1  GI:33808618
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
```

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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
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Db         15 AAAAAAAAAAAAAAA 1


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LOCUS       CF330668                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF330668
VERSION     CF330668.1  GI:33809572
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


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CF330668/c
LOCUS       CF330668                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF330668
VERSION     CF330668.1  GI:33809572
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2852
CF332178
LOCUS       CF332178                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-J10, mRNA sequence.
ACCESSION   CF332178
VERSION     CF332178.1  GI:33812580
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2853
CF332178/c
LOCUS       CF332178                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-J10, mRNA sequence.
ACCESSION   CF332178
VERSION     CF332178.1  GI:33812580
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2854
CF336202
LOCUS       CF336202                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-C20, mRNA sequence.
ACCESSION   CF336202
VERSION     CF336202.1  GI:33820794
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
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Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2855
CF336202/c
LOCUS       CF336202                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-C20, mRNA sequence.
ACCESSION   CF336202
VERSION     CF336202.1  GI:33820794
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2856
BQ590507/c
LOCUS       BQ590507                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION   BQ590507
VERSION     BQ590507.1  GI:26120090
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 19  row: M  column: 04
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189608"
                     /db_xref="taxon:161934"
                     /clone="024-019-M04"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2857
BQ595369/c
LOCUS       BQ595369                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013317-024-022-P02-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION   BQ595369
VERSION     BQ595369.1  GI:26124952
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 22  row: P  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
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                     /db_xref="taxon:161934"
                     /clone="024-022-P02"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
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Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
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Db         15 AAAAAAAAAAAAAAA 1
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RESULT 2858
CF296130/c
LOCUS CF296130 16 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--06-F22, mRNA sequence.
ACCESSION CF296130
VERSION CF296130.1 GI:33665163
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
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Db         15 AAAAAAAAAAAAAAA 1
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RESULT 2859
CF314013/c
LOCUS CF314013 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-G01, mRNA sequence.
ACCESSION CF314013
VERSION CF314013.1 GI:33685774
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HD--02-G01"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         15 AAAAAAAAAAAAAAA 1
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RESULT 2860
CF329320/c
LOCUS CF329320 16 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-J17, mRNA sequence.
ACCESSION CF329320
VERSION CF329320.1 GI:33806877
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .16

/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
/clone="NACL--04-J17"
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/lab_host="E.coli DH10B"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
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Db 15 AAAAAAAAAAAAAAA 1

RESULT 2861
BQ590207
LOCUS BQ590207 16 bp mRNA linear EST 06-DEC-2002
DEFINITION E012843-024-019-O15-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-019-O15 3-PRIME, mRNA sequence.
ACCESSION BQ590207
VERSION BQ590207.1 GI:26119790
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 19 row: O column: 15
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .16
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/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189913"
/db_xref="taxon:161934"
/clone="024-019-O15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
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Db 1 TTTTTTTTTTTTTTT 15

RESULT 2862
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LOCUS BQ590207 16 bp mRNA linear EST 06-DEC-2002
DEFINITION E012843-024-019-O15-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-019-O15 3-PRIME, mRNA sequence.
ACCESSION BQ590207
VERSION BQ590207.1 GI:26119790
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 19 row: O column: 15
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189913"
/db_xref="taxon:161934"
/clone="024-019-O15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
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Db 15 AAAAAAAAAAAAAAA 1

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RESULT 2863
CF291803
LOCUS       CF291803                 16 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION   CF291803
VERSION     CF291803.1  GI:33660836
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-G05"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              |||||||||||||||
Db          2 GAAAAAAAAAAAAAA 16


RESULT 2864
CF312586
LOCUS       CF312586                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--08-G13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-G13, mRNA sequence.
ACCESSION   CF312586
VERSION     CF312586.1  GI:33684347
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--08-G13"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2865
CF318894
LOCUS       CF318894                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-D06, mRNA sequence.
ACCESSION   CF318894
VERSION     CF318894.1  GI:33690655
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--09-D06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
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  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2866
CF318894/c
LOCUS       CF318894                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-D06, mRNA sequence.
ACCESSION   CF318894
VERSION     CF318894.1  GI:33690655
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--09-D06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2867
CF327923
LOCUS       CF327923                  16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-J18, mRNA sequence.
ACCESSION   CF327923
VERSION     CF327923.1  GI:33804096
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2868
CF327923/c
LOCUS       CF327923                  16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-J18, mRNA sequence.
ACCESSION   CF327923
VERSION     CF327923.1  GI:33804096
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2869
CF328223
LOCUS       CF328223                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-A10, mRNA sequence.
ACCESSION   CF328223
VERSION     CF328223.1  GI:33804692
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2870
CF328223/c
LOCUS       CF328223                 16 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-A10, mRNA sequence.
ACCESSION   CF328223
VERSION     CF328223.1  GI:33804692
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2871
CF298341
LOCUS       CF298341                 17 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-K24, mRNA sequence.
ACCESSION   CF298341
VERSION     CF298341.1  GI:33670102
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 2872
CF301359
LOCUS CF301359 18 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--06-D05, mRNA sequence.
ACCESSION CF301359
VERSION CF301359.1 GI:33673120
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-D05"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 2873
CF325356
LOCUS CF325356 19 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT1--03-A08.g1 AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-A08, mRNA sequence.
ACCESSION CF325356
VERSION CF325356.1 GI:33798994
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT1--03-A08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 2874
CF325356/c
LOCUS CF325356 19 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT1--03-A08.g1 AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-A08, mRNA sequence.
ACCESSION CF325356
VERSION CF325356.1 GI:33798994
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT1--03-A08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
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Db 15 AAAAAAAAAAAAAAA 1

RESULT 2875
AZ856873/c
LOCUS AZ856873 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0161O19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0161O19 F, genomic survey sequence.
ACCESSION AZ856873
VERSION AZ856873.1 GI:13048296
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0161 row: O column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0161O19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAA 2799
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Db 15 GAAAAAAAAAAAAAA 1

RESULT 2876
AZ950028
LOCUS AZ950028 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0213L19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0213L19 R, genomic survey sequence.
ACCESSION AZ950028
VERSION AZ950028.1 GI:13821255
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0213 row: L column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0213L19"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAA 2799
              |||||||||||||||
Db          5 GAAAAAAAAAAAAAA 19
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RESULT 2877
CF301222
LOCUS CF301222 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-P21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-P21, mRNA sequence.
ACCESSION CF301222
VERSION CF301222.1 GI:33672983
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-P21"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2173 TTTTTTTTTTTTTTA 2187
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Db          2 TTTTTTTTTTTTTTA 16
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RESULT 2878
AZ316368
LOCUS AZ316368 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0034L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0034L22 F, genomic survey sequence.
ACCESSION AZ316368
VERSION AZ316368.1 GI:10364124
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: L column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034L22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
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Db          1 AAAAAAAAAAAAAAA 15
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RESULT 2879
CF331733
LOCUS CF331733 20 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--07-P15.b1 Rice callus plasmid cDNA library (NACL) Oryza

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            sativa cDNA clone NACL--07-P15, mRNA sequence.
ACCESSION   CF331733
VERSION     CF331733.1  GI:33811693
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--07-P15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2880
CF331733/c
LOCUS       CF331733                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-P15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-P15, mRNA sequence.
ACCESSION   CF331733
VERSION     CF331733.1  GI:33811693
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--07-P15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
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Db         15 TTTTTTTTTTTTTTT 1


RESULT 2881
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LOCUS       AZ341108                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0073O14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0073O14 F, genomic survey sequence.
ACCESSION   AZ341108
VERSION     AZ341108.1  GI:10417030
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0073  row: O  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0073O14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
```

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15
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RESULT 2882
CF309614/c
LOCUS CF309614 21 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--03-N20.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-N20, mRNA sequence.
ACCESSION CF309614
VERSION CF309614.1 GI:33681375
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--03-N20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
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Db         18 AAAAAAAAAAAAAAA 4
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RESULT 2883
CF282313
LOCUS CF282313 21 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-M08.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--09-M08, mRNA sequence.
ACCESSION CF282313
VERSION CF282313.1 GI:33659700
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-M08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          7 AAAAAAAAAAAAAAA 21
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RESULT 2884
CF282313/c
LOCUS CF282313 21 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-M08.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--09-M08, mRNA sequence.
ACCESSION CF282313
VERSION CF282313.1 GI:33659700
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

```
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--09-M08"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         21 TTTTTTTTTTTTTTT 7


RESULT 2885
AZ785791/c
LOCUS       AZ785791                  21 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0030O19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0030O19 F, genomic survey sequence.
ACCESSION   AZ785791
VERSION     AZ785791.1  GI:12922904
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0030  row: O  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0030O19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              |||||||||||||||
Db         15 GAAAAAAAAAAAAAA 1


RESULT 2886
AZ818565
LOCUS       AZ818565                  21 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0088K10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0088K10 R, genomic survey sequence.
ACCESSION   AZ818565
VERSION     AZ818565.1  GI:12988473
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0088  row: K  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0088K10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15
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RESULT 2887
AZ818565/c
LOCUS       AZ818565                 21 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0088K10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0088K10 R, genomic survey sequence.
ACCESSION   AZ818565
VERSION     AZ818565.1  GI:12988473
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0088  row: K  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0088K10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1
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RESULT 2888
AZ963501
LOCUS       AZ963501                 21 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0232M07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0232M07 R, genomic survey sequence.
ACCESSION   AZ963501
VERSION     AZ963501.1  GI:13834728
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0232M07"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
```

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
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RESULT 2889
AZ963501/c
LOCUS       AZ963501                21 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0232M07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0232M07 R, genomic survey sequence.
ACCESSION   AZ963501
VERSION     AZ963501.1  GI:13834728
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0232M07"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
```

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
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Db         15 AAAAAAAAAAAAAAA 1
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RESULT 2890
AZ317017/c
LOCUS       AZ317017                22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0035P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0035P09 F, genomic survey sequence.
ACCESSION   AZ317017
VERSION     AZ317017.1  GI:10365400
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0035  row: P  column: 09
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0035P09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
```

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         22 AAAAAAAAAAAAAAA 8
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RESULT 2891
CF308058/c

```
LOCUS       CF308058                 23 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-L15.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-L15, mRNA sequence.
ACCESSION   CF308058
VERSION     CF308058.1  GI:33679819
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--01-L15"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
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Query Match 0.5%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2801
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Db         23 AGTGTTAGTAAAAAAAAAAAAA 1
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RESULT 2892

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AZ390689
LOCUS       AZ390689                 23 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0152A18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0152A18 F, genomic survey sequence.
ACCESSION   AZ390689
VERSION     AZ390689.1  GI:10505732
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0152  row: A  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0152A18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

Query Match 0.5%; Score 15; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAA 2799
              |||||||||||||||
Db          9 GAAAAAAAAAAAAAA 23
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RESULT 2893
AZ654389/c

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LOCUS       AZ654389                 23 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0528H06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0528H06 R, genomic survey sequence.
ACCESSION   AZ654389
VERSION     AZ654389.1  GI:11791535
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0528  row: H  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0528H06"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.5e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        250 GGTCCCCCACCTCTCCTCCGCCG 272
              | |||||||||| || |  |||
Db         23 GCTCCCCCACCTCACCACACCCG 1


RESULT 2894
AZ771221
LOCUS       AZ771221                 23 bp    DNA     linear   GSS 16-FEB-2001
```

```
DEFINITION  1M0573A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0573A16 F, genomic survey sequence.
ACCESSION   AZ771221
VERSION     AZ771221.1  GI:12893248
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0573  row: A  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0573A16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2895
AZ771221/c
LOCUS       AZ771221                 23 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0573A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
```

```
          clone UUGC1M0573A16 F, genomic survey sequence.
ACCESSION AZ771221
VERSION   AZ771221.1  GI:12893248
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
  ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1  (bases 1 to 23)
  AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
  JOURNAL Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000   Std Error: 0.00
          Plate: 0573  row: A  column: 16
          Seq primer: CGTTGTAAAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0573A16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2896
AZ810709/c
LOCUS       AZ810709                23 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0076M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0076M20 F, genomic survey sequence.
ACCESSION   AZ810709
VERSION     AZ810709.1  GI:12978228
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0076  row: M  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0076M20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.5e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1817 TAAGTTTTAGAATCTTTTAAATA 1839
              |||||||| ||| |||   |||
Db         23 TAAGTTTTAAAATTTTTATTATA 1


RESULT 2897
TA120E05P
LOCUS       TA120E05P               23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 120e05, forward sequence,
            genomic survey sequence.
ACCESSION   AL464555
```

```
VERSION     AL464555.1  GI:11833135
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="120e05"

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2898
TA155F12Q
LOCUS       TA155F12Q                 24 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 155f12, reverse sequence,
            genomic survey sequence.
ACCESSION   AL472698
VERSION     AL472698.1  GI:11838089
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="155f12"

  Query Match             0.5%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2899
TA319G03Q/c
LOCUS       TA319G03Q                 26 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 319g03, reverse sequence,
            genomic survey sequence.
ACCESSION   AL492820
VERSION     AL492820.1  GI:11867590
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="319g03"

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 2900
AW246455/c
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LOCUS       AW246455                 27 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821693.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821693 3',
            mRNA sequence.
ACCESSION   AW246455
VERSION     AW246455.1  GI:6589448
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821693.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 27 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: H  column: 14
            High quality sequence stop: 10.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821693"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 15;  DB 1;  Length 27;
  Best Local Similarity   78.3%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAAA 2804
              ||  |||||||| |  |||||||
Db         26 ATAAAAAAAAAACATGAAAAAAA 4


RESULT 2901
TA224C08P
LOCUS       TA224C08P                29 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 224c08, forward sequence,
            genomic survey sequence.
ACCESSION   AL480654
VERSION     AL480654.1  GI:11846423
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="224c08"

  Query Match             0.5%;  Score 15;  DB 1;  Length 29;
  Best Local Similarity   78.3%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2801
              ||||  |   |||||||||||||
Db          7 AGAAGGGGGGAAAAAAAAAAAAA 29


RESULT 2902
AZ504854
LOCUS       AZ504854                 33 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0345D16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0345D16 F, genomic survey sequence.
ACCESSION   AZ504854
VERSION     AZ504854.1  GI:10686170
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0345  row: D  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
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          High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0345D16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.5%;  Score 15;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          2 AAAAAAAAAAAAAAA 16


RESULT 2903
CF329020/c
LOCUS       CF329020                 18 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-D03, mRNA sequence.
ACCESSION   CF329020
VERSION     CF329020.1  GI:33806277
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-D03"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              ||  |||||||||||||||
Db         18 GAGTAAAAAAAAAAAAAA 1


RESULT 2904
AW246505
LOCUS       AW246505                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3',
            mRNA sequence.
ACCESSION   AW246505
VERSION     AW246505.1  GI:6589498
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821585.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washingtion Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 18
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 18 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: D  column: 2
            High quality sequence stop: 18.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821585"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
```

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  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2183
              |||||||||| ||| |||
Db          1 TTTTTTTTTCTTTATTT 18


RESULT 2905
AW246505/c
LOCUS       AW246505                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3',
            mRNA sequence.
ACCESSION   AW246505
VERSION     AW246505.1  GI:6589498
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821585.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 18
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 18 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: D  column: 2
            High quality sequence stop: 18.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821585"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||| ||| ||||||||||
Db         18 AAATAAAGAAAAAAAAAA 1


RESULT 2906
AW247875/c
LOCUS       AW247875                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820433.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820433 3',
            mRNA sequence.
ACCESSION   AW247875
VERSION     AW247875.1  GI:6590868
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820433.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 18 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM4  row: D  column: 2
            High quality sequence stop: 10.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820433"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAA 2795
              |||  ||||||||||||||
Db         18 TAGGCTTGAAAAAAAAAA 1


RESULT 2907
CF309858
LOCUS       CF309858                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--04-D16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--04-D16, mRNA sequence.
```

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ACCESSION   CF309858
VERSION     CF309858.1  GI:33681619
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--04-D16"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||||| | |
Db          2 AAAAAAAAAAAAAACATA 19


RESULT 2908
AZ475079
LOCUS       AZ475079                 19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0293B17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0293B17 F, genomic survey sequence.
ACCESSION   AZ475079
VERSION     AZ475079.1  GI:10633204
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0293  row: B  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0293B17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        898 GGCTGAAGTACAGAGGCG 915
              ||| |||| |||||||||
Db          2 GGCGGAAGCACAGAGGCG 19


RESULT 2909
AZ789309
LOCUS       AZ789309                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0036L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0036L22 R, genomic survey sequence.
ACCESSION   AZ789309
VERSION     AZ789309.1  GI:12929974
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
```

```
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0036  row: L  column: 22
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0036L22"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2182
              |||||||||||| |||| |
Db          2 CTTTTTTTTTTCTTTTCT 19


RESULT 2910
AZ789309/c
LOCUS       AZ789309                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0036L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0036L22 R, genomic survey sequence.
ACCESSION   AZ789309
VERSION     AZ789309.1  GI:12929974
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0036  row: L  column: 22
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
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                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0036L22"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| |||||||||| |
Db         18 GAAAAGAAAAAAAAAAGA 1


RESULT 2911
AZ962226/c
LOCUS       AZ962226                 19 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0231A02 F, genomic survey sequence.
ACCESSION   AZ962226
VERSION     AZ962226.1  GI:13833453
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
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            Plate: 0231  row: A  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0231A02"
                      /sex="Female"
                      /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC2M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (female) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTT 2172
              ||||||| ||| ||||||
Db         18 TTTTTTTTTCCATTTTTT 1


RESULT 2912
CF297010/c
LOCUS       CF297010                 20 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-J24.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--07-J24, mRNA sequence.
ACCESSION   CF297010
VERSION     CF297010.1  GI:33666043
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="30DGS--07-J24"
                      /tissue_type="leaf"
                      /dev_stage="30 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||  ||||||||||||||
Db         18 GACCAAAAAAAAAAAAAA 1


RESULT 2913
CF313751/c
LOCUS       CF313751                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-P23.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.
ACCESSION   CF313751
VERSION     CF313751.1  GI:33685512
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="HD--01-P23"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                      /lab_host="E.coli DH10B"
                      /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                      reverse transcribed and then used for PCR. mRNA was
                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||  ||||||||||||||
Db         18 GAGCAAAAAAAAAAAAAA 1


RESULT 2914
CF313752
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LOCUS       CF313752                20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-P23.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.
ACCESSION   CF313752
VERSION     CF313752.1  GI:33685513
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--01-P23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||  ||||||||||||||
Db          3 GAGCAAAAAAAAAAAAAA 20


RESULT 2915
AZ828826/c
LOCUS       AZ828826                20 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0106O01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0106O01 F, genomic survey sequence.
ACCESSION   AZ828826
VERSION     AZ828826.1  GI:12998734
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0106  row: O  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0106O01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2528 TATATATACAGGGTATTA 2545
              |||||||| | |||||||
Db         20 TATATATAAATGGTATTA 3


RESULT 2916
AZ625662
LOCUS       AZ625662                21 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0465C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0465C23 F, genomic survey sequence.
ACCESSION   AZ625662
VERSION     AZ625662.1  GI:11747852
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
```

```
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0465  row: C  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0465C23"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||||||||||| | |
Db          2 AAAAAAAAAAAAAATATA 19


RESULT 2917
AU254546/c
LOCUS       AU254546                 21 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU254546 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0002442 3', mRNA sequence.
ACCESSION   AU254546
VERSION     AU254546.1  GI:20316429
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /db_xref="taxon:10090"
                      /clone="BED0002442"
                      /tissue_type="brain"
                      /clone_lib="3'-directed mouse cDNA library"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              |||||| ||||||||| |
Db         20 TTGAAAGAAAAAAAAAGA 3


RESULT 2918
AZ331619/c
LOCUS       AZ331619                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0059K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0059K09 R, genomic survey sequence.
ACCESSION   AZ331619
VERSION     AZ331619.1  GI:10394486
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0059  row: K  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES              Location/Qualifiers
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                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0059K09"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1771 TTTTTTTTTTTGAACCCC 1788
              |||||||||||  || |||
Db         18 TTTTTTTTTTTAAAACCC 1
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RESULT 2919
AZ984045/c
LOCUS AZ984045 23 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0265I23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0265I23 F, genomic survey sequence.
ACCESSION AZ984045
VERSION AZ984045.1 GI:13855272
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0265 row: I column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0265I23"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.8; DB 1; Length 23;
Best Local Similarity 88.9%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAAAAAA 2800
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Db         18 TTAAAAAAAAAAAATAAA 1
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RESULT 2920
AZ349008/c
LOCUS AZ349008 24 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0085O13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0085O13 R, genomic survey sequence.
ACCESSION AZ349008
VERSION AZ349008.1 GI:10428245
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: O column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
FEATURES Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0085O13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.8; DB 1; Length 24;
Best Local Similarity 88.9%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||  ||
Db         24 AAAAAAAAAAAAAACGAA 7
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RESULT 2921
AZ782507/c
LOCUS AZ782507 24 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0022L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0022L22 R, genomic survey sequence.
ACCESSION AZ782507
VERSION AZ782507.1 GI:12916299
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0022 row: L column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
FEATURES Location/Qualifiers
source 1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0022L22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.8; DB 1; Length 24;
Best Local Similarity 88.9%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2803
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Db         21 AAACAACAAAAAAAAAAA 4
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RESULT 2922
AU264164/c
LOCUS AU264164 27 bp mRNA linear EST 10-MAY-2002
DEFINITION AU264164 VS Dictyostelium discoideum cDNA clone VSD517 5', mRNA sequence.
ACCESSION AU264164
VERSION AU264164.1 GI:20522962
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 27)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .27
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSD517"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.5%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy       2176 TTTTTTTTTTAACTTTGAAAGTTAA 2201
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Db         27 TTTTTTTTTCAATATTAAAAAAAAA 2
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RESULT 2923
AZ346714/c
LOCUS AZ346714 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0082N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0082N05 F, genomic survey sequence.
ACCESSION AZ346714
VERSION AZ346714.1 GI:10425951
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

```
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0082  row: N  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0082N05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAA 2188
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Db         21 TTTTTTTTTTGTATTATGTAA 1


RESULT 2924
AZ483617/c
LOCUS       AZ483617                 21 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0309A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0309A05 R, genomic survey sequence.
ACCESSION   AZ483617
VERSION     AZ483617.1  GI:10647772
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0309  row: A  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0309A05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
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Db         21 TTGTTTTGTTTTTGTTGTTTT 1


RESULT 2925
AZ787674/c
LOCUS       AZ787674                 21 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0034H14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0034H14 F, genomic survey sequence.
ACCESSION   AZ787674
VERSION     AZ787674.1  GI:12926701
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
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```
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0034  row: H  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0034H14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2674 GTGTGTGTGGGTGAAATGGAG 2694
              ||||||||| |||| |  |||
Db         21 GTGTGTGTGTGTGAGAGAGAG 1


RESULT 2926
AZ788269
LOCUS       AZ788269                21 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0035D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0035D18 F, genomic survey sequence.
ACCESSION   AZ788269
VERSION     AZ788269.1  GI:12927898
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0035  row: D  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0035D18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2674 GTGTGTGTGGGTGAAATGGAG 2694
              ||||||||||||    ||||
Db          1 GTGTGTGTGGGTGTGTAGGAG 21


RESULT 2927
AZ845735/c
LOCUS       AZ845735                22 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0145J07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0145J07 R, genomic survey sequence.
ACCESSION   AZ845735
VERSION     AZ845735.1  GI:13015643
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
```

```
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0145  row: J  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0145J07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAA 2799
              | ||   ||||||||||||||
Db         21 AAAAGCCAAAAAAAAAAAAAA 1


RESULT 2928
AZ470212
LOCUS       AZ470212                 22 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0284L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0284L09 F, genomic survey sequence.
ACCESSION   AZ470212
VERSION     AZ470212.1  GI:10628337
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0284  row: L  column: 09
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0284L09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTT 2182
              ||   ||| ||||||||||||
Db          1 CTGGGTTTCTTTTTTTTTTT 21


RESULT 2929
AA888191/c
LOCUS       AA888191                 22 bp    mRNA    linear   EST 31-MAR-1998
DEFINITION  of82a05.s1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:1436816 3'
            similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ;, mRNA sequence.
ACCESSION   AA888191
VERSION     AA888191.1  GI:3003866
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
```

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            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html

           Trace considered overall poor quality
           Seq primer: -40m13 fwd. ET from Amersham
           High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1436816"
                     /tissue_type="hepatic adenoma"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Li5"
                     /note="Organ: liver; Vector: pCMV-SPORT4; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 0.8 kb."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTT 2177
              || |||| ||||| |||| ||
Db         22 TTGTTCTTCTTTTATTTTGTT 2

RESULT 2930
AI184101/c
LOCUS       AI184101                 22 bp    mRNA    linear   EST 29-OCT-1998
DEFINITION  qe24d08.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:1739919 3' similar to TR:O00483 O00483 NADH:UBIQUINONE
            OXIDOREDUCTASE MLRQ SUBUNIT. ;, mRNA sequence.
ACCESSION   AI184101
VERSION     AI184101.1  GI:3734739
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 2216   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1739919"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. This library was constructed
                     from the same fetus as the fetal heart library, Soares
                     fetal heart NbHH19W."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2262 GCATATTTATTTCAGATGTTT 2282
              |||| || | | |||||||||
Db         21 GCATGTTCAATCCAGATGTTT 1

RESULT 2931
BQ595200/c
LOCUS       BQ595200                 22 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012709-024-023-E04-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-023-E04 5-PRIME, mRNA sequence.
ACCESSION   BQ595200
VERSION     BQ595200.1  GI:26124783
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 22   Std Error: 0.00
            Plate: 23  row: E  column: 04
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:191654"
                     /db_xref="taxon:161934"
                     /clone="024-023-E04"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy       1775 TTTTTTTGAACCCCATTCTTT 1795
              |||||||  |||||| || |||
Db         22 TTTTTTGAAACCCCCTTTTTT 2


RESULT 2932
BX563723
LOCUS       BX563723                 22 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX563723 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse68e02_p1c, mRNA sequence.
ACCESSION   BX563723
VERSION     BX563723.1  GI:33430936
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse68e02_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTT 2181
              |||   | ||||||||||||||
Db          2 TCTAAATATTTTTTTTTTTTT 22


RESULT 2933
AZ326642/c
LOCUS       AZ326642                 22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0049D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0049D09 R, genomic survey sequence.
ACCESSION   AZ326642
VERSION     AZ326642.1  GI:10384599
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0049  row: D  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0049D09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTT 2176
              || || |||| |||||| |||
Db         22 TTGTTGCTCCATTTTTTATTT 2


RESULT 2934
AZ854229/c
LOCUS       AZ854229                 22 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0157C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0157C14 R, genomic survey sequence.
ACCESSION   AZ854229
VERSION     AZ854229.1  GI:13043139
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
```

```
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0157  row: C  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0157C14"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||| |||| | | |||
Db         22 TTTTTTTTCTTTTCTCTCTTT 2


RESULT 2935
AU267170/c
LOCUS       AU267170                  23 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU267170 VS Dictyostelium discoideum cDNA clone VSH269 5', mRNA
            sequence.
ACCESSION   AU267170
VERSION     AU267170.1  GI:20525968
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="Dictyostelium discoideum"
                      /mol_type="mRNA"
                      /strain="AX4"
                      /db_xref="taxon:44689"
                      /clone="VSH269"
                      /sex="mat A"
                      /dev_stage="vegetative"
                      /clone_lib="VS"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||| ||| | || |
Db         23 TTTTTTTTTTATTTCTATTGT 3


RESULT 2936
AW332764/c
LOCUS       AW332764                  23 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S12F12 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION   AW332764
VERSION     AW332764.1  GI:6829121
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
  ORGANISM  Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="Pneumocystis carinii"
                      /mol_type="mRNA"
                      /db_xref="taxon:4754"
                      /lab_host="E. coli"
                      /clone_lib="AGS-1"
                      /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                      P. carinii organisms (3x10e9) from a single rat (99-1-6,
                      sacrificed on 3/17/99)  at Cincinnati VA facilities.
                      Trizol extracted RNA.  Oligo dT priming, standard
                      conditions described by  vendor, Stratagene. Further
                      details see www.uky.edu/Project/Pneumocystis/"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACT 2190
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              |||||| | |||| ||||| |
Db         23 TTTTTTATCTTTTCTTTAATT 3


RESULT 2937
CF292525
LOCUS       CF292525                 23 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--01-G03.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--01-G03, mRNA sequence.
ACCESSION   CF292525
VERSION     CF292525.1  GI:33661558
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--01-G03"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||   ||| |
Db          1 TTTTTTTTTTTTTGCATTACC 21


RESULT 2938
AZ390689/c
LOCUS       AZ390689                 23 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0152A18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0152A18 F, genomic survey sequence.
ACCESSION   AZ390689
VERSION     AZ390689.1  GI:10505732
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0152  row: A  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0152A18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCATT 1791
              ||||||||||||   |||| ||
Db         21 TTTTTTTTTTTTCCCCCCCTT 1


RESULT 2939
CF312586/c
LOCUS       CF312586                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--08-G13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-G13, mRNA sequence.
ACCESSION   CF312586
VERSION     CF312586.1  GI:33684347
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="ABF--08-G13"
                      /tissue_type="leaf"
                      /dev_stage="14 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="ABF3-overexpressing transgenic rice plasmid
                      cDNA library (ABF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                      for 2hrs. Oligo-capped mRNA was reverse transcribed and
                      then used for PCR. mRNA was prepared from ABA-responsive
                      element binding transcription factor 3 overexpression
                      line."

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || |||||||||||||
Db         16 TTTAAAAAAAAAAAAA 1


RESULT 2940
CF317778
LOCUS       CF317778                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-J13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-J13, mRNA sequence.
ACCESSION   CF317778
VERSION     CF317778.1  GI:33689539
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="HD--07-J13"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                      /lab_host="E.coli DH10B"
                      /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                      reverse transcribed and then used for PCR. mRNA was
                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2181
              ||| |||||||||||||
Db          1 TTTGTTTTTTTTTTT 16


RESULT 2941
CF317778/c
LOCUS       CF317778                  16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-J13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-J13, mRNA sequence.
ACCESSION   CF317778
VERSION     CF317778.1  GI:33689539
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="HD--07-J13"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                      /lab_host="E.coli DH10B"
                      /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                      reverse transcribed and then used for PCR. mRNA was
                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              ||||||||||||| |||
Db         16 AAAAAAAAAAAACAAA 1


RESULT 2942
AW247165
LOCUS       AW247165                  17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819675.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819675 3',
            mRNA sequence.
ACCESSION   AW247165
VERSION     AW247165.1  GI:6590158
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819675.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 17
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 17 contiguous distinct
            peaks following vector sequence.
            Plate: LLCM2  row: D  column: 12
            High quality sequence stop: 17.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819675"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2181
              ||||||||||  |||||
Db          2 TTTTTTTTTGTTTTT 17


RESULT 2943
AW247165/c
LOCUS       AW247165                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819675.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819675 3',
            mRNA sequence.
ACCESSION   AW247165
VERSION     AW247165.1  GI:6590158
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819675.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 17
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 17 contiguous distinct
            peaks following vector sequence.
            Plate: LLCM2  row: D  column: 12
            High quality sequence stop: 17.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819675"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              |||||  ||||||||||
Db         17 AAAAACAAAAAAAAA 2


RESULT 2944
AZ774536/c
LOCUS       AZ774536                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0004P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0004P01 F, genomic survey sequence.
ACCESSION   AZ774536
VERSION     AZ774536.1  GI:12900089
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0004  row: P  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
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          Class: plasmid ends
          High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0004P01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGAA 1784
              ||||||||||||| ||
Db         19 GCTTTTTTTTTTTTAA 4


RESULT 2945
CF196152
LOCUS       CF196152                 22 bp    mRNA    linear   EST 31-JUL-2003
DEFINITION  Azvi1.2_E03 AZ-VI Oryza sativa (japonica cultivar-group) cDNA clone
            AZ-VI1.2E03 5', mRNA sequence.
ACCESSION   CF196152
VERSION     CF196152.1  GI:33380809
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Ventelon-Debout,M., Thi-Thu Huang,N., Wissocq,A., Berger,C.,
            Michele,L., Piegu,B., Cooke,R., Ghesquiere,A., Delseny,M. and
            Brugidou,C.
  TITLE     Metabolism and Photosynthesis gene expression is affected in
            response to rice yellow mottle virus infection in Oryza sativa
            indica and japonica culltivars
  JOURNAL   Mol. Genet. Genomics (2003) In press
COMMENT     Contact: Brugidou C
            IRD
            BP 64501, 34394 Montpellier cedex 5 France
            Tel: 33 4 67 41 67 39
            Fax: 33 4 67 41 61 81
            PCR PRimers
            FORWARD: 5'AATTAACCCTCACTAAAGGG3'
            BACKWARD: 5'CGGGATATCACTCAGCATAATG3'
            Plate: 1.2  row: E  column: 3.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Azucena"
                     /db_xref="taxon:39947"
                     /clone="AZ-VI1.2E03"
                     /tissue_type="leaves"
                     /dev_stage="3 weeks-old plants"
                     /lab_host="SOLR strain (Stratagene)"
                     /clone_lib="AZ-VI"
                     /note="Vector: pBluescript SK (+/-); Site_1: Eco RI;
                     Site_2: Xho I; Sample name: AZ-VI; Plant growth place:
                     greenhouse; Soil conditions: standard; Sowing date:
                     28/02/2000; Harvesting date: 18/03/2000; Stress date:
                     15/03/2000; Cultivar: azucena; Description: Az-RYMV
                     inoculated leaves cDNA library; experimental condition:
                     rymv inoculation;"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   78.9%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAAC 2189
              ||||||||||||    |||
Db          1 TTTTTTTTTTTTNNNAAAC 19


RESULT 2946
TA120E05P/c
LOCUS       TA120E05P                23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 120e05, forward sequence,
            genomic survey sequence.
ACCESSION   AL464555
VERSION     AL464555.1  GI:11833135
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="120e05"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 23;
  Best Local Similarity   93.8%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || ||||||||||||
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```
Db         16 TTTAAAAAAAAAAAAA 1


RESULT 2947
BZ767540/c
LOCUS       BZ767540                  25 bp    DNA     linear   GSS 13-MAR-2003
DEFINITION  SALK_139012.18.15.n Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_139012.18.15.n, genomic
            survey sequence.
ACCESSION   BZ767540
VERSION     BZ767540.1  GI:28940093
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_139012.18.15.n"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 25;
  Best Local Similarity   75.0%;  Pred. No. 3.6e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||   ||| ||||| ||| |||||
Db         24 AAGACAAACAAAAATAAATAAAAA 1


RESULT 2948
AZ785639
LOCUS       AZ785639                  27 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0029O12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0029O12 R, genomic survey sequence.
ACCESSION   AZ785639
VERSION     AZ785639.1  GI:12922599
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0029  row: O  column: 12
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0029O12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 27;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || ||||||||||||||
Db         12 TTAAAAAAAAAAAAAA 27


RESULT 2949
AZ766990
LOCUS       AZ766990                  19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0564H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0564H19 R, genomic survey sequence.
ACCESSION   AZ766990
VERSION     AZ766990.1  GI:12884624
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0564  row: H  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0564H19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||   ||
Db          1 AAAAAAAAAAAAAATGGAA 19


RESULT 2950
AZ962226
LOCUS       AZ962226                 19 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0231A02 F, genomic survey sequence.
ACCESSION   AZ962226
VERSION     AZ962226.1  GI:13833453
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0231  row: A  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0231A02"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||   ||||||||||
Db          1 AAAAAATGGAAAAAAAAAA 19


RESULT 2951
AI364573
LOCUS       AI364573                 19 bp    mRNA    linear   EST 15-FEB-1999
DEFINITION  qw37g03.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:1993300 3'
            similar to TR:Q39835 Q39835 EXTENSIN. ;, mRNA sequence.
ACCESSION   AI364573
VERSION     AI364573.1  GI:4124262
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1632 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1993300"
/tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut4"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        292 CGCGCCACCCCTCTCCCAC 310
              | ||||||||| | |||||
Db          1 CCCGCCACCCCCCCCCCAC 19
```

RESULT 2952
AI371092
LOCUS AI371092 19 bp mRNA linear EST 16-FEB-1999
DEFINITION ta07g09.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2043424 3' similar to TR:Q26195 Q26195 PVA1 GENE. ;contains L1.b3 L1 repetitive element ;, mRNA sequence.
ACCESSION AI371092
VERSION AI371092.1 GI:4149845
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 536 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2043424"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn23"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2160 TTCTCCTTTTTTTTTTTTT 2178
              || |||||||||| | ||||
Db          1 TTTTCCTTTTTTCTCTTTT 19
```

RESULT 2953
CF337608/c
LOCUS CF337608 19 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--08-C02.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--08-C02, mRNA sequence.
ACCESSION CF337608
VERSION CF337608.1 GI:33823602
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--08-C02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2157 TTTTTCTCCTTTTTTTTTT 2175
                ||||  |||||  |||  ||||
Db         19 TTTTCCTCCTCTTTCTTTT 1
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RESULT 2954
AZ328922
LOCUS AZ328922 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0052L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0052L22 R, genomic survey sequence.
ACCESSION AZ328922
VERSION AZ328922.1 GI:10389127
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: L column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
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/db_xref="taxon:10090"
/clone="UUGC1M0052L22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2157 TTTTTCTCCTTTTTTTTTT 2175
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Db          1 TTTTTCTACTTTTCTTCTT 19
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RESULT 2955
AZ408157/c
LOCUS AZ408157 19 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0179A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0179A16 F, genomic survey sequence.
ACCESSION AZ408157
VERSION AZ408157.1 GI:10532170
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0179 row: A column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0179A16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db         19 TTTTTTTTTTAATAATTTT 1


RESULT 2956
AZ775624
LOCUS       AZ775624                19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0008E01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0008E01 R, genomic survey sequence.
ACCESSION   AZ775624
VERSION     AZ775624.1  GI:12902356
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0008  row: E  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0008E01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Db          1 ACACACAAAAAAAAAAAAA 19


RESULT 2957
AZ775624/c
LOCUS       AZ775624                19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0008E01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0008E01 R, genomic survey sequence.
ACCESSION   AZ775624
VERSION     AZ775624.1  GI:12902356
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0008  row: E  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0008E01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
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Db         19 TTTTTTTTTTTTTGTGTGT 1
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RESULT 2958
CF340627/c
LOCUS       CF340627                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  RCL1--08-K02.g1 Regenerated callus lambda phage cDNA library (RCL1)
            Oryza sativa cDNA clone RCL1--08-K02, mRNA sequence.
ACCESSION   CF340627
VERSION     CF340627.1  GI:33829609
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="RCL1--08-K02"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli SOLR"
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                     /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
                     XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
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                     induced on 2N6 media for 30 days and cultured for 36hrs on
                     regenerated media"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||   ||||||||
Db         20 AAAAAAAAGGGAAAAAAAA 2


RESULT 2959
CF297010
LOCUS       CF297010                 20 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-J24.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--07-J24, mRNA sequence.
ACCESSION   CF297010
VERSION     CF297010.1  GI:33666043
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="30DGS--07-J24"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
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Db          1 TTTTTTTTTTTTTTGGTCT 19


RESULT 2960
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LOCUS       AL587630                 20 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587630 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS060A07, mRNA sequence.
ACCESSION   AL587630
VERSION     AL587630.1  GI:13192664
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
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     source          1. .20
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                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"
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  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTT 2177
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Db          2 TTTCCAGTTTTTTTTTTTT 20


RESULT 2961
AU257221
LOCUS       AU257221                 20 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU257221 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0010046 3', mRNA sequence.
ACCESSION   AU257221
VERSION     AU257221.1  GI:20321628
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="BED0010046"
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                     /clone_lib="3'-directed mouse cDNA library"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATTAA 2478
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Db          1 GATCCAATTTGATTATCAA 19


RESULT 2962
CF339443
LOCUS       CF339443                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  RCL1--04-O03.g1 Regenerated callus lambda phage cDNA library (RCL1)
            Oryza sativa cDNA clone RCL1--04-O03, mRNA sequence.
ACCESSION   CF339443
VERSION     CF339443.1  GI:33827271
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="RCL1--04-O03"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli SOLR"
                     /clone_lib="Regenerated callus lambda phage cDNA library
                     (RCL1)"
                     /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
                     XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
                     end with SstI and 3' end with XhoI site. Callus was
                     induced on 2N6 media for 30 days and cultured for 36hrs on
                     regenerated media"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              |||||||  |||||||| |
Db          1 GCGGCGGCAGCGGCGGCGG 19


RESULT 2963
AZ304038/c
LOCUS       AZ304038                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0003L08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0003L08 R, genomic survey sequence.
ACCESSION   AZ304038
VERSION     AZ304038.1  GI:10339611
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0003  row: L  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0003L08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
```

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||||| | |||| ||||||
Db         19 GAAAAGATAAAAGAAAAAA 1
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RESULT 2964
AZ308410/c
LOCUS AZ308410 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0011A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0011A24 F, genomic survey sequence.
ACCESSION AZ308410
VERSION AZ308410.1 GI:10348378
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: A column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0011A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        290 CCCGCGCCACCCCTCTCCC 308
              |||||||| |||| | |||
Db         20 CCCGCGCCCCCCCGCCCCC 2
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RESULT 2965
AZ345646/c
LOCUS AZ345646 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080K20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080K20 F, genomic survey sequence.
ACCESSION AZ345646
VERSION AZ345646.1 GI:10424883
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: K column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080K20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTG 2193
              ||||||||||| |  ||||
Db         20 TTTTTTTTTTTAATGTTTG 2
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RESULT 2966
AZ346143/c

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LOCUS       AZ346143                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0081P11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0081P11 F, genomic survey sequence.
ACCESSION   AZ346143
VERSION     AZ346143.1  GI:10425380
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0081  row: P  column: 11
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0081P11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

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  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2183
              |||||||||| ||| | ||
Db         19 CTTTTTTTTTCTTTGTCTT 1
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RESULT 2967
AZ426873/c

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LOCUS       AZ426873                 20 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0208L05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0208L05 R, genomic survey sequence.
ACCESSION   AZ426873
VERSION     AZ426873.1  GI:10550886
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0208  row: L  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0208L05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTTTTT 2178
              | |  ||||||||||||||
Db         19 TACATCTTTTTTTTTTTTT 1
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RESULT 2968
AZ345540/c
LOCUS       AZ345540                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080P05 F, genomic survey sequence.
ACCESSION   AZ345540
VERSION     AZ345540.1  GI:10424777
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: P  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080P05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||| || ||||||| ||||
Db         21 AAAGAAGAAAAAAAGAAAA 3
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RESULT 2969
AZ346717/c
LOCUS       AZ346717                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0082O02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0082O02 F, genomic survey sequence.
ACCESSION   AZ346717
VERSION     AZ346717.1  GI:10425954
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0082  row: O  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0082O02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAAA 2804
              ||||||||| ||| ||| ||
Db         21 AAAAAAAAGAAAGAAAGAA 3
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RESULT 2970
AZ339966/c
LOCUS       AZ339966                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0071L11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0071L11 R, genomic survey sequence.
ACCESSION   AZ339966
VERSION     AZ339966.1  GI:10414760
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0071  row: L  column: 11
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0071L11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
```

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAAA 2804
              || || |||||||| ||||
Db         19 AAGAAGAAAAAAAAGAAAA 1
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RESULT 2971
AW248826
LOCUS       AW248826                 21 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821056.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821056 3',
            mRNA sequence.
ACCESSION   AW248826
VERSION     AW248826.1  GI:6591819
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821056.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 21
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 21 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: N  column: 1
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821056"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
```

adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1771 TTTTTTTTTTTGAACCCCA 1789
              |||||||||| | |||| |
Db          1 TTTTTTTTTTGGGACCCTA 19
```

RESULT 2972
AZ331046
LOCUS AZ331046 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0056K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0056K08 R, genomic survey sequence.
ACCESSION AZ331046
VERSION AZ331046.1 GI:10393185
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: K column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0056K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2517 GGTTTTATTCATATATATA 2535
              ||| |||| |||| |||||
Db          2 GGTATTATACATACATATA 20
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RESULT 2973
AZ629111
LOCUS AZ629111 21 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0481D22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0481D22 R, genomic survey sequence.
ACCESSION AZ629111
VERSION AZ629111.1 GI:11751301
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0481 row: D column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0481D22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2674 GTGTGTGTGGGTGAAATGG 2692
              ||||||||| ||| || ||
Db          2 GTGTGTGTGTGTGTAAGGG 20
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RESULT 2974
AZ471736
LOCUS AZ471736 22 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0286I12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286I12 R, genomic survey sequence.
ACCESSION AZ471736
VERSION AZ471736.1 GI:10629957
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0286 row: I column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0286I12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 22;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||  | |||||||
Db          3 AAAAAAAACCATAAAAAAA 21
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RESULT 2975
AZ468097/c
LOCUS AZ468097 23 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0279K22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0279K22 R, genomic survey sequence.
ACCESSION AZ468097
VERSION AZ468097.1 GI:10626222
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0279 row: K column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES Location/Qualifiers
source 1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0279K22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 23;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||| ||| |||||
Db         22 AAAAACAAACAAACAAAAA 4
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RESULT 2976
AW245956/c
LOCUS AW245956 23 bp mRNA linear EST 07-JAN-2000
DEFINITION 2823002.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823002 3', mRNA sequence.
ACCESSION AW245956
VERSION AW245956.1 GI:6588949
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 23)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2823002.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 9 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 23 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM10 row: O column: 3
High quality sequence stop: 9.
FEATURES Location/Qualifiers
source 1. .23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2823002"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 14.2; DB 1; Length 23;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||| ||||| |||
Db         20 AAAAATAAAGAAAAAGAAA 2
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RESULT 2977
AZ308225/c
LOCUS AZ308225 24 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0011E06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0011E06 F, genomic survey sequence.
ACCESSION AZ308225
VERSION AZ308225.1 GI:10348004
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: E column: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES Location/Qualifiers
source 1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0011E06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 24;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||| ||| ||| |||||||
Db         21 AAACAAACAAACAAAAAAA 3
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RESULT 2978
AU265714
LOCUS       AU265714                 26 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU265714 VS Dictyostelium discoideum cDNA clone VSF741 5', mRNA
            sequence.
ACCESSION   AU265714
VERSION     AU265714.1  GI:20524512
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSF741"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 26;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAAA 2804
              ||||||||   ||||||||
Db          2 AAAAAAAAGGGAAAAAAAA 20


RESULT 2979
AZ808163/c
LOCUS       AZ808163                 30 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0071N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0071N08 R, genomic survey sequence.
ACCESSION   AZ808163
VERSION     AZ808163.1  GI:12973424
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0071  row: N  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0071N08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 30;
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Db         28 AAACAAACAAACAAAAAAA 10


RESULT 2980
BQ586422
LOCUS       BQ586422                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013307-024-013-O02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-013-O02 3-PRIME, mRNA sequence.
ACCESSION   BQ586422
VERSION     BQ586422.1  GI:26116004
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     line)"
                     /db_xref="GABI:186441"
                     /db_xref="taxon:161934"
                     /clone="024-013-O02"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTT 14


RESULT 2981
BQ586422/c
LOCUS       BQ586422                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013307-024-013-O02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-013-O02 3-PRIME, mRNA sequence.
ACCESSION   BQ586422
VERSION     BQ586422.1  GI:26116004
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
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            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     line)"
                     /db_xref="GABI:186441"
                     /db_xref="taxon:161934"
                     /clone="024-013-O02"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 2982
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LOCUS       BQ587890                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013302-024-009-B02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-009-B02 3-PRIME, mRNA sequence.
ACCESSION   BQ587890
VERSION     BQ587890.1  GI:26117472
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 9  row: B  column: 02
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:161934"
                     /clone="024-009-B02"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
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SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTTT 14
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RESULT 2983
BQ587890/c
LOCUS BQ587890 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S013302-024-009-B02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-009-B02 3-PRIME, mRNA sequence.
ACCESSION BQ587890
VERSION BQ587890.1 GI:26117472
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 9 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGGC.
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/db_xref="GABI:184980"
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SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1
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RESULT 2984
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LOCUS BQ589191 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S014009-024-015-I20-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-015-I20 3-PRIME, mRNA sequence.
ACCESSION BQ589191
VERSION BQ589191.1 GI:26118774
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGGC.
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/db_xref="taxon:161934"
/clone="024-015-I20"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTTT 14
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RESULT 2985
BQ589191/c
LOCUS BQ589191 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S014009-024-015-I20-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-015-I20 3-PRIME, mRNA sequence.

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ACCESSION   BQ589191
VERSION     BQ589191.1  GI:26118774
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
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            Seq primer: T7; GTAATACGACTCACTATAGGGC.
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                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
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                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         14 AAAAAAAAAAAAAA 1


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LOCUS       BQ590242                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012840-024-019-E16-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-E16 5-PRIME, mRNA sequence.
ACCESSION   BQ590242
VERSION     BQ590242.1  GI:26119825
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 19  row: E  column: 16
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTTT 14


RESULT 2987
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LOCUS       BQ590242                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012840-024-019-E16-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-E16 5-PRIME, mRNA sequence.
ACCESSION   BQ590242
VERSION     BQ590242.1  GI:26119825
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
```

```
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaa@mpiz-koeln.mpg.de
          Insert Length: 14   Std Error: 0.00
          Plate: 19  row: E  column: 16
          Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
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                     /cultivar="KWS2320 (double haploid, monogerm breeding
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                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2988
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LOCUS       BQ590261                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-K14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-K14 3-PRIME, mRNA sequence.
ACCESSION   BQ590261
VERSION     BQ590261.1  GI:26119844
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 19  row: K  column: 14
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     line)"
                     /db_xref="GABI:189851"
                     /db_xref="taxon:161934"
                     /clone="024-019-K14"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2989
BQ590261/c
LOCUS       BQ590261                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012844-024-019-K14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-K14 3-PRIME, mRNA sequence.
ACCESSION   BQ590261
VERSION     BQ590261.1  GI:26119844
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 19  row: K  column: 14
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     line)"
                     /db_xref="GABI:189851"
                     /db_xref="taxon:161934"
                     /clone="024-019-K14"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
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                    Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                    b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                    orientation:
                    SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                    Sequencing granted in the context of the GABI-Beet
                    project, local PI: Dr. Katharina Schneider, coordinator:
                    Prof. Christian Jung;  Sequence submission managed by
                    RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2990
BQ591168
LOCUS       BQ591168                14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-H18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-H18 3-PRIME, mRNA sequence.
ACCESSION   BQ591168
VERSION     BQ591168.1  GI:26120751
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: H  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /db_xref="taxon:161934"
                     /clone="024-017-H18"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2991
BQ591168/c
LOCUS       BQ591168                14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-H18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-H18 3-PRIME, mRNA sequence.
ACCESSION   BQ591168
VERSION     BQ591168.1  GI:26120751
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: H  column: 18
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188939"
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                     /clone="024-017-H18"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
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                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
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                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2992
BQ591176
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LOCUS       BQ591176                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-N20-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-N20 3-PRIME, mRNA sequence.
ACCESSION   BQ591176
VERSION     BQ591176.1  GI:26120759
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: N  column: 20
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188947"
                     /db_xref="taxon:161934"
                     /clone="024-017-N20"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

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  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2993
BQ591176/c
LOCUS       BQ591176                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-N20-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-N20 3-PRIME, mRNA sequence.
ACCESSION   BQ591176
VERSION     BQ591176.1  GI:26120759
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: N  column: 20
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
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                     /db_xref="GABI:188947"
                     /db_xref="taxon:161934"
                     /clone="024-017-N20"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 2994
BQ591207
LOCUS       BQ591207                  14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-B04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-B04 3-PRIME, mRNA sequence.
ACCESSION   BQ591207
VERSION     BQ591207.1  GI:26120790
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
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COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: B  column: 04
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
     source           1. .14
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                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
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                      /db_xref="GABI:188904"
                      /db_xref="taxon:161934"
                      /clone="024-017-B04"
                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
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                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2995
BQ591207/c
LOCUS       BQ591207                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012715-024-017-B04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-B04 3-PRIME, mRNA sequence.
ACCESSION   BQ591207
VERSION     BQ591207.1  GI:26120790
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: B  column: 04
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:188904"
                      /db_xref="taxon:161934"
                      /clone="024-017-B04"
                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-storage root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2996
BQ591380
LOCUS       BQ591380                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012714-024-017-B15-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-B15 3-PRIME, mRNA sequence.
ACCESSION   BQ591380
VERSION     BQ591380.1  GI:26120963
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: B  column: 15
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
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                      /mol_type="mRNA"
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                      line)"
                      /db_xref="GABI:188734"
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                      /clone="024-017-B15"
                      /tissue_type="storage root"
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/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTT 2179
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Db 1 TTTTTTTTTTTTT 14

RESULT 2997
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LOCUS BQ591380 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012714-024-017-B15-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-B15 3-PRIME, mRNA sequence.
ACCESSION BQ591380
VERSION BQ591380.1 GI:26120963
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGGC.
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line)"
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/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2799
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Db 14 AAAAAAAAAAAAAA 1

RESULT 2998
BQ591482
LOCUS BQ591482 14 bp mRNA linear EST 06-DEC-2002
DEFINITION E012713-024-017-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-M04 3-PRIME, mRNA sequence.
ACCESSION BQ591482
VERSION BQ591482.1 GI:26121065
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: M column: 04
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188633"
/db_xref="taxon:161934"
/clone="024-017-M04"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTT 2179
||||||||||||||
Db 1 TTTTTTTTTTTTT 14

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RESULT 2999
BQ591482/c
LOCUS       BQ591482                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012713-024-017-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-M04 3-PRIME, mRNA sequence.
ACCESSION   BQ591482
VERSION     BQ591482.1  GI:26121065
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 17  row: M  column: 04
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .14
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188633"
                     /db_xref="taxon:161934"
                     /clone="024-017-M04"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3000
BQ593052
LOCUS       BQ593052                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012375-024-028-C03-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-028-C03 5-PRIME, mRNA sequence.
ACCESSION   BQ593052
VERSION     BQ593052.1  GI:26122635
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 28  row: C  column: 03
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
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                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
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                     /db_xref="GABI:193808"
                     /db_xref="taxon:161934"
                     /clone="024-028-C03"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3001
BQ593052/c
LOCUS       BQ593052                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012375-024-028-C03-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-028-C03 5-PRIME, mRNA sequence.
ACCESSION   BQ593052
VERSION     BQ593052.1  GI:26122635
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
```

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  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 28  row: C  column: 03
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
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                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:193808"
                     /db_xref="taxon:161934"
                     /clone="024-028-C03"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3002
CF277935
LOCUS       CF277935                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--03-K11.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--03-K11, mRNA sequence.
ACCESSION   CF277935
VERSION     CF277935.1  GI:33655321
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--03-K11"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3003
CF277935/c
LOCUS       CF277935                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--03-K11.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--03-K11, mRNA sequence.
ACCESSION   CF277935
VERSION     CF277935.1  GI:33655321
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3004
CF278001
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LOCUS       CF278001                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--03-L21.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--03-L21, mRNA sequence.
ACCESSION   CF278001
VERSION     CF278001.1  GI:33655387
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--03-L21"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3005
CF278001/c
LOCUS       CF278001                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--03-L21.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--03-L21, mRNA sequence.
ACCESSION   CF278001
VERSION     CF278001.1  GI:33655387
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
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                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3006
CF278452
LOCUS       CF278452                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-F22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--04-F22, mRNA sequence.
ACCESSION   CF278452
VERSION     CF278452.1  GI:33655838
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
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                     /clone="14ETL--04-F22"
                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
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Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14
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CF278452/c
LOCUS       CF278452                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-F22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--04-F22, mRNA sequence.
ACCESSION   CF278452
VERSION     CF278452.1  GI:33655838
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3008
CF279473
LOCUS       CF279473                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--05-M14.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--05-M14, mRNA sequence.
ACCESSION   CF279473
VERSION     CF279473.1  GI:33656859
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3009
CF279473/c
LOCUS       CF279473                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--05-M14.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--05-M14, mRNA sequence.
ACCESSION   CF279473
VERSION     CF279473.1  GI:33656859
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1
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RESULT 3010
CF279992
LOCUS       CF279992                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--06-I01, mRNA sequence.
ACCESSION   CF279992
VERSION     CF279992.1  GI:33657378
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
             ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14
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RESULT 3011
CF279992/c
LOCUS       CF279992                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--06-I01, mRNA sequence.
ACCESSION   CF279992
VERSION     CF279992.1  GI:33657378
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1
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RESULT 3012
CF281958
LOCUS       CF281958                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-D24.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-D24, mRNA sequence.
ACCESSION   CF281958
VERSION     CF281958.1  GI:33659345
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
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  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3013
CF281958/c
LOCUS       CF281958                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-D24.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-D24, mRNA sequence.
ACCESSION   CF281958
VERSION     CF281958.1  GI:33659345
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3014
CF282350
LOCUS       CF282350                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.
ACCESSION   CF282350
VERSION     CF282350.1  GI:33659737
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3015
CF282350/c
LOCUS       CF282350                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.
ACCESSION   CF282350
VERSION     CF282350.1  GI:33659737
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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(14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2799
||||||||||||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 3016
CF294449
LOCUS CF294449 14 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--03-P15, mRNA sequence.
ACCESSION CF294449
VERSION CF294449.1 GI:33663482
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTT 2179
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Db 1 TTTTTTTTTTTTTT 14

RESULT 3017
CF294449/c
LOCUS CF294449 14 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--03-P15, mRNA sequence.
ACCESSION CF294449
VERSION CF294449.1 GI:33663482
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--03-P15"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2799
||||||||||||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 3018
CF295570
LOCUS CF295570 14 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--05-J06.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--05-J06, mRNA sequence.
ACCESSION CF295570
VERSION CF295570.1 GI:33664603
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--05-J06"
/tissue_type="leaf"
/dev_stage="30 days after germination"

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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3019
CF295570/c
LOCUS       CF295570                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-J06.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-J06, mRNA sequence.
ACCESSION   CF295570
VERSION     CF295570.1  GI:33664603
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="30DGS--05-J06"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3020
CF296120
LOCUS       CF296120                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--06-F17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--06-F17, mRNA sequence.
ACCESSION   CF296120
VERSION     CF296120.1  GI:33665153
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3021
CF296120/c
LOCUS       CF296120                  14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--06-F17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--06-F17, mRNA sequence.
ACCESSION   CF296120
VERSION     CF296120.1  GI:33665153
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /dev_stage="30 days after germination"
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3022
CF297969
LOCUS       CF297969                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-C16, mRNA sequence.
ACCESSION   CF297969
VERSION     CF297969.1  GI:33669730
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTTT 14


RESULT 3023
CF297969/c
LOCUS       CF297969                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-C16, mRNA sequence.
ACCESSION   CF297969
VERSION     CF297969.1  GI:33669730
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
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Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3024
CF298109
LOCUS       CF298109                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-F19, mRNA sequence.
ACCESSION   CF298109
VERSION     CF298109.1  GI:33669870
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3025
CF298109/c
LOCUS       CF298109                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-F19, mRNA sequence.
ACCESSION   CF298109
VERSION     CF298109.1  GI:33669870
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3026
CF299368
LOCUS       CF299368                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-F21, mRNA sequence.
ACCESSION   CF299368
VERSION     CF299368.1  GI:33671129
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3027
CF299368/c
LOCUS       CF299368                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-F21, mRNA sequence.
ACCESSION   CF299368
VERSION     CF299368.1  GI:33671129
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3028
CF300542
LOCUS       CF300542                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION   CF300542
VERSION     CF300542.1  GI:33672303
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-B01"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3029
CF300542/c
LOCUS       CF300542                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION   CF300542
VERSION     CF300542.1  GI:33672303
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-B01"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3030
CF301020
LOCUS       CF301020                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
ACCESSION   CF301020
VERSION     CF301020.1  GI:33672781
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3031
CF301020/c
LOCUS       CF301020                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
ACCESSION   CF301020
VERSION     CF301020.1  GI:33672781
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3032
CF301083
LOCUS       CF301083                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-M19, mRNA sequence.
ACCESSION   CF301083
VERSION     CF301083.1  GI:33672844
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-M19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3033
CF301083/c
LOCUS       CF301083                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-M19, mRNA sequence.
ACCESSION   CF301083
VERSION     CF301083.1  GI:33672844
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3034
CF301380
LOCUS       CF301380                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-D16, mRNA sequence.
ACCESSION   CF301380
VERSION     CF301380.1  GI:33673141
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--06-D16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2179
              |||||||||||||
Db          1 TTTTTTTTTTTTT 14


RESULT 3035
CF301380/c
LOCUS       CF301380                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-D16, mRNA sequence.
ACCESSION   CF301380
VERSION     CF301380.1  GI:33673141
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3036
CF302675
LOCUS       CF302675                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-G18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-G18, mRNA sequence.
ACCESSION   CF302675
VERSION     CF302675.1  GI:33674436
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
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                     /mol_type="mRNA"
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3037
CF302675/c
LOCUS       CF302675                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-G18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-G18, mRNA sequence.
ACCESSION   CF302675
VERSION     CF302675.1  GI:33674436
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3038
CF302846
LOCUS       CF302846                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-M05, mRNA sequence.
ACCESSION   CF302846
VERSION     CF302846.1  GI:33674607
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTTT 14


RESULT 3039
CF302846/c
LOCUS       CF302846                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-M05, mRNA sequence.
ACCESSION   CF302846
VERSION     CF302846.1  GI:33674607
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

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Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3040
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LOCUS       CF308006                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-K10, mRNA sequence.
ACCESSION   CF308006
VERSION     CF308006.1  GI:33679767
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3041
CF308006/c
LOCUS       CF308006                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-K10, mRNA sequence.
ACCESSION   CF308006
VERSION     CF308006.1  GI:33679767
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3042
CF308220
LOCUS       CF308220                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.
ACCESSION   CF308220
VERSION     CF308220.1  GI:33679981
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
```

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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /mol_type="mRNA"
                      /cultivar="Nackdong"
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                      /clone_lib="ABF3-overexpressing transgenic rice plasmid
                      cDNA library (ABF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                      for 2hrs. Oligo-capped mRNA was reverse transcribed and
                      then used for PCR. mRNA was prepared from ABA-responsive
                      element binding transcription factor 3 overexpression
                      line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3043
CF308220/c
LOCUS       CF308220                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.
ACCESSION   CF308220
VERSION     CF308220.1  GI:33679981
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      cDNA library (ABF)"
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                      for 2hrs. Oligo-capped mRNA was reverse transcribed and
                      then used for PCR. mRNA was prepared from ABA-responsive
                      element binding transcription factor 3 overexpression
                      line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3044
CF308445
LOCUS       CF308445                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.
ACCESSION   CF308445
VERSION     CF308445.1  GI:33680206
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                      /dev_stage="14 days after germination"
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                      /clone_lib="ABF3-overexpressing transgenic rice plasmid
                      cDNA library (ABF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                      element binding transcription factor 3 overexpression
                      line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3045
CF308445/c
LOCUS       CF308445                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.
ACCESSION   CF308445
VERSION     CF308445.1  GI:33680206
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
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           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1  (bases 1 to 14)
  AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE    Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL  Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3046
CF308918
LOCUS      CF308918                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
           library (ABF) Oryza sativa cDNA clone ABF--02-O16, mRNA sequence.
ACCESSION  CF308918
VERSION    CF308918.1  GI:33680679
KEYWORDS   EST.
SOURCE     Oryza sativa
  ORGANISM Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1  (bases 1 to 14)
  AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE    Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL  Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3047
CF308918/c
LOCUS      CF308918                 14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
           library (ABF) Oryza sativa cDNA clone ABF--02-O16, mRNA sequence.
ACCESSION  CF308918
VERSION    CF308918.1  GI:33680679
KEYWORDS   EST.
SOURCE     Oryza sativa
  ORGANISM Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1  (bases 1 to 14)
  AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  JOURNAL  Unpublished (2003)
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           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
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Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1
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RESULT 3048
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LOCUS       CF310714                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-I11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--05-I11, mRNA sequence.
ACCESSION   CF310714
VERSION     CF310714.1  GI:33682475
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3049
CF310714/c
LOCUS       CF310714                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-I11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--05-I11, mRNA sequence.
ACCESSION   CF310714
VERSION     CF310714.1  GI:33682475
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--05-I11"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3050
CF311201
LOCUS       CF311201                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-F09, mRNA sequence.
ACCESSION   CF311201
VERSION     CF311201.1  GI:33682962
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
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  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3051
CF311201/c
LOCUS       CF311201                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-F09, mRNA sequence.
ACCESSION   CF311201
VERSION     CF311201.1  GI:33682962
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--06-F09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3052
CF311813
LOCUS       CF311813                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.
ACCESSION   CF311813
VERSION     CF311813.1  GI:33683574
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3053
CF311813/c
LOCUS       CF311813                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.
ACCESSION   CF311813
VERSION     CF311813.1  GI:33683574
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--07-D22"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2799
||||||||||||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 3054
CF318323
LOCUS CF318323 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--08-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-G13, mRNA sequence.
ACCESSION CF318323
VERSION CF318323.1 GI:33690084
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTT 2179
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Db 1 TTTTTTTTTTTTTT 14

RESULT 3055
CF318323/c
LOCUS CF318323 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--08-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-G13, mRNA sequence.
ACCESSION CF318323
VERSION CF318323.1 GI:33690084
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/clone="HD--08-G13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2799
||||||||||||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 3056
CF318450
LOCUS CF318450 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--08-J08.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-J08, mRNA sequence.
ACCESSION CF318450
VERSION CF318450.1 GI:33690211
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea

```
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--08-J08"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3057
CF318450/c
LOCUS       CF318450                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-J08.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--08-J08, mRNA sequence.
ACCESSION   CF318450
VERSION     CF318450.1  GI:33690211
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--08-J08"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3058
CF319826
LOCUS       CF319826                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-H16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.
ACCESSION   CF319826
VERSION     CF319826.1  GI:33691587
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3059
CF319826/c
LOCUS       CF319826                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-H16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.
ACCESSION   CF319826
VERSION     CF319826.1  GI:33691587
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3060
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LOCUS       CF321246                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--12-G24.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--12-G24, mRNA sequence.
ACCESSION   CF321246
VERSION     CF321246.1  GI:33693007
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  JOURNAL   Unpublished (2003)
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
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                     line."

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Qy       2166 TTTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTTT 14


RESULT 3061
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LOCUS       CF321246                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--12-G24.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--12-G24, mRNA sequence.
ACCESSION   CF321246
VERSION     CF321246.1  GI:33693007
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     derived from rice Histone Deacetylase overexpression
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3062
CF327097
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LOCUS       CF327097                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-H01, mRNA sequence.
ACCESSION   CF327097
VERSION     CF327097.1  GI:33802449
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
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Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3063
CF327097/c
LOCUS       CF327097                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-H01, mRNA sequence.
ACCESSION   CF327097
VERSION     CF327097.1  GI:33802449
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Db         14 AAAAAAAAAAAAAA 1


RESULT 3064
CF327119
LOCUS       CF327119                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-H14, mRNA sequence.
ACCESSION   CF327119
VERSION     CF327119.1  GI:33802493
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Qy       2166 TTTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTTT 14


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CF327119/c
LOCUS       CF327119                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF327119
VERSION     CF327119.1  GI:33802493
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3066
CF327445
LOCUS       CF327445                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF327445
VERSION     CF327445.1  GI:33803149
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Db          1 TTTTTTTTTTTTTT 14


RESULT 3067
CF327445/c
LOCUS       CF327445                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF327445
VERSION     CF327445.1  GI:33803149
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Db         14 AAAAAAAAAAAAAA 1
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RESULT 3068
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LOCUS       CF328490                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF328490
VERSION     CF328490.1  GI:33805226
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3069
CF328490/c
LOCUS       CF328490                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF328490
VERSION     CF328490.1  GI:33805226
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          14 AAAAAAAAAAAAAA 1


RESULT 3070
CF328540
LOCUS       CF328540                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-H24, mRNA sequence.
ACCESSION   CF328540
VERSION     CF328540.1  GI:33805324
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-H24"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTTT 14
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CF328540/c
LOCUS       CF328540                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-H24, mRNA sequence.
ACCESSION   CF328540
VERSION     CF328540.1  GI:33805324
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="NACL--03-H24"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3072
CF328669
LOCUS       CF328669                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-K23, mRNA sequence.
ACCESSION   CF328669
VERSION     CF328669.1  GI:33805587
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3073
CF328669/c
LOCUS       CF328669                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-K23, mRNA sequence.
ACCESSION   CF328669
VERSION     CF328669.1  GI:33805587
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1
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RESULT 3074
CF328994
LOCUS       CF328994                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-C11, mRNA sequence.
ACCESSION   CF328994
VERSION     CF328994.1  GI:33806228
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3075
CF328994/c
LOCUS       CF328994                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-C11, mRNA sequence.
ACCESSION   CF328994
VERSION     CF328994.1  GI:33806228
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3076
CF329217
LOCUS       CF329217                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-H10, mRNA sequence.
ACCESSION   CF329217
VERSION     CF329217.1  GI:33806672
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTTT 14


RESULT 3077
CF329217/c
LOCUS       CF329217                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-H10, mRNA sequence.
ACCESSION   CF329217
VERSION     CF329217.1  GI:33806672
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3078
CF329990
LOCUS       CF329990                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-I11, mRNA sequence.
ACCESSION   CF329990
VERSION     CF329990.1  GI:33808202
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 3079
CF329990/c
LOCUS       CF329990                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF329990
VERSION     CF329990.1  GI:33808202
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
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Db         14 TTTTTTTTTTTTTT 1


RESULT 3080
CF330784
LOCUS       CF330784                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-K10, mRNA sequence.
ACCESSION   CF330784
VERSION     CF330784.1  GI:33809790
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3081
CF330784/c
LOCUS       CF330784                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-K10, mRNA sequence.
ACCESSION   CF330784
VERSION     CF330784.1  GI:33809790
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-K10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          14 AAAAAAAAAAAAAA 1


RESULT 3082
CF331272
LOCUS       CF331272                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION   CF331272
VERSION     CF331272.1  GI:33810755
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--07-F09"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3083
CF331272/c
LOCUS       CF331272                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION   CF331272
VERSION     CF331272.1  GI:33810755
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--07-F09"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3084
CF331861
LOCUS       CF331861                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-C10, mRNA sequence.
ACCESSION   CF331861
VERSION     CF331861.1  GI:33811945
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3085
CF331861/c
LOCUS       CF331861                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-C10, mRNA sequence.
ACCESSION   CF331861
VERSION     CF331861.1  GI:33811945
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /cultivar="Nackdong"
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                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3086
CF333214
LOCUS       CF333214                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-A10.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
ACCESSION   CF333214
VERSION     CF333214.1  GI:33814707
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
             ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3087
CF333214/c
LOCUS       CF333214                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-A10.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
ACCESSION   CF333214
VERSION     CF333214.1  GI:33814707
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3088
CF333215
LOCUS       CF333215                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
ACCESSION   CF333215
VERSION     CF333215.1  GI:33814709
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAA 2799
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Db          1 AAAAAAAAAAAAAA 14
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RESULT 3089
CF333215/c
LOCUS CF333215 14 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
ACCESSION CF333215
VERSION CF333215.1 GI:33814709
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/organism="Oryza sativa"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTT 2179
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Db         14 TTTTTTTTTTTTTT 1
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RESULT 3090
CF333399
LOCUS CF333399 14 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-E12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-E12, mRNA sequence.
ACCESSION CF333399
VERSION CF333399.1 GI:33815074
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/organism="Oryza sativa"
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/tissue_type="leaf"
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTT 2179
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Db          1 TTTTTTTTTTTTTT 14
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RESULT 3091
CF333399/c
LOCUS CF333399 14 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-E12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-E12, mRNA sequence.
ACCESSION CF333399
VERSION CF333399.1 GI:33815074
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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                     /clone="JMT--02-E12"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
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Qy       2786 AAAAAAAAAAAAAA 2799
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Db         14 AAAAAAAAAAAAAA 1


RESULT 3092
CF334202
LOCUS       CF334202                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-G11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-G11, mRNA sequence.
ACCESSION   CF334202
VERSION     CF334202.1  GI:33816736
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3093
CF334202/c
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LOCUS       CF334202                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-G11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-G11, mRNA sequence.
ACCESSION   CF334202
VERSION     CF334202.1  GI:33816736
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="14 days after germination"
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                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3094
CF334281
LOCUS       CF334281                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-I05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-I05, mRNA sequence.
ACCESSION   CF334281
VERSION     CF334281.1  GI:33816894
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
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           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--03-I05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3095
CF334281/c
LOCUS       CF334281                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-I05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-I05, mRNA sequence.
ACCESSION   CF334281
VERSION     CF334281.1  GI:33816894
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3096
CF334290
LOCUS       CF334290                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-I11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-I11, mRNA sequence.
ACCESSION   CF334290
VERSION     CF334290.1  GI:33816914
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="14 days after germination"
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                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3097
CF334290/c
LOCUS       CF334290                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-I11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-I11, mRNA sequence.
ACCESSION   CF334290
VERSION     CF334290.1  GI:33816914
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3098
CF335781
LOCUS       CF335781                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--05-J13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--05-J13, mRNA sequence.
ACCESSION   CF335781
VERSION     CF335781.1  GI:33819936
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3099
CF335781/c
LOCUS       CF335781                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--05-J13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--05-J13, mRNA sequence.
ACCESSION   CF335781
VERSION     CF335781.1  GI:33819936
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3100
CF336094
LOCUS       CF336094                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-A10, mRNA sequence.
ACCESSION   CF336094
VERSION     CF336094.1  GI:33820566
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="14 days after germination"
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3101
CF336094/c
LOCUS       CF336094                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-A10, mRNA sequence.
ACCESSION   CF336094
VERSION     CF336094.1  GI:33820566
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3102
CF336106
LOCUS       CF336106                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-A17.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-A17, mRNA sequence.
ACCESSION   CF336106
VERSION     CF336106.1  GI:33820590
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
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Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3103
CF336106/c
LOCUS       CF336106                 14 bp    mRNA    linear   EST 18-AUG-2003
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DEFINITION  JMT--06-A17.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-A17, mRNA sequence.
ACCESSION   CF336106
VERSION     CF336106.1  GI:33820590
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

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Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3104
CF336287
LOCUS       CF336287                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-E15.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.
ACCESSION   CF336287
VERSION     CF336287.1  GI:33820962
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3105
CF336287/c
LOCUS       CF336287                 14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-E15.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.
ACCESSION   CF336287
VERSION     CF336287.1  GI:33820962
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
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              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3106
CF336906
LOCUS       CF336906                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--07-C05, mRNA sequence.
ACCESSION   CF336906
VERSION     CF336906.1  GI:33822182
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
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                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3107
CF336906/c
LOCUS       CF336906                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--07-C05, mRNA sequence.
ACCESSION   CF336906
VERSION     CF336906.1  GI:33822182
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3108
CF295100/c
LOCUS       CF295100                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--04-O02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--04-O02, mRNA sequence.
ACCESSION   CF295100
VERSION     CF295100.1  GI:33664133
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
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  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3109
CF296652
LOCUS       CF296652                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--07-C02, mRNA sequence.
ACCESSION   CF296652
VERSION     CF296652.1  GI:33665685
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3110
CF296652/c
LOCUS       CF296652                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--07-C02, mRNA sequence.
ACCESSION   CF296652
VERSION     CF296652.1  GI:33665685
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3111
CF329379
LOCUS       CF329379                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-K23, mRNA sequence.
ACCESSION   CF329379
VERSION     CF329379.1  GI:33806995
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
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  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          2 TTTTTTTTTTTTTT 15


RESULT 3112
CF329379/c
LOCUS       CF329379                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-K23, mRNA sequence.
ACCESSION   CF329379
VERSION     CF329379.1  GI:33806995
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         15 AAAAAAAAAAAAAA 2


RESULT 3113
CF291803/c
LOCUS       CF291803                 16 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION   CF291803
VERSION     CF291803.1  GI:33660836
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-G05"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         16 TTTTTTTTTTTTTT 3


RESULT 3114
AW250784
LOCUS       AW250784                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822335.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822335 3',
            mRNA sequence.
ACCESSION   AW250784
VERSION     AW250784.1  GI:6593777
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822335.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence.
            Plate: LLCM9  row: C  column: 8.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:2822335"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||   ||||||||||||
Db          1 TTNNNTTTTTTTTTTT 17
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RESULT 3115
AW250784/c
LOCUS AW250784 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2822335.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822335 3', mRNA sequence.
ACCESSION AW250784
VERSION AW250784.1 GI:6593777
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2822335.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence.
Plate: LLCM9 row: C column: 8.
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822335"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||   ||
Db         17 AAAAAAAAAAAANNNAA 1
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RESULT 3116
BG673623/c
LOCUS BG673623 17 bp mRNA linear EST 30-APR-2001
DEFINITION DRNAAQC09 Rat DRG Library Rattus norvegicus cDNA clone DRNAAQC09 5', mRNA sequence.
ACCESSION BG673623
VERSION BG673623.1 GI:13895722
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 17)
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C., Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D., Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
TITLE Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
MEDLINE 22056133
PUBMED 12060780
COMMENT Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR PRimers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA=No.
FEATURES Location/Qualifiers
source 1. .17
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRNAAQC09"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2175 TTTTTTTTTTTTAA 2188
              ||||||||||||||
Db         17 TTTTTTTTTTTTAA 4
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RESULT 3117

```
AZ465954/c
LOCUS       AZ465954                19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0276E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0276E16 F, genomic survey sequence.
ACCESSION   AZ465954
VERSION     AZ465954.1  GI:10624079
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0276  row: E  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0276E16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         19 AAAAAAAAAAAAAA 6


RESULT 3118
AZ856873
```

```
LOCUS       AZ856873                19 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0161O19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0161O19 F, genomic survey sequence.
ACCESSION   AZ856873
VERSION     AZ856873.1  GI:13048296
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0161  row: O  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0161O19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3119
AZ950028/c
LOCUS       AZ950028                19 bp    DNA     linear   GSS 27-APR-2001
```

```
DEFINITION  2M0213L19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0213L19 R, genomic survey sequence.
ACCESSION   AZ950028
VERSION     AZ950028.1  GI:13821255
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0213  row: L  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0213L19"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         19 TTTTTTTTTTTTTT 6


RESULT 3120
CF332005/c
LOCUS       CF332005                  19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-F13.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-F13, mRNA sequence.
ACCESSION   CF332005
VERSION     CF332005.1  GI:33812230
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-F13"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||||||||
Db         14 GAAAAAAAAAAAAA 1


RESULT 3121
CF313751
LOCUS       CF313751                  20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-P23.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.
ACCESSION   CF313751
VERSION     CF313751.1  GI:33685512
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
```

```
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--01-P23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
             ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3122
CF313752/c
LOCUS       CF313752                  20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-P23.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.
ACCESSION   CF313752
VERSION     CF313752.1  GI:33685513
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--01-P23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
             ||||||||||||||
Db          20 TTTTTTTTTTTTTT 7


RESULT 3123
AZ785791
LOCUS       AZ785791                  21 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0030O19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0030O19 F, genomic survey sequence.
ACCESSION   AZ785791
VERSION     AZ785791.1  GI:12922904
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0030  row: O  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0030O19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
             ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14
```

```
RESULT 3124
AZ375417
LOCUS       AZ375417                 22 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0128E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0128E13 R, genomic survey sequence.
ACCESSION   AZ375417
VERSION     AZ375417.1  GI:10489117
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0128  row: E  column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0128E13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          7 AAAAAAAAAAAAAA 20
```

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RESULT 3125
AZ854229
LOCUS       AZ854229                 22 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0157C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0157C14 R, genomic survey sequence.
ACCESSION   AZ854229
VERSION     AZ854229.1  GI:13043139
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0157  row: C  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0157C14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 14;  DB 1;  Length 22;
  Best Local Similarity   77.3%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2800
              | ||  || |||| ||||||||
Db          1 AAAAGAGAGAAAAGAAAAAAA 22
```

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RESULT 3126
CF196152/c
LOCUS       CF196152                 22 bp    mRNA    linear   EST 31-JUL-2003
DEFINITION  Azvi1.2_E03 AZ-VI Oryza sativa (japonica cultivar-group) cDNA clone
            AZ-VI1.2E03 5', mRNA sequence.
ACCESSION   CF196152
VERSION     CF196152.1  GI:33380809
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Ventelon-Debout,M., Thi-Thu Huang,N., Wissocq,A., Berger,C.,
            Michele,L., Piegu,B., Cooke,R., Ghesquiere,A., Delseny,M. and
            Brugidou,C.
  TITLE     Metabolism and Photosynthesis gene expression is affected in
            response to rice yellow mottle virus infection in Oryza sativa
            indica and japonica culltivars
  JOURNAL   Mol. Genet. Genomics (2003) In press
COMMENT     Contact: Brugidou C
            IRD
            BP 64501, 34394 Montpellier cedex 5 France
            Tel: 33 4 67 41 67 39
            Fax: 33 4 67 41 61 81
            PCR PRimers
            FORWARD: 5'AATTAACCCTCACTAAAGGG3'
            BACKWARD: 5'CGGGATATCACTCAGCATAATG3'
            Plate: 1.2  row: E  column: 3.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Azucena"
                     /db_xref="taxon:39947"
                     /clone="AZ-VI1.2E03"
                     /tissue_type="leaves"
                     /dev_stage="3 weeks-old plants"
                     /lab_host="SOLR strain (Stratagene)"
                     /clone_lib="AZ-VI"
                     /note="Vector: pBluescript SK (+/-); Site_1: Eco RI;
                     Site_2: Xho I; Sample name: AZ-VI; Plant growth place:
                     greenhouse; Soil conditions: standard; Sowing date:
                     28/02/2000; Harvesting date: 18/03/2000; Stress date:
                     15/03/2000; Cultivar: azucena; Description: Az-RYMV
                     inoculated leaves cDNA library; experimental condition:
                     rymv inoculation;"

  Query Match             0.5%;  Score 14;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              ||   ||||||||||||
Db         17 TTNNNAAAAAAAAAAAA 1


RESULT 3127
AU267617/c
LOCUS       AU267617                 23 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU267617 VS Dictyostelium discoideum cDNA clone VSH555 5', mRNA
            sequence.
ACCESSION   AU267617
VERSION     AU267617.1  GI:20526415
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSH555"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.5%;  Score 14;  DB 1;  Length 23;
  Best Local Similarity   77.3%;  Pred. No. 3.8e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTAACTTTGAA 2195
              ||||||||||  |||  ||  ||
Db         23 TTTTTTTTTACTAAATTCTAA 2


RESULT 3128
CF295238/c
LOCUS       CF295238                 24 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-B07.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-B07, mRNA sequence.
ACCESSION   CF295238
VERSION     CF295238.1  GI:33664271
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--05-B07"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 14;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         24 AAAAAAAAAAAAAA 11


RESULT 3129
CNS00HLD/c
LOCUS       CNS00HLD                  24 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR35D24 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL073529
VERSION     AL073529.1  GI:4953410
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR35D24"
                     /clone_lib="RPCI-98"
                     /note="end : T7"

  Query Match             0.5%;  Score 14;  DB 1;  Length 24;
  Best Local Similarity   78.9%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||| : |||| |||
Db         23 AAAAAAAANHBAAAACAAA 5


RESULT 3130
AU012885
LOCUS       AU012885                  25 bp    mRNA    linear   EST 03-AUG-1998
DEFINITION  AU012885 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc07426, mRNA sequence.
ACCESSION   AU012885
VERSION     AU012885.1  GI:3357794
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Schizosaccharomyces pombe"
                     /mol_type="mRNA"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc07426"
                     /sex="h minus"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"

  Query Match             0.5%;  Score 14;  DB 1;  Length 25;
  Best Local Similarity   77.3%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAA 2802
              || | |||   ||||||||||
Db          4 AACTCAAAGCTAAAAAAAAAA 25


RESULT 3131
AZ510128
LOCUS       AZ510128                  25 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0354L23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0354L23 F, genomic survey sequence.
ACCESSION   AZ510128
VERSION     AZ510128.1  GI:10691444
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0354  row: L  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0354L23"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14; DB 1; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2804
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Db          1 TTAAAAAAAAAAAAACCATACA 22
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RESULT 3132
AZ997733
LOCUS AZ997733 25 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0284E22F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0284E22 F, genomic survey sequence.
ACCESSION AZ997733
VERSION AZ997733.1 GI:13868960
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0284 row: E column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
FEATURES Location/Qualifiers
source 1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0284E22"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAA 2799
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Db          1 AAAAAAAAAAAAAA 14
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RESULT 3133
AW246446
LOCUS AW246446 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821601.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821601 3', mRNA sequence.
ACCESSION AW246446
VERSION AW246446.1 GI:6589439
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821601.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 9 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: D column: 18
High quality sequence stop: 9.
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:2821601"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1922 TTTTTTTTCAGTGTTAA 1938
|||||||| |||||||
Db 1 TTTTTTTTTTGTGTTAA 17

RESULT 3134
AW247949
LOCUS AW247949 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2820605.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820605 3', mRNA sequence.
ACCESSION AW247949
VERSION AW247949.1 GI:6591037
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2820605.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM4 row: K column: 6.
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820605"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2182
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Db 1 TTTTTTTTTTACTTTTT 17

RESULT 3135
AW247949/c
LOCUS AW247949 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2820605.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820605 3', mRNA sequence.
ACCESSION AW247949
VERSION AW247949.1 GI:6591037
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2820605.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM4 row: K column: 6.
FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820605"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||  ||||||||||
Db         17 AAAAAGTAAAAAAAAAA 1


RESULT 3136
AW247976
LOCUS       AW247976                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820717.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820717 3',
            mRNA sequence.
ACCESSION   AW247976
VERSION     AW247976.1  GI:6591064
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820717.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM4  row: O  column: 22.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820717"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAACTTTG 2193
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Db          1 TTTTTTTTTTAACAATG 17


RESULT 3137
AW248779/c
LOCUS       AW248779                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821015.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821015 3',
            mRNA sequence.
ACCESSION   AW248779
VERSION     AW248779.1  GI:6591772
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821015.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM5  row: L  column: 8.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:2821015"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAA 2794
              |||  ||||||||||||
Db         17 TAGGCTTGAAAAAAAAA 1


RESULT 3138
BQ797972
LOCUS       BQ797972                 17 bp    mRNA    linear   EST 30-JUL-2002
DEFINITION  EST 6910 Ripening Grape berries Lambda Zap II Library Vitis
            vinifera cDNA clone RT092F02 3', mRNA sequence.
ACCESSION   BQ797972
VERSION     BQ797972.1  GI:22012938
KEYWORDS    EST.
SOURCE      Vitis vinifera
  ORGANISM  Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
```

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REFERENCE   1  (bases 1 to 17)
  AUTHORS   Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
  TITLE     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Romieu C.
            Unite de Recherche des Produits de la Vigne
            Institut National de la Recherche Agronomique
            2, place Viala, 34 060 Montpellier Cedex 01, France
            Tel: 00-33-(0)4-99-61-28-62
            Fax: 00-33-(0)4-99-61-28-57
            Email: romieu@ensam.inra.fr
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Vitis vinifera"
                     /mol_type="mRNA"
                     /cultivar="Shiraz"
                     /db_xref="taxon:29760"
                     /clone="RT092F02"
                     /dev_stage="ripening stage"
                     /clone_lib="Ripening Grape berries Lambda Zap II Library"
                     /note="Organ: Fruit; Vector: Lambda Zap II; Site_1: Eco
                     RI; Site_2: XhoI; Oriented library, construction described
                     in Generation of ESTs from grape Berry (skin, pulp or
                     seeds) at various developmental stages by Terrier,N.,
                     Ageorges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158
                     (12): 1575-83 2001"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1129 TGAAGCCGAATTTCCTA 1145
              ||||||| ||||||||
Db          1 TGAAGCCCCATTTCCTA 17


RESULT 3139
AW249856
LOCUS       AW249856                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821566.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821566 3',
            mRNA sequence.
ACCESSION   AW249856
VERSION     AW249856.1  GI:6592849
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821566.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 18 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM7  row: C  column: 7
            High quality sequence stop: 9.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821566"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||||||  |||  ||
Db          1 TTTTTTTTTTNTTTGCTT 18


RESULT 3140
AW249856/c
LOCUS       AW249856                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821566.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821566 3',
            mRNA sequence.
ACCESSION   AW249856
VERSION     AW249856.1  GI:6592849
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821566.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 18 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM7  row: C  column: 7
            High quality sequence stop: 9.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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```
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821566"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
                ||  ||| ||||||||||
Db         18 AAGCAAANAAAAAAAAAA 1


RESULT 3141
AW250449
LOCUS       AW250449                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822458.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822458 3',
            mRNA sequence.
ACCESSION   AW250449
VERSION     AW250449.1  GI:6593442
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822458.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 18
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 18 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM9  row: H  column: 11
            High quality sequence stop: 18.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822458"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAACTTTG 2193
                ||||||||||  |||||
Db          1 TTTTTTTTTTCCCTTTG 17


RESULT 3142
AZ924200/c
LOCUS       AZ924200                 18 bp    DNA     linear   GSS 01-APR-2001
DEFINITION  4906.ic27n17.s1 Saccharomyces mikatae IFO 1815 Saccharomyces
            mikatae genomic clone 4906.ic27n17.s1, genomic survey sequence.
ACCESSION   AZ924200
VERSION     AZ924200.1  GI:13495098
KEYWORDS    GSS.
SOURCE      Saccharomyces mikatae
  ORGANISM  Saccharomyces mikatae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cliften,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T.,
            Gish,W.R., Waterston,R.H. and Johnston,M.
  TITLE     Surveying Saccharomyces genomes to identify functional elements by
            comparative DNA sequence analysis
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Johnston M
            Department of Genetics
            Washington University Medical School
            Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
            Tel: 314 362 2735
            Fax: 314 362 7855
            Email: mj@genetics.wustl.edu
            Class: random plasmid subclone.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Saccharomyces mikatae"
                     /mol_type="genomic DNA"
                     /strain="IFO 1815"
                     /db_xref="taxon:114525"
                     /clone="4906.ic27n17.s1"
                     /clone_lib="Saccharomyces mikatae IFO 1815"
                     /note="Random genomic sequence "

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAA 2188
                ||||||||  | ||||||
Db         17 TTTTTTTGTCTTTTAA 1


RESULT 3143
CF295672/c
LOCUS       CF295672                 19 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-L12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-L12, mRNA sequence.
ACCESSION   CF295672
VERSION     CF295672.1  GI:33664705
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="30DGS--05-L12"
                      /tissue_type="leaf"
                      /dev_stage="30 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              ||  ||||||||||||||
Db         17 TGTTAAAAAAAAAAAAA 1


RESULT 3144
AZ323986
LOCUS       AZ323986                 19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0045P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0045P09 R, genomic survey sequence.
ACCESSION   AZ323986
VERSION     AZ323986.1  GI:10379252
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0045  row: P  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0045P09"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||  ||| ||||
Db          3 CCTTTTTTGTTTGTTTT 19


RESULT 3145
AZ854647/c
LOCUS       AZ854647                 19 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0158P15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0158P15 F, genomic survey sequence.
ACCESSION   AZ854647
VERSION     AZ854647.1  GI:13043971
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0158  row: P  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0158P15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              | |||||||||||| |||
Db         17 GGGGCGGGGGCGGGGGC 1


RESULT 3146
AZ304038
LOCUS       AZ304038                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0003L08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0003L08 R, genomic survey sequence.
ACCESSION   AZ304038
VERSION     AZ304038.1  GI:10339611
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0003  row: L  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0003L08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              |||||| ||||| ||||
Db          1 TTTTTTCTTTTATCTTT 17


RESULT 3147
AZ469472
LOCUS       AZ469472                 20 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0283A06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0283A06 F, genomic survey sequence.
ACCESSION   AZ469472
VERSION     AZ469472.1  GI:10627597
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0283  row: A  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
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                     /db_xref="taxon:10090"
                     /clone="UUGC1M0283A06"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTT 2177
              ||| ||||| |||||||
Db          4 TCTGCTTTTGTTTTTTT 20


RESULT 3148
AZ512414
LOCUS       AZ512414                 20 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0357J21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0357J21 R, genomic survey sequence.
ACCESSION   AZ512414
VERSION     AZ512414.1  GI:10693730
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0357  row: J  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0357J21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         49 GCGCGGCGGGGGCGGCG 65
              | |||||||||||||  |
Db          4 GGGCGGCGGGGGCGGGG 20


RESULT 3149
AZ331619
LOCUS       AZ331619                 21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0059K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0059K09 R, genomic survey sequence.
ACCESSION   AZ331619
VERSION     AZ331619.1  GI:10394486
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0059  row: K  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0059K09"
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                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              || |||||||||||  ||
Db          5 TTTAAAAAAAAAAACAA 21


RESULT 3150
AZ788269/c
LOCUS       AZ788269                 21 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0035D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0035D18 F, genomic survey sequence.
ACCESSION   AZ788269
VERSION     AZ788269.1  GI:12927898
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0035  row: D  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0035D18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1851 CCAACAGACCCACACAC 1867
              || ||| ||||||||||
Db         19 CCTACACACCCACACAC 3


RESULT 3151
AZ386904/c
LOCUS       AZ386904                 21 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0146C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0146C12 F, genomic survey sequence.
ACCESSION   AZ386904
VERSION     AZ386904.1  GI:10500604
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0146  row: C  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0146C12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.8; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1941 TAATGGTTGGTTTTTGT 1957
              | |||||||||||  |||
Db         17 TCATGGTTGGTTTGTGT 1

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RESULT 3152
AW249550/c
LOCUS AW249550 23 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821204.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821204 3', mRNA sequence.
ACCESSION AW249550
VERSION AW249550.1 GI:6592543
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 23)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821204.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washingtion Genome Center. Vector Trimming: cross_match from University of Washingtion Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 9 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 23 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM6 row: D column: 5
High quality sequence stop: 9.
FEATURES Location/Qualifiers
source 1. .23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821204"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.8; DB 1; Length 23;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2781 AATTGAAAAAAAAAAAA 2797
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Db         17 AATTGTTAAAAAAAAAA 1

```

RESULT 3153
AI560179
LOCUS AI560179 25 bp mRNA linear EST 24-MAR-1999
DEFINITION tq59h01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2213137 3' similar to SW:NU5M_ASCSU P24884 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;contains element MER30 repetitive element ;, mRNA sequence.
ACCESSION AI560179
VERSION AI560179.1 GI:4510520
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2213137"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut1"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

Query Match 0.5%; Score 13.8; DB 1; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||| |||| |||||||
Db          1 AAAACAAAAGAAAAAAA 17
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RESULT 3154
AZ426873
LOCUS AZ426873 20 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0208L05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0208L05 R, genomic survey sequence.
ACCESSION AZ426873
VERSION AZ426873.1 GI:10550886
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0208 row: L column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0208L05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       1979 AAAAAAAGAAAAGTGTGTAT 1998
              ||||||| ||||   |||||
Db          1 AAAAAAAAAAAAAGATGTAT 20
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RESULT 3155
AZ303903/c
LOCUS AZ303903 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0003B18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0003B18 R, genomic survey sequence.
ACCESSION AZ303903
VERSION AZ303903.1 GI:10339339
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: B column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0003B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        450 CCACAGGCAGCCAGCAGCAG 469
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Db         20 CCAAAGGAAGCCAGGAACAG 1


RESULT 3156
AZ387841/c
LOCUS       AZ387841                 20 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0147H24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0147H24 R, genomic survey sequence.
ACCESSION   AZ387841
VERSION     AZ387841.1  GI:10501549
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0147  row: H  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0147H24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
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Db         20 GAAAAAAGAAATGAAAAAGA 1


RESULT 3157
AZ479732
LOCUS       AZ479732                 20 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0300A09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0300A09 R, genomic survey sequence.
ACCESSION   AZ479732
VERSION     AZ479732.1  GI:10639901
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0300  row: A  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0300A09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAACCCCATT 1791
              ||||||||||   |||| ||
Db          1 TTTTTTTTTTTCCCCCTTT 20
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RESULT 3158
AZ645269
LOCUS       AZ645269                 20 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0510B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0510B10 R, genomic survey sequence.
ACCESSION   AZ645269
VERSION     AZ645269.1  GI:11774602
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0510  row: B  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0510B10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCCC 308
              |||| | || |||||| |||
Db          1 CCCCCCCCCCCCCCTCCCCC 20
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RESULT 3159
AZ786781
LOCUS       AZ786781                 20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0032C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0032C05 R, genomic survey sequence.
ACCESSION   AZ786781
VERSION     AZ786781.1  GI:12924886
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0032  row: C  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0032C05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTT 2180
              || | || | ||||||||||
Db          1 TCCCATTATATTTTTTTTT 20
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RESULT 3160
AU267211/c
LOCUS       AU267211                  23 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU267211 VS Dictyostelium discoideum cDNA clone VSH291 5', mRNA
            sequence.
ACCESSION   AU267211
VERSION     AU267211.1  GI:20526009
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSH291"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 3.9e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAACCCCATT 1791
              |||||||||||  |   | |||
Db         23 TTTTTTTTTTGTATACAATT 4


RESULT 3161
CK277017/c
LOCUS       CK277017                  23 bp    mRNA    linear   EST 12-DEC-2003
DEFINITION  EST723095 potato abiotic stress cDNA library Solanum tuberosum cDNA
            clone POADX19 3' end, mRNA sequence.
ACCESSION   CK277017
VERSION     CK277017.1  GI:39833995
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
  TITLE     Generation of ESTs from abiotic stressed potato tissue
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: EST723094
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Clones can be requested from TIGR via potato@tigr.org
            Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="POADX19"
                     /tissue_type="abiotic stress treated leaf and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="potato abiotic stress cDNA library"
                     /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                     supplier: Solanum tuberosum var. Kennebec plants were
                     grown from cuttings on a 16hr light/8 hr dark cycle at 25
                     C for 3-4 weeks. Abiotic stress conditions were applied to
                     four separate sets of plants. Set 1 involved saturation of
                     the soil with 150 mM NaCl and tissues were harvested at
                     following application of the salt stress (leaves: 2hr,
                     6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
                     Set 2 were grown under the standard conditions and then
                     were water stressed by withdrawal of further watering
                     applications. Drought stressed plants were harvested after
                     cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
                     and 5d). Set 3 were grown under the standard conditions
                     and then were cold stressed by placement at 4 C. Cold
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d. Set 4 were grown under the standard conditions and
                     then were heat stressed by placement at 35 C. Heat
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d and 4d and heat-stressed roots were harvested at 6 hr,
                     12 hr, 1 d, and 4d. RNA was isolated from all tissues and
                     equal RNA from each tissue and stress was pooled to
                     construct the cDNA library. RNA sample."

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 23;
  Best Local Similarity   80.0%;  Pred. No. 3.9e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              || | ||||||| ||| |||
Db         21 TTAAGAAAAAAAGAAATAAA 2


RESULT 3162
CF290849
LOCUS       CF290849                  15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION   CF290849
VERSION     CF290849.1  GI:33659882
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-A17"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
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                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||| |||||||||
Db          1 AAAAATAAAAAAAAA 15


RESULT 3163
CF290849/c
LOCUS       CF290849                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION   CF290849
VERSION     CF290849.1  GI:33659882
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||| |||||
Db         15 TTTTTTTTTATTTTT 1


RESULT 3164
CF291030
LOCUS       CF291030                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION   CF291030
VERSION     CF291030.1  GI:33660063
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-E19"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||| |||||||
Db          1 AAAAAAATAAAAAAA 15


RESULT 3165
CF291030/c
LOCUS       CF291030                 15 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION   CF291030
VERSION     CF291030.1  GI:33660063
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-E19"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2180
              ||||||| |||||||
Db         15 TTTTTTTATTTTTTT 1


RESULT 3166
CF301470
LOCUS       CF301470                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-F15, mRNA sequence.
ACCESSION   CF301470
VERSION     CF301470.1  GI:33673231
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--06-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2180
              | ||||||||||||||
Db          1 TGTTTTTTTTTTTT 15


RESULT 3167
CF301470/c
LOCUS       CF301470                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-F15, mRNA sequence.
ACCESSION   CF301470
VERSION     CF301470.1  GI:33673231
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--06-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2800
              ||||||||||||| |
Db         15 AAAAAAAAAAAAACA 1


RESULT 3168
CF330669/c
LOCUS       CF330669                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-H16.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-H16, mRNA sequence.
ACCESSION   CF330669
VERSION     CF330669.1  GI:33809573
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-H16"
                     /tissue_type="callus"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2178 TTTTTTTTTAACTTT 2192
||||||||||| |||
Db 15 TTTTTTTTTAATTTT 1

RESULT 3169
CF543203/c
LOCUS CF543203 15 bp mRNA linear EST 22-SEP-2003
DEFINITION S014679-024-030-D05-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-030-D05 5-PRIME, mRNA sequence.
ACCESSION CF543203
VERSION CF543203.1 GI:34891643
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 30 row: D column: 05
Seq primer: SP6.
FEATURES Location/Qualifiers
source 1. .15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:936579"
/db_xref="taxon:161934"
/clone="024-030-D05"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2175 TTTTTTTTTTTTAAC 2189
||||||||||||| ||
Db 15 TTTTTTTTTTTTGAC 1

RESULT 3170
BQ583458/c
LOCUS BQ583458 16 bp mRNA linear EST 06-DEC-2002
DEFINITION E011979-024-005-J11-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-005-J11 5-PRIME, mRNA sequence.
ACCESSION BQ583458
VERSION BQ583458.1 GI:26113035
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 5 row: J column: 11
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:183240"
/db_xref="taxon:161934"
/clone="024-005-J11"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2162 CTCCTTTTTTTTTTT 2176
| ||||||||||||||
Db 15 CCCCTTTTTTTTTTT 1

RESULT 3171
CF319827/c
LOCUS CF319827 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-H16.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA

```
            library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.
ACCESSION   CF319827
VERSION     CF319827.1  GI:33691588
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-H16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAACTT 2191
              ||||||||||||| ||
Db         15 TTTTTTTTTTAATTT 1


RESULT 3172
BG673623
LOCUS       BG673623                 17 bp    mRNA    linear   EST 30-APR-2001
DEFINITION  DRNAAQC09 Rat DRG Library Rattus norvegicus cDNA clone DRNAAQC09
            5', mRNA sequence.
ACCESSION   BG673623
VERSION     BG673623.1  GI:13895722
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
            Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
            Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
  TITLE     Identification of gene expression profile of dorsal root ganglion
            in the rat peripheral axotomy model of neuropathic pain
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
  MEDLINE   22056133
   PUBMED   12060780
COMMENT     Contact: Zhang Xu
            Laboratory of Sensory System
            Institute of Neuroscience
            320 Yue Yang Road, Shanghai 200031, P.R.China
            Tel: 86-21-64748700-121
            Fax: 86-21-64713446
            Email: xu.zhang@ion.ac.cn
            This clone is also available at Chinese National Human Genome
            Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
            Pudong New Area, P.R.China. Please contact with Zhang Xu
            (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
            PCR PRimers
            FORWARD: T3
            BACKWARD: T7
            Seq primer: T3
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="DRNAAQC09"
                     /sex="male"
                     /tissue_type="dorsal root ganglion"
                     /dev_stage="adult"
                     /clone_lib="Rat DRG Library"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAA 2797
              || |||||||||||||
Db          3 TTTAAAAAAAAAAAA 17


RESULT 3173
AZ803756
LOCUS       AZ803756                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0064M15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0064M15 F, genomic survey sequence.
ACCESSION   AZ803756
VERSION     AZ803756.1  GI:12956079
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0064  row: M  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
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/clone="UUGC2M0064M15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2625 CTTTGTCTCGTTCCT 2639
              ||||| |||||||||
Db          2 CTTTGCCTCGTTCCT 16
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RESULT 3174
AZ810717
LOCUS AZ810717 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0076N24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0076N24 F, genomic survey sequence.
ACCESSION AZ810717
VERSION AZ810717.1 GI:12978242
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: N column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0076N24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAAA 2797
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Db          5 TTGGAAAAAAAAAAA 19
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RESULT 3175
AZ387816/c
LOCUS AZ387816 20 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0147B22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0147B22 R, genomic survey sequence.
ACCESSION AZ387816
VERSION AZ387816.1 GI:10501524
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0147 row: B column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0147B22"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1492 GGAGAAAATGGAGAA 1506
              ||||||||||||| |
Db         17 GGAGAAAATGGAGTA 3
```

RESULT 3176
AZ772074
LOCUS AZ772074 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0574M10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0574M10 R, genomic survey sequence.
ACCESSION AZ772074
VERSION AZ772074.1 GI:12895006
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0574 row: M column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0574M10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2672 CAGTGTGTGTGGGTG 2686
              ||||||||||| |||
Db          3 CAGTGTGTGTGTGTG 17
```

RESULT 3177
AZ836069
LOCUS AZ836069 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0130J11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0130J11 R, genomic survey sequence.
ACCESSION AZ836069
VERSION AZ836069.1 GI:13005977
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0130 row: J column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0130J11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1299 TCGCCCCAGTCTTGG 1313
              ||||||||  ||||||
Db          6 TCGCCCCATTCTTGG 20
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RESULT 3178
AZ957966
LOCUS AZ957966 20 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0225I01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0225I01 F, genomic survey sequence.
ACCESSION AZ957966
VERSION AZ957966.1 GI:13829193
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: I column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0225I01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2162 CTCCTTTTTTTTTTT 2176
              | ||||||||||||||
Db          6 CCCCTTTTTTTTTTT 20
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RESULT 3179
BX563723/c
LOCUS BX563723 22 bp mRNA linear EST 10-OCT-2003
DEFINITION BX563723 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse68e02_p1c, mRNA sequence.
ACCESSION BX563723
VERSION BX563723.1 GI:33430936
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 22)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.
FEATURES Location/Qualifiers
source 1. .22
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse68e02_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with

T.brucei"

Query Match 0.5%; Score 13.4; DB 1; Length 22;
Best Local Similarity 93.3%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAA 2800
              ||||||||||||| |
Db         22 AAAAAAAAAAAATA 8
```

RESULT 3180
AU008929
LOCUS AU008929 25 bp mRNA linear EST 31-JUL-1998
DEFINITION AU008929 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc04231, mRNA sequence.
ACCESSION AU008929
VERSION AU008929.1 GI:3345387
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
REFERENCE 1 (bases 1 to 25)
AUTHORS Morimyo,M. and Mita,K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
FEATURES Location/Qualifiers
source 1. .25
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc04231"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"

Query Match 0.5%; Score 13.4; DB 1; Length 25;
Best Local Similarity 73.9%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       2773 CTTGTTAGAATTGAAAAAAAAAA 2795
              | | | | | || ||||||||||
Db          3 CATATCAAAGTTAAAAAAAAAAA 25
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RESULT 3181
AZ445446
LOCUS AZ445446 32 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0241G14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0241G14 F, genomic survey sequence.
ACCESSION AZ445446
VERSION AZ445446.1 GI:10595276
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 32)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0241 row: G column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
FEATURES Location/Qualifiers
source 1. .32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0241G14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 32;
Best Local Similarity 64.5%; Pred. No. 2.8e+03;
Matches 20; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy       2764 AAAAGTATTCTTGTTAGAATTGAAAAAAAAA 2794
              ||||  ||   |   | || ||| |||||||
Db          2 AAAAAAATATCTCAAACAAATGAGAAAAAAA 32
```

RESULT 3182
AW247875
LOCUS AW247875 18 bp mRNA linear EST 07-JAN-2000
DEFINITION 2820433.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820433 3', mRNA sequence.
ACCESSION AW247875
VERSION AW247875.1 GI:6590868
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820433.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 18 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM4  row: D  column: 2
            High quality sequence stop: 10.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820433"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAACCCCA 1789
              ||||||||||  ||  || |
Db          1 TTTTTTTTTTCAAGCCTA 18


RESULT 3183
CF314887
LOCUS       CF314887                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--03-J15.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--03-J15, mRNA sequence.
ACCESSION   CF314887
VERSION     CF314887.1  GI:33686648
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--03-J15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAACT 2190
              ||||||||||  ||| |
Db          1 TTTTTTTTTTACTAAAT 18


RESULT 3184
CF314887/c
LOCUS       CF314887                 18 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--03-J15.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--03-J15, mRNA sequence.
ACCESSION   CF314887
VERSION     CF314887.1  GI:33686648
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--03-J15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
```

```
  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAA 2799
              ||| |  ||||||||||
Db         18 ATTTAGTAAAAAAAAAAA 1


RESULT 3185
CF332005
LOCUS       CF332005                 19 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-F13.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-F13, mRNA sequence.
ACCESSION   CF332005
VERSION     CF332005.1  GI:33812230
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-F13"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTGAACCCC 1788
              ||||||||||   ||||
Db          1 TTTTTTTTTTTTCCCCC 18


RESULT 3186
AA878744/c
LOCUS       AA878744                 19 bp    mRNA    linear   EST 25-MAR-1998
DEFINITION  of85a08.s1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:1437110 3'
            similar to TR:Q67633 Q67633 ECO Q PROTEIN. [1] ;contains TAR1.t2
            TAR1 repetitive element ;, mRNA sequence.
ACCESSION   AA878744
VERSION     AA878744.1  GI:2987709
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            unknown library type
            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1437110"
                     /tissue_type="hepatic adenoma"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Li5"
                     /note="Organ: liver; Vector: pCMV-SPORT4; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 0.8 kb."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGCAGA 70
              || ||||| || ||||||
Db         19 GGGGGGGGGGGGGGCAGA 2


RESULT 3187
AI476315/c
LOCUS       AI476315                 19 bp    mRNA    linear   EST 09-MAR-1999
DEFINITION  ta15c09.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2044144 3'
            similar to TR:Q61431 Q61431 PROCOLLAGEN TYPE V ALPHA 2. ;contains
            OFR.b3 MSR1 repetitive element ;, mRNA sequence.
ACCESSION   AI476315
VERSION     AI476315.1  GI:4329360
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mark Raffeld, M.D.
             cDNA Library Preparation: Stratagene, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2044144"
                     /tissue_type="follicular lymphoma"
                     /lab_host="SOLR (Stratagene, kanamycin resistant)"
                     /clone_lib="NCI_CGAP_Lym5"
                     /note="Organ: lymph node; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
```

Oligo dT. Average insert size 1.2 kb. Non-amplified library. ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        481 CCGCCAGAGCCAGGAGGG 498
              || |||| |||||| |||
Db         18 CCCCCAGGGCCAGGGGGG 1
```

RESULT 3188
AW247975
LOCUS AW247975 19 bp mRNA linear EST 07-JAN-2000
DEFINITION 2820669.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820669 3', mRNA sequence.
ACCESSION AW247975
VERSION AW247975.1 GI:6591063
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2820669.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM4 row: M column: 22.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820669"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1771 TTTTTTTTTTTGAACCCC 1788
```

```
              ||||||||| ||||| |
Db          2 TTTTTTTTTAGGAACCTC 19
```

RESULT 3189
AW248167/c
LOCUS AW248167 19 bp mRNA linear EST 07-JAN-2000
DEFINITION 2819811.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819811 5', mRNA sequence.
ACCESSION AW248167
VERSION AW248167.1 GI:6591160
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2819811.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 14 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Possible Inverted Insert: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this clone probably contains an inverted cDNA insert. EST# does not reflect transcript orientation. Possible Chimera: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of this sequence and at the beginning of the sequence from the 3' read of this clone, this cDNA insert appears to be chimeric.
Plate: LLCM2 row: J column: 4
High quality sequence stop: 14.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819811"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2782 ATTGAAAAAAAAAAAAAA 2799
              || | || ||||||||||
Db         18 ATGGGAAGAAAAAAAAAA 1
```

```
RESULT 3190
AW248934
LOCUS       AW248934                19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819262.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819262 3',
            mRNA sequence.
ACCESSION   AW248934
VERSION     AW248934.1  GI:6591927
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819262.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 19 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM1  row: C  column: 7
            High quality sequence stop: 8.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819262"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTT 2192
              ||||||||||   |||||
Db          1 TTTTTTTTTTGGGACTTT 18


RESULT 3191
AW249918/c
LOCUS       AW249918                19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821753.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821753 3',
            mRNA sequence.
ACCESSION   AW249918
VERSION     AW249918.1  GI:6592911
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821753.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 11
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 19 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: K  column: 2
            High quality sequence stop: 11.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821753"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              ||||  | ||||||||||
Db         18 TTGATGACAAAAAAAAAA 1


RESULT 3192
AW250451
LOCUS       AW250451                19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822502.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822502 3',
            mRNA sequence.
ACCESSION   AW250451
VERSION     AW250451.1  GI:6593444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
```

```
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822502.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 19
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 19 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM9  row: J  column: 7
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2822502"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_7"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAACCCCA 1789
              ||||||||||  ||| |
Db          1 TTTTTTTTTGGCCCCAA 18


RESULT 3193
BQ588375
LOCUS       BQ588375                 19 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012307-024-008-P19-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-008-P19 5-PRIME, mRNA sequence.
ACCESSION   BQ588375
VERSION     BQ588375.1  GI:26117958
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 19   Std Error: 0.00
            Plate: 8  row: P  column: 19
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:184440"
                      /db_xref="taxon:161934"
                      /clone="024-008-P19"
                      /tissue_type="leaf"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-leaf"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||  |||||||  ||||||
Db          1 AACAAAAAAATCAAAAAA 18


RESULT 3194
BQ588375/c
LOCUS       BQ588375                 19 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012307-024-008-P19-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-008-P19 5-PRIME, mRNA sequence.
ACCESSION   BQ588375
VERSION     BQ588375.1  GI:26117958
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 19   Std Error: 0.00
            Plate: 8  row: P  column: 19
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
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FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184440"
                     /db_xref="taxon:161934"
                     /clone="024-008-P19"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||  ||||||| ||
Db         18 TTTTTTGATTTTTTTGTT 1


RESULT 3195
AZ447864
LOCUS       AZ447864                 19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0245A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0245A14 F, genomic survey sequence.
ACCESSION   AZ447864
VERSION     AZ447864.1  GI:10600087
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0245  row: A  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0245A14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2467 TTTTAATATTAACTTTTA 2484
              ||||  |||||  | |||||
Db          1 TTTTTATATTCATTTTTA 18


RESULT 3196
AZ514792
LOCUS       AZ514792                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0361B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0361B17 R, genomic survey sequence.
ACCESSION   AZ514792
VERSION     AZ514792.1  GI:10696108
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0361  row: B  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0361B17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2803
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Db          1 AAAAAAAAACAAGAAATA 18
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RESULT 3197
AZ514792/c
LOCUS AZ514792 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0361B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0361B17 R, genomic survey sequence.
ACCESSION AZ514792
VERSION AZ514792.1 GI:10696108
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: B column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361B17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2157 TTTTTCTCCTTTTTTTTT 2174
              | |||||  |||||||||
Db         18 TATTTCTTGTTTTTTTTT 1
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RESULT 3198
AZ579133/c
LOCUS AZ579133 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0363B04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0363B04 R, genomic survey sequence.
ACCESSION AZ579133
VERSION AZ579133.1 GI:11693594
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: B column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0363B04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2670 TACAGTGTGTGTGGGTGA 2687
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Db         19 TTCAGTTTGTGTGGGTCA 2
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RESULT 3199
AZ648404
LOCUS AZ648404 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0517I23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0517I23 F, genomic survey sequence.
ACCESSION AZ648404
VERSION AZ648404.1 GI:11780837
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0517 row: I column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0517I23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1900 AGATCAACAGATCAACAA 1917
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Db          2 ACAACAACAGAACAACAA 19
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RESULT 3200
AZ841555/c
LOCUS AZ841555 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0139P06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0139P06 R, genomic survey sequence.
ACCESSION AZ841555
VERSION AZ841555.1 GI:13011463
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: P column: 06
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0139P06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1861 CACACACTTAGCCATTGA 1878
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Db         19 CACACATTTAGCGATTCA 2
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RESULT 3201
AZ850833
LOCUS       AZ850833                19 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0152P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0152P13 R, genomic survey sequence.
ACCESSION   AZ850833
VERSION     AZ850833.1  GI:13036226
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0152  row: P  column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0152P13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAA 2188
              |||| ||| || ||||||
Db          1 TTTTGTTTGTTATTTTAA 18
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RESULT 3202
AZ345646
LOCUS       AZ345646                20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080K20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080K20 F, genomic survey sequence.
ACCESSION   AZ345646
VERSION     AZ345646.1  GI:10424883
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: K  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080K20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||| |  ||||||||||||
Db          3 AAACATTAAAAAAAAAAA 20
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RESULT 3203
AZ346143
LOCUS       AZ346143                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0081P11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0081P11 F, genomic survey sequence.
ACCESSION   AZ346143
VERSION     AZ346143.1  GI:10425380
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0081  row: P  column: 11
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0081P11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

```
  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              || | |||  |||||||||
Db          1 AAGACAAAGAAAAAAAAA 18
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RESULT 3204
AZ387841
LOCUS       AZ387841                 20 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0147H24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0147H24 R, genomic survey sequence.
ACCESSION   AZ387841
VERSION     AZ387841.1  GI:10501549
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0147  row: H  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0147H24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
```

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2165 CTTTTTTTTTTTTTTTT 2182
              ||||||  ||| ||||||
Db          2 CTTTTTCATTTCTTTTTT 19
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RESULT 3205
AU264645/c
LOCUS AU264645 20 bp mRNA linear EST 10-MAY-2002
DEFINITION AU264645 VS Dictyostelium discoideum cDNA clone VSD846 5', mRNA sequence.
ACCESSION AU264645
VERSION AU264645.1 GI:20523443
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 20)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .20
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSD846"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2175 TTTTTTTTTTTTAACTTT 2192
              ||||||||||  || |||
Db         20 TTTTTTTTTTAAAAATTT 3
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RESULT 3206
AU267884/c
LOCUS AU267884 20 bp mRNA linear EST 10-MAY-2002
DEFINITION AU267884 VS Dictyostelium discoideum cDNA clone VSH730 3', mRNA sequence.
ACCESSION AU267884
VERSION AU267884.1 GI:20526682
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 20)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .20
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH730"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAAAAAAA 2802
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Db         19 GAGAAAAAAGCAAAAAAA 2
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RESULT 3207
AW249928
LOCUS AW249928 20 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821805.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821805 3', mRNA sequence.
ACCESSION AW249928
VERSION AW249928.1 GI:6592921
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821805.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 9 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 20 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: M column: 6

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          High quality sequence stop: 9.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821805"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAACCCCA 1789
              ||||||||||   ||| |
Db          1 TTTTTTTTTTGGGCCCAA 18


RESULT 3208
C53693/c
LOCUS       C53693                    20 bp    mRNA    linear   EST 11-SEP-1997
DEFINITION  C53693 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
            clone yk323c3 3', mRNA sequence.
ACCESSION   C53693
VERSION     C53693.1  GI:2391450
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
            Sano,M., Miyata,A. and Nishigaki,A.
  TITLE     Expression map of the C.elegans genome
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Yuji Kohara
            Genome Biology Lab.
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Caenorhabditis elegans"
                     /mol_type="mRNA"
                     /strain="CB1489 him-8(e1489)"
                     /db_xref="taxon:6239"
                     /clone="yk323c3"
                     /sex="hermaphrodite, male"
                     /tissue_type="whole animal"
                     /dev_stage="varied"
                     /clone_lib="Yuji Kohara unpublished cDNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2564 GGCTCTGTTCTTGGCTTG 2581
              |||  ||||||||  ||||
Db         20 GGCCCTGTTCTTTTCTTG 3


RESULT 3209
CF302574
LOCUS       CF302574                  20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-E02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-E02, mRNA sequence.
ACCESSION   CF302574
VERSION     CF302574.1  GI:33674335
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-E02"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAA 2798
              | ||  ||||||||||||
Db          3 ACTTCCAAAAAAAAAAAA 20


RESULT 3210
CF302574/c
LOCUS       CF302574                  20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-E02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-E02, mRNA sequence.
ACCESSION   CF302574
VERSION     CF302574.1  GI:33674335
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
```

```
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
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Db         20 TTTTTTTTTTTTGGAAGT 3


RESULT 3211
CF302637
LOCUS       CF302637                 20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-F12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-F12, mRNA sequence.
ACCESSION   CF302637
VERSION     CF302637.1  GI:33674398
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-F12"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGAA 1784
              ||  ||||||||||| ||
Db          1 AAAATTTTTTTTTTTAAA 18


RESULT 3212
CF322590
LOCUS       CF322590                 20 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  HDN--01-I03.g1 OsHDAC1-overexpressing transgenic rice lambda phage
            cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-I03, mRNA
            sequence.
ACCESSION   CF322590
VERSION     CF322590.1  GI:33793421
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HDN--01-I03"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli SOLR"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice lambda
                     phage cDNA library II (HDN)"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
                     5' end with EcoRI and 3' end with XhoI site. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              ||||||||||||   ||||
Db          1 TTTTTTTTTTTCCCCCCC 18


RESULT 3213
AZ764505/c
LOCUS       AZ764505                 20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0560M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0560M06 R, genomic survey sequence.
ACCESSION   AZ764505
VERSION     AZ764505.1  GI:12879537
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
```

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            plasmid inserts
  JOURNAL   Unpublished (2000)
 COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0560  row: M  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0560M06"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         43 GCCCGCGCGCGGCGGGGG 60
              ||||| ||| || |||||
Db         19 GCCCGGGCGGGGGGGGGG 2


RESULT 3214
AZ789280/c
LOCUS       AZ789280                 20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0037A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0037A08 F, genomic survey sequence.
ACCESSION   AZ789280
VERSION     AZ789280.1  GI:12930134
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
 COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0037  row: A  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC2M0037A08"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTG 2193
                | ||||||||||| |||
Db         18 TATTTTTTTTTAATGTTG 1


RESULT 3215
AU254546
LOCUS       AU254546                 21 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU254546 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0002442 3', mRNA sequence.
ACCESSION   AU254546
VERSION     AU254546.1  GI:20316429
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
 COMMENT    Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
```

```
          Tel: 81-743-72-5581
          Fax: 81-743-72-5589
          Email: kkato@bs.aist-nara.ac.jp,
          URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="BED0002442"
                     /tissue_type="brain"
                     /clone_lib="3'-directed mouse cDNA library"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAA 2188
              | ||||||||| ||| ||
Db          3 TCTTTTTTTTTCTTTCAA 20


RESULT 3216
AZ483617
LOCUS       AZ483617                 21 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0309A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0309A05 R, genomic survey sequence.
ACCESSION   AZ483617
VERSION     AZ483617.1  GI:10647772
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0309  row: A  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0309A05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||| || ||||| ||||
Db          1 AAAACAACAAAAACAAAA 18


RESULT 3217
AZ632757/c
LOCUS       AZ632757                 23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0487M05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0487M05 R, genomic survey sequence.
ACCESSION   AZ632757
VERSION     AZ632757.1  GI:11754947
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0487  row: M  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0487M05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
```

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              || |||||| |||||||
Db         23 AACAAAAAAGGAAAAAAA 6
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RESULT 3218
AU267694/c
LOCUS AU267694 26 bp mRNA linear EST 10-MAY-2002
DEFINITION AU267694 VS Dictyostelium discoideum cDNA clone VSH605 5', mRNA sequence.
ACCESSION AU267694
VERSION AU267694.1 GI:20526492
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 26)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .26
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH605"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.5%; Score 13.2; DB 1; Length 26;
Best Local Similarity 69.2%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy       2177 TTTTTTTTTTAACTTTGAAAGTTAAC 2202
              |||||||||||   | | |   |||
Db         26 TTTTTTTTTTAATAATAACAACAAAC 1
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RESULT 3219
AI623404
LOCUS AI623404 28 bp mRNA linear EST 14-DEC-1999
DEFINITION ts35a07.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230548 3' similar to SW:YM04_PARTE P15605 HYPOTHETICAL 18.8 KD PROTEIN ;, mRNA sequence.
ACCESSION AI623404
VERSION AI623404.1 GI:4648335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 28)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1577 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
FEATURES Location/Qualifiers
source 1. .28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2230548"
/tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut4"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

Query Match 0.5%; Score 13.2; DB 1; Length 28;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              || || | ||||||||||
Db          3 AACAACAGAAAAAAAAAA 20
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RESULT 3220
BQ583549
LOCUS BQ583549 13 bp mRNA linear EST 06-DEC-2002
DEFINITION EO11978-024-005-C14-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-005-C14 5-PRIME, mRNA sequence.
ACCESSION BQ583549
VERSION BQ583549.1 GI:26113126
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 13)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ

```
           Max-Planck-Institute for Plant Breeding Research
           Carl-von-Linne Weg 10, 50829 Koeln, Germany
           Fax: 00492215062851
           Email: weisshaa@mpiz-koeln.mpg.de
           Insert Length: 13   Std Error: 0.00
           Plate: 5  row: C  column: 14
           Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:183152"
                     /db_xref="taxon:161934"
                     /clone="024-005-C14"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3221
BQ583549/c
LOCUS       BQ583549                 13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E011978-024-005-C14-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-005-C14 5-PRIME, mRNA sequence.
ACCESSION   BQ583549
VERSION     BQ583549.1  GI:26113126
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
            Plate: 5  row: C  column: 14
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:183152"
                     /db_xref="taxon:161934"
                     /clone="024-005-C14"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3222
BQ589180
LOCUS       BQ589180                 13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S014009-024-015-I22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-015-I22 3-PRIME, mRNA sequence.
ACCESSION   BQ589180
VERSION     BQ589180.1  GI:26118763
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
            Plate: 15  row: I  column: 22
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
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                     /db_xref="GABI:187886"
                     /db_xref="taxon:161934"
                     /clone="024-015-I22"
                     /tissue_type="storage root"
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                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
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cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13
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RESULT 3223
BQ589180/c
LOCUS BQ589180 13 bp mRNA linear EST 06-DEC-2002
DEFINITION S014009-024-015-I22-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-015-I22 3-PRIME, mRNA sequence.
ACCESSION BQ589180
VERSION BQ589180.1 GI:26118763
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 13)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 15 row: I column: 22
Seq primer: T7; GTAATACGACTCACTATAGGGC.
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/cultivar="KWS2320 (double haploid, monogerm breeding line)"
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/db_xref="taxon:161934"
/clone="024-015-I22"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          13 AAAAAAAAAAAAA 1
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RESULT 3224
BQ590337
LOCUS BQ590337 13 bp mRNA linear EST 06-DEC-2002
DEFINITION E012840-024-019-G12-SP6 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-019-G12 5-PRIME, mRNA sequence.
ACCESSION BQ590337
VERSION BQ590337.1 GI:26119920
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 13)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 19 row: G column: 12
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
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/db_xref="GABI:189780"
/db_xref="taxon:161934"
/clone="024-019-G12"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13
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RESULT 3225

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BQ590337/c
LOCUS       BQ590337                 13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012840-024-019-G12-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-G12 5-PRIME, mRNA sequence.
ACCESSION   BQ590337
VERSION     BQ590337.1  GI:26119920
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
            Plate: 19  row: G  column: 12
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189780"
                     /db_xref="taxon:161934"
                     /clone="024-019-G12"
                     /tissue_type="storage root"
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                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3226
CF278426
LOCUS       CF278426                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-F09.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--04-F09, mRNA sequence.
ACCESSION   CF278426
VERSION     CF278426.1  GI:33655812
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
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                     /clone_lib="Rice etiolated leaf plasmid cDNA library
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3227
CF278426/c
LOCUS       CF278426                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-F09.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--04-F09, mRNA sequence.
ACCESSION   CF278426
VERSION     CF278426.1  GI:33655812
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
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/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAA 2798
||||||||||||||
Db 13 AAAAAAAAAAAAA 1

RESULT 3228
CF280420
LOCUS CF280420 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-B11.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--07-B11, mRNA sequence.
ACCESSION CF280420
VERSION CF280420.1 GI:33657806
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTT 2178
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Db 1 TTTTTTTTTTTTT 13

RESULT 3229
CF280420/c
LOCUS CF280420 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-B11.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--07-B11, mRNA sequence.
ACCESSION CF280420
VERSION CF280420.1 GI:33657806
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/cultivar="Nackdong"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAA 2798
||||||||||||||
Db 13 AAAAAAAAAAAAA 1

RESULT 3230
CF280707
LOCUS CF280707 13 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--07-H19, mRNA sequence.
ACCESSION CF280707
VERSION CF280707.1 GI:33658093
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"

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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3231
CF280707/c
LOCUS       CF280707                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--07-H19, mRNA sequence.
ACCESSION   CF280707
VERSION     CF280707.1  GI:33658093
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--07-H19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3232
CF280757
LOCUS       CF280757                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-I21.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--07-I21, mRNA sequence.
ACCESSION   CF280757
VERSION     CF280757.1  GI:33658143
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--07-I21"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3233
CF280757/c
LOCUS       CF280757                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-I21.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--07-I21, mRNA sequence.
ACCESSION   CF280757
VERSION     CF280757.1  GI:33658143
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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    source          1. .13
                    /organism="Oryza sativa"
                    /mol_type="mRNA"
                    /cultivar="Nackdong"
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                    /clone="14ETL--07-I21"
                    /tissue_type="leaf"
                    /dev_stage="14 days after germination"
                    /lab_host="E.coli DH10B"
                    /clone_lib="Rice etiolated leaf plasmid cDNA library
                    (14ETL)"
                    /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                    with oligoribonucleotides and then used as templates for
                    RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3234
CF282369
LOCUS       CF282369                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-N16.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-N16, mRNA sequence.
ACCESSION   CF282369
VERSION     CF282369.1  GI:33659756
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--09-N16"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3235
CF282369/c
LOCUS       CF282369                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--09-N16.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--09-N16, mRNA sequence.
ACCESSION   CF282369
VERSION     CF282369.1  GI:33659756
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="14ETL--09-N16"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3236
CF290970
LOCUS       CF290970                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-D13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-D13, mRNA sequence.
ACCESSION   CF290970
VERSION     CF290970.1  GI:33660003
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
```

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           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-D13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3237
CF290970/c
LOCUS       CF290970                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-D13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-D13, mRNA sequence.
ACCESSION   CF290970
VERSION     CF290970.1  GI:33660003
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-D13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3238
CF290971
LOCUS       CF290971                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-D13, mRNA sequence.
ACCESSION   CF290971
VERSION     CF290971.1  GI:33660004
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3239
CF290971/c
LOCUS       CF290971                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-D13, mRNA sequence.
ACCESSION   CF290971
VERSION     CF290971.1  GI:33660004
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
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                     /clone="14ROOT--01-D13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3240
CF291011
LOCUS       CF291011                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-E10, mRNA sequence.
ACCESSION   CF291011
VERSION     CF291011.1  GI:33660044
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
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                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3241
CF291011/c
LOCUS       CF291011                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-E10, mRNA sequence.
ACCESSION   CF291011
VERSION     CF291011.1  GI:33660044
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-E10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3242
CF291060
LOCUS       CF291060                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION   CF291060
VERSION     CF291060.1  GI:33660093
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-F11"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3243
CF291060/c
LOCUS       CF291060                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION   CF291060
VERSION     CF291060.1  GI:33660093
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-F11"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3244
CF291061
LOCUS       CF291061                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION   CF291061
VERSION     CF291061.1  GI:33660094
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-F11"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3245
CF291061/c
LOCUS       CF291061                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-F11, mRNA sequence.
ACCESSION   CF291061
VERSION     CF291061.1  GI:33660094
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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           of Bioscience and Bioinformatics, MyongJi University
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           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-F11"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3246
CF291167
LOCUS       CF291167                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-H20.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-H20, mRNA sequence.
ACCESSION   CF291167
VERSION     CF291167.1  GI:33660200
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-H20"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3247
CF291167/c
LOCUS       CF291167                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-H20.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-H20, mRNA sequence.
ACCESSION   CF291167
VERSION     CF291167.1  GI:33660200
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-H20"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3248
CF291214
LOCUS       CF291214                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-I22.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-I22, mRNA sequence.
ACCESSION   CF291214
VERSION     CF291214.1  GI:33660247
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-I22"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3249
CF291214/c
LOCUS       CF291214                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-I22.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-I22, mRNA sequence.
ACCESSION   CF291214
VERSION     CF291214.1  GI:33660247
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-I22"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3250
CF291427
LOCUS       CF291427                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-N14.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION   CF291427
VERSION     CF291427.1  GI:33660460
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-N14"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3251
CF291427/c
LOCUS       CF291427                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-N14.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION   CF291427
VERSION     CF291427.1  GI:33660460
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-N14"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3252
CF291469
LOCUS       CF291469                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-O12, mRNA sequence.
ACCESSION   CF291469
VERSION     CF291469.1  GI:33660502
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-O12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3253
CF291469/c
LOCUS       CF291469                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-O12, mRNA sequence.
ACCESSION   CF291469
VERSION     CF291469.1  GI:33660502
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-O12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3254
CF291479
LOCUS       CF291479                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O17.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-O17, mRNA sequence.
ACCESSION   CF291479
VERSION     CF291479.1  GI:33660512
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

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  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-O17"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3255
CF291479/c
LOCUS       CF291479                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-O17.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-O17, mRNA sequence.
ACCESSION   CF291479
VERSION     CF291479.1  GI:33660512
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-O17"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3256
CF291514
LOCUS       CF291514                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-P13, mRNA sequence.
ACCESSION   CF291514
VERSION     CF291514.1  GI:33660547
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-P13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3257
CF291514/c
LOCUS       CF291514                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-P13, mRNA sequence.
ACCESSION   CF291514
VERSION     CF291514.1  GI:33660547
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-P13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3258
CF291515
LOCUS       CF291515                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-P13, mRNA sequence.
ACCESSION   CF291515
VERSION     CF291515.1  GI:33660548
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-P13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         1 AAAAAAAAAAAAA 13


RESULT 3259
CF291515/c
LOCUS       CF291515                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-P13, mRNA sequence.
ACCESSION   CF291515
VERSION     CF291515.1  GI:33660548
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-P13"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3260
CF291596
LOCUS       CF291596                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-B12, mRNA sequence.
ACCESSION   CF291596
VERSION     CF291596.1  GI:33660629
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
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  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-B12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3261
CF291596/c
LOCUS       CF291596                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-B12, mRNA sequence.
ACCESSION   CF291596
VERSION     CF291596.1  GI:33660629
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-B12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          13 AAAAAAAAAAAAA 1


RESULT 3262
CF291597
LOCUS       CF291597                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-B12, mRNA sequence.
ACCESSION   CF291597
VERSION     CF291597.1  GI:33660630
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-B12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3263
CF291597/c
LOCUS       CF291597                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-B12, mRNA sequence.
ACCESSION   CF291597
VERSION     CF291597.1  GI:33660630
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-B12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3264
CF291726
LOCUS       CF291726                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-E10, mRNA sequence.
ACCESSION   CF291726
VERSION     CF291726.1  GI:33660759
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-E10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3265
CF291726/c
LOCUS       CF291726                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-E10, mRNA sequence.
ACCESSION   CF291726
VERSION     CF291726.1  GI:33660759
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-E10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3266
CF291903
LOCUS       CF291903                  13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-I10, mRNA sequence.
ACCESSION   CF291903
VERSION     CF291903.1  GI:33660936
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-I10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3267
CF291903/c
LOCUS       CF291903                 13 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-I10, mRNA sequence.
ACCESSION   CF291903
VERSION     CF291903.1  GI:33660936
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-I10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          13 TTTTTTTTTTTTT 1


RESULT 3268
CF298590
LOCUS       CF298590                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A19, mRNA sequence.
ACCESSION   CF298590
VERSION     CF298590.1  GI:33670351
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3269
CF298590/c
LOCUS       CF298590                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A19, mRNA sequence.
ACCESSION   CF298590
VERSION     CF298590.1  GI:33670351
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="7LEAF--02-A19"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3270
CF298592
LOCUS       CF298592                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A21, mRNA sequence.
ACCESSION   CF298592
VERSION     CF298592.1  GI:33670353
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .13
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
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                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3271
CF298592/c
LOCUS       CF298592                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A21, mRNA sequence.
ACCESSION   CF298592
VERSION     CF298592.1  GI:33670353
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /organism="Oryza sativa"
                      /mol_type="mRNA"
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                      /tissue_type="leaf"
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                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3272
CF298736
LOCUS       CF298736                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-E22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-E22, mRNA sequence.
ACCESSION   CF298736
VERSION     CF298736.1  GI:33670497
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
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                     /clone="7LEAF--02-E22"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3273
CF298736/c
LOCUS       CF298736                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-E22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-E22, mRNA sequence.
ACCESSION   CF298736
VERSION     CF298736.1  GI:33670497
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3274
CF298764
LOCUS       CF298764                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-F20, mRNA sequence.
ACCESSION   CF298764
VERSION     CF298764.1  GI:33670525
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-F20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3275
CF298764/c
LOCUS       CF298764                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-F20, mRNA sequence.
ACCESSION   CF298764
VERSION     CF298764.1  GI:33670525
KEYWORDS    EST.
SOURCE      Oryza sativa
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  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-F20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3276
CF298795
LOCUS       CF298795                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-G14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-G14, mRNA sequence.
ACCESSION   CF298795
VERSION     CF298795.1  GI:33670556
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-G14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3277
CF298795/c
LOCUS       CF298795                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-G14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-G14, mRNA sequence.
ACCESSION   CF298795
VERSION     CF298795.1  GI:33670556
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-G14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3278
CF298908
LOCUS       CF298908                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-K03, mRNA sequence.
ACCESSION   CF298908
VERSION     CF298908.1  GI:33670669
KEYWORDS    EST.
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SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-K03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3279
CF298908/c
LOCUS       CF298908                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-K03, mRNA sequence.
ACCESSION   CF298908
VERSION     CF298908.1  GI:33670669
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-K03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3280
CF299133
LOCUS       CF299133                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-A06, mRNA sequence.
ACCESSION   CF299133
VERSION     CF299133.1  GI:33670894
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-A06"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3281
CF299133/c
LOCUS       CF299133                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-A06, mRNA sequence.
ACCESSION   CF299133
VERSION     CF299133.1  GI:33670894
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KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-A06"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3282
CF299359
LOCUS       CF299359                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-F15, mRNA sequence.
ACCESSION   CF299359
VERSION     CF299359.1  GI:33671120
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3283
CF299359/c
LOCUS       CF299359                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-F15, mRNA sequence.
ACCESSION   CF299359
VERSION     CF299359.1  GI:33671120
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="7LEAF--03-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3284
CF299937
LOCUS       CF299937                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-C12, mRNA sequence.
ACCESSION   CF299937
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VERSION     CF299937.1  GI:33671698
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3285
CF299937/c
LOCUS       CF299937                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-C12, mRNA sequence.
ACCESSION   CF299937
VERSION     CF299937.1  GI:33671698
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
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            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-C12"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3286
CF300118
LOCUS       CF300118                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-G10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-G10, mRNA sequence.
ACCESSION   CF300118
VERSION     CF300118.1  GI:33671879
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-G10"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3287
CF300118/c
LOCUS       CF300118                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-G10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-G10, mRNA sequence.
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ACCESSION   CF300118
VERSION     CF300118.1  GI:33671879
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-G10"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3288
CF300587
LOCUS       CF300587                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-C01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-C01, mRNA sequence.
ACCESSION   CF300587
VERSION     CF300587.1  GI:33672348
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-C01"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3289
CF300587/c
LOCUS       CF300587                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-C01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-C01, mRNA sequence.
ACCESSION   CF300587
VERSION     CF300587.1  GI:33672348
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3290
CF300658
LOCUS       CF300658                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-D14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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            sativa cDNA clone 7LEAF--05-D14, mRNA sequence.
ACCESSION   CF300658
VERSION     CF300658.1  GI:33672419
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-D14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3291
CF300658/c
LOCUS       CF300658                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-D14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-D14, mRNA sequence.
ACCESSION   CF300658
VERSION     CF300658.1  GI:33672419
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /cultivar="Nackdong"
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                     /clone="7LEAF--05-D14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3292
CF300929
LOCUS       CF300929                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION   CF300929
VERSION     CF300929.1  GI:33672690
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-J11"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3293
CF300929/c
LOCUS       CF300929                 13 bp    mRNA    linear   EST 15-AUG-2003
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DEFINITION  7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-J11, mRNA sequence.
ACCESSION   CF300929
VERSION     CF300929.1  GI:33672690
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-J11"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3294
CF301247
LOCUS       CF301247                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-A15, mRNA sequence.
ACCESSION   CF301247
VERSION     CF301247.1  GI:33673008
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3295
CF301247/c
LOCUS       CF301247                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-A15, mRNA sequence.
ACCESSION   CF301247
VERSION     CF301247.1  GI:33673008
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="7LEAF--06-A15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3296
CF301286
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LOCUS       CF301286                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-B15, mRNA sequence.
ACCESSION   CF301286
VERSION     CF301286.1  GI:33673047
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--06-B15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3297
CF301286/c
LOCUS       CF301286                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-B15, mRNA sequence.
ACCESSION   CF301286
VERSION     CF301286.1  GI:33673047
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /clone="7LEAF--06-B15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3298
CF302158
LOCUS       CF302158                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-G20, mRNA sequence.
ACCESSION   CF302158
VERSION     CF302158.1  GI:33673919
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-G20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3299
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CF302158/c
LOCUS       CF302158                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-G20, mRNA sequence.
ACCESSION   CF302158
VERSION     CF302158.1  GI:33673919
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-G20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3300
CF302830
LOCUS       CF302830                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-L16, mRNA sequence.
ACCESSION   CF302830
VERSION     CF302830.1  GI:33674591
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-L16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3301
CF302830/c
LOCUS       CF302830                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-L16, mRNA sequence.
ACCESSION   CF302830
VERSION     CF302830.1  GI:33674591
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-L16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1
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RESULT 3302
CF302898
LOCUS       CF302898                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-N08, mRNA sequence.
ACCESSION   CF302898
VERSION     CF302898.1  GI:33674659
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3303
CF302898/c
LOCUS       CF302898                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-N08, mRNA sequence.
ACCESSION   CF302898
VERSION     CF302898.1  GI:33674659
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3304
CF310516
LOCUS       CF310516                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION   CF310516
VERSION     CF310516.1  GI:33682277
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
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Db          1 TTTTTTTTTTTTT 13


RESULT 3305
CF310516/c
LOCUS       CF310516                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION   CF310516
VERSION     CF310516.1  GI:33682277
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3306
CF310517
LOCUS       CF310517                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION   CF310517
VERSION     CF310517.1  GI:33682278
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
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                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3307
CF310517/c
LOCUS       CF310517                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION   CF310517
VERSION     CF310517.1  GI:33682278
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         13 TTTTTTTTTTTTT 1
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RESULT 3308
CF312721
LOCUS CF312721 13 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--08-J13, mRNA sequence.
ACCESSION CF312721
VERSION CF312721.1 GI:33684482
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTT 13
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RESULT 3309
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DEFINITION ABF--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--08-J13, mRNA sequence.
ACCESSION CF312721
VERSION CF312721.1 GI:33684482
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
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Query Match 0.5%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         13 AAAAAAAAAAAAA 1
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RESULT 3310
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LOCUS CF313171 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--01-D10.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.
ACCESSION CF313171
VERSION CF313171.1 GI:33684932
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTT 2178
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Db 1 TTTTTTTTTTTTT 13

RESULT 3311
CF313171/c
LOCUS CF313171 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--01-D10.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.
ACCESSION CF313171
VERSION CF313171.1 GI:33684932
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
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Qy 2786 AAAAAAAAAAAAA 2798
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Db 13 AAAAAAAAAAAAA 1

RESULT 3312
CF314239
LOCUS CF314239 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-L01.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-L01, mRNA sequence.
ACCESSION CF314239
VERSION CF314239.1 GI:33686000
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
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/clone="HD--02-L01"
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/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTT 2178
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Db 1 TTTTTTTTTTTTT 13

RESULT 3313
CF314239/c
LOCUS CF314239 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-L01.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-L01, mRNA sequence.
ACCESSION CF314239
VERSION CF314239.1 GI:33686000
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

```
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3314
CF314874
LOCUS       CF314874                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--03-J07.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--03-J07, mRNA sequence.
ACCESSION   CF314874
VERSION     CF314874.1  GI:33686635
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3315
CF314874/c
LOCUS       CF314874                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--03-J07.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
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ACCESSION   CF314874
VERSION     CF314874.1  GI:33686635
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     derived from rice Histone Deacetylase overexpression
                     line."

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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3316
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LOCUS       CF315395                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-E20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--04-E20, mRNA sequence.
ACCESSION   CF315395
VERSION     CF315395.1  GI:33687156
KEYWORDS    EST.
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              Ehrhartoideae; Oryzeae; Oryza.
  REFERENCE   1  (bases 1 to 13)
    AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    TITLE     Large-scale Sequencing Analysis of Rice ESTs
    JOURNAL   Unpublished (2003)
  COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, MyongJi University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
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                       reverse transcribed and then used for PCR. mRNA was
                       derived from rice Histone Deacetylase overexpression
                       line."

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    Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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  Db          1 TTTTTTTTTTTTT 13


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              library (HD) Oryza sativa cDNA clone HD--04-E20, mRNA sequence.
  ACCESSION   CF315395
  VERSION     CF315395.1  GI:33687156
  KEYWORDS    EST.
  SOURCE      Oryza sativa
    ORGANISM  Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
  REFERENCE   1  (bases 1 to 13)
    AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    TITLE     Large-scale Sequencing Analysis of Rice ESTs
    JOURNAL   Unpublished (2003)
  COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, MyongJi University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
  FEATURES             Location/Qualifiers
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                       derived from rice Histone Deacetylase overexpression
                       line."

    Query Match             0.5%;  Score 13;  DB 1;  Length 13;
    Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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              library (HD) Oryza sativa cDNA clone HD--05-L17, mRNA sequence.
  ACCESSION   CF316439
  VERSION     CF316439.1  GI:33688200
  KEYWORDS    EST.
  SOURCE      Oryza sativa
    ORGANISM  Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
  REFERENCE   1  (bases 1 to 13)
    AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    TITLE     Large-scale Sequencing Analysis of Rice ESTs
    JOURNAL   Unpublished (2003)
  COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, MyongJi University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
  FEATURES             Location/Qualifiers
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                       /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                       /lab_host="E.coli DH10B"
                       /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                       cDNA library (HD)"
                       /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                       treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                       reverse transcribed and then used for PCR. mRNA was
                       derived from rice Histone Deacetylase overexpression
                       line."

    Query Match             0.5%;  Score 13;  DB 1;  Length 13;
    Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
    Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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  Db          1 TTTTTTTTTTTTT 13
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RESULT 3319
CF316439/c
LOCUS       CF316439                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-L17.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--05-L17, mRNA sequence.
ACCESSION   CF316439
VERSION     CF316439.1  GI:33688200
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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Qy       2786 AAAAAAAAAAAAA 2798
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Db         13 AAAAAAAAAAAAA 1


RESULT 3320
CF316440
LOCUS       CF316440                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-L17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--05-L17, mRNA sequence.
ACCESSION   CF316440
VERSION     CF316440.1  GI:33688201
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3321
CF316440/c
LOCUS       CF316440                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-L17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--05-L17, mRNA sequence.
ACCESSION   CF316440
VERSION     CF316440.1  GI:33688201
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
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derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTT 2178
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Db         13 TTTTTTTTTTTTT 1
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RESULT 3322
CF316637
LOCUS CF316637 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--06-A04.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--06-A04, mRNA sequence.
ACCESSION CF316637
VERSION CF316637.1 GI:33688398
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/cultivar="Nackdong"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
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/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTT 13
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RESULT 3323
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LOCUS CF316637 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--06-A04.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--06-A04, mRNA sequence.
ACCESSION CF316637
VERSION CF316637.1 GI:33688398
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAA 2798
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Db         13 AAAAAAAAAAAAA 1
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RESULT 3324
CF318290
LOCUS CF318290 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--08-F19.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.
ACCESSION CF318290
VERSION CF318290.1 GI:33690051
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nackdong"

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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3325
CF318290/c
LOCUS       CF318290                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-F19.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.
ACCESSION   CF318290
VERSION     CF318290.1  GI:33690051
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3326
CF319066
LOCUS       CF319066                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-H02.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-H02, mRNA sequence.
ACCESSION   CF319066
VERSION     CF319066.1  GI:33690827
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3327
CF319066/c
LOCUS       CF319066                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-H02.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-H02, mRNA sequence.
ACCESSION   CF319066
VERSION     CF319066.1  GI:33690827
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3328
CF319531
LOCUS       CF319531                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-B03.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
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ACCESSION   CF319531
VERSION     CF319531.1  GI:33691292
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /tissue_type="callus"
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                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                      reverse transcribed and then used for PCR. mRNA was
                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3329
CF319531/c
LOCUS       CF319531                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-B03.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.
ACCESSION   CF319531
VERSION     CF319531.1  GI:33691292
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:4530"
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                      /lab_host="E.coli DH10B"
                      /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                      reverse transcribed and then used for PCR. mRNA was
                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3330
CF319532
LOCUS       CF319532                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-B03.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.
ACCESSION   CF319532
VERSION     CF319532.1  GI:33691293
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:4530"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3331
CF319532/c
LOCUS       CF319532                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-B03.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.
ACCESSION   CF319532
VERSION     CF319532.1  GI:33691293
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3332
CF319919
LOCUS       CF319919                 13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-J17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-J17, mRNA sequence.
ACCESSION   CF319919
VERSION     CF319919.1  GI:33691680
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13
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RESULT 3333
CF319919/c
LOCUS       CF319919                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-J17.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-J17, mRNA sequence.
ACCESSION   CF319919
VERSION     CF319919.1  GI:33691680
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3334
CF320017
LOCUS       CF320017                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-L20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.
ACCESSION   CF320017
VERSION     CF320017.1  GI:33691778
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3335
CF320017/c
LOCUS       CF320017                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-L20.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.
ACCESSION   CF320017
VERSION     CF320017.1  GI:33691778
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
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            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     line."
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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3336
CF320018
LOCUS       CF320018                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-L20.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.
ACCESSION   CF320018
VERSION     CF320018.1  GI:33691779
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3337
CF320018/c
LOCUS       CF320018                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-L20.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.
ACCESSION   CF320018
VERSION     CF320018.1  GI:33691779
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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            Tel: 82 31 330 6193
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            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3338
CF320143
LOCUS       CF320143                  13 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-O13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-O13, mRNA sequence.
ACCESSION   CF320143
VERSION     CF320143.1  GI:33691904
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="HD--10-O13"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTT 2178
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Db          1 TTTTTTTTTTTTT 13
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RESULT 3339
CF320143/c
LOCUS CF320143 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-O13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--10-O13, mRNA sequence.
ACCESSION CF320143
VERSION CF320143.1 GI:33691904
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAA 2798
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Db         13 AAAAAAAAAAAAA 1
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RESULT 3340
CF320938
LOCUS CF320938 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--12-A06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--12-A06, mRNA sequence.
ACCESSION CF320938
VERSION CF320938.1 GI:33692699
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--12-A06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTT 13
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RESULT 3341
CF320938/c
LOCUS CF320938 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--12-A06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--12-A06, mRNA sequence.
ACCESSION CF320938
VERSION CF320938.1 GI:33692699
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea

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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
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                      /tissue_type="callus"
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                      /lab_host="E.coli DH10B"
                      /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                      reverse transcribed and then used for PCR. mRNA was
                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
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Db         13 AAAAAAAAAAAAA 1


RESULT 3342
CF326844
LOCUS       CF326844                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-B12, mRNA sequence.
ACCESSION   CF326844
VERSION     CF326844.1  GI:33801943
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /organism="Oryza sativa"
                      /mol_type="mRNA"
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                      /db_xref="taxon:4530"
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                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3343
CF326844/c
LOCUS       CF326844                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-B12, mRNA sequence.
ACCESSION   CF326844
VERSION     CF326844.1  GI:33801943
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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                      /organism="Oryza sativa"
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                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3344
CF327070
LOCUS       CF327070                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-G09, mRNA sequence.
ACCESSION   CF327070
VERSION     CF327070.1  GI:33802396
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
```

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COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3345
CF327070/c
LOCUS       CF327070                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-G09, mRNA sequence.
ACCESSION   CF327070
VERSION     CF327070.1  GI:33802396
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3346
CF327339
LOCUS       CF327339                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-M15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-M15, mRNA sequence.
ACCESSION   CF327339
VERSION     CF327339.1  GI:33802936
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
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            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
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Db          1 TTTTTTTTTTTTT 13


RESULT 3347
CF327339/c
LOCUS       CF327339                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-M15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-M15, mRNA sequence.
ACCESSION   CF327339
VERSION     CF327339.1  GI:33802936
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3348
CF327340
LOCUS       CF327340                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-M15.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-M15, mRNA sequence.
ACCESSION   CF327340
VERSION     CF327340.1  GI:33802938
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         1 AAAAAAAAAAAAA 13


RESULT 3349
CF327340/c
LOCUS       CF327340                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-M15.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-M15, mRNA sequence.
ACCESSION   CF327340
VERSION     CF327340.1  GI:33802938
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3350
CF327576
LOCUS       CF327576                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-B22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-B22, mRNA sequence.
ACCESSION   CF327576
VERSION     CF327576.1  GI:33803404
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

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  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3351
CF327576/c
LOCUS       CF327576                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-B22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-B22, mRNA sequence.
ACCESSION   CF327576
VERSION     CF327576.1  GI:33803404
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3352
CF327888
LOCUS       CF327888                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-I22, mRNA sequence.
ACCESSION   CF327888
VERSION     CF327888.1  GI:33804024
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3353
CF327888/c
LOCUS       CF327888                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-I22, mRNA sequence.
ACCESSION   CF327888
VERSION     CF327888.1  GI:33804024
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3354
CF327939
LOCUS       CF327939                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-K02.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-K02, mRNA sequence.
ACCESSION   CF327939
VERSION     CF327939.1  GI:33804127
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3355
CF327939/c
LOCUS       CF327939                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-K02.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-K02, mRNA sequence.
ACCESSION   CF327939
VERSION     CF327939.1  GI:33804127
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     with oligoribonucleotides and then used as templates for
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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3356
CF328153
LOCUS       CF328153                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-O19.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-O19, mRNA sequence.
ACCESSION   CF328153
VERSION     CF328153.1  GI:33804556
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
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  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3357
CF328153/c
LOCUS       CF328153                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-O19.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF328153
VERSION     CF328153.1  GI:33804556
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3358
CF328228
LOCUS       CF328228                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-A13.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-A13, mRNA sequence.
ACCESSION   CF328228
VERSION     CF328228.1  GI:33804702
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3359
CF328228/c
LOCUS       CF328228                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-A13.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-A13, mRNA sequence.
ACCESSION   CF328228
VERSION     CF328228.1  GI:33804702
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3360
CF328807
LOCUS       CF328807                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-O07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-O07, mRNA sequence.
ACCESSION   CF328807
VERSION     CF328807.1  GI:33805856
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3361
CF328807/c
LOCUS       CF328807                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-O07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-O07, mRNA sequence.
ACCESSION   CF328807
VERSION     CF328807.1  GI:33805856
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-O07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3362
CF329075
LOCUS       CF329075                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-E07, mRNA sequence.
ACCESSION   CF329075
VERSION     CF329075.1  GI:33806393
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-E07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3363
CF329075/c
LOCUS       CF329075                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-E07, mRNA sequence.
ACCESSION   CF329075
VERSION     CF329075.1  GI:33806393
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="NACL--04-E07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3364
CF329076
LOCUS       CF329076                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-E07.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-E07, mRNA sequence.
ACCESSION   CF329076
VERSION     CF329076.1  GI:33806395
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-E07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3365
CF329076/c
LOCUS       CF329076                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-E07.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-E07, mRNA sequence.
ACCESSION   CF329076
VERSION     CF329076.1  GI:33806395
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="NACL--04-E07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3366
CF329417
LOCUS       CF329417                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-L19.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-L19, mRNA sequence.
ACCESSION   CF329417
VERSION     CF329417.1  GI:33807072
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-L19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3367
CF329417/c
LOCUS       CF329417                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-L19.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-L19, mRNA sequence.
ACCESSION   CF329417
VERSION     CF329417.1  GI:33807072
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3368
CF329460
LOCUS       CF329460                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-M18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-M18, mRNA sequence.
ACCESSION   CF329460
VERSION     CF329460.1  GI:33807156
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="NACL--04-M18"
                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3369
CF329460/c
LOCUS       CF329460                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-M18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-M18, mRNA sequence.
ACCESSION   CF329460
VERSION     CF329460.1  GI:33807156
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3370
CF329729
LOCUS       CF329729                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-C14, mRNA sequence.
ACCESSION   CF329729
VERSION     CF329729.1  GI:33807674
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3371
CF329729/c
LOCUS       CF329729                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-C14, mRNA sequence.
ACCESSION   CF329729
VERSION     CF329729.1  GI:33807674
KEYWORDS    EST.
SOURCE      Oryza sativa
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  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
             |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3372
CF329800
LOCUS       CF329800                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION   CF329800
VERSION     CF329800.1  GI:33807817
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--05-E04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
             |||||||||||||
Db         1 TTTTTTTTTTTTT 13


RESULT 3373
CF329800/c
LOCUS       CF329800                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION   CF329800
VERSION     CF329800.1  GI:33807817
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--05-E04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
             |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3374
CF329801
LOCUS       CF329801                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION   CF329801
VERSION     CF329801.1  GI:33807819
KEYWORDS    EST.
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SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--05-E04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3375
CF329801/c
LOCUS       CF329801                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION   CF329801
VERSION     CF329801.1  GI:33807819
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3376
CF329869
LOCUS       CF329869                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-F18, mRNA sequence.
ACCESSION   CF329869
VERSION     CF329869.1  GI:33807959
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3377
CF329869/c
LOCUS       CF329869                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-F18, mRNA sequence.
ACCESSION   CF329869
VERSION     CF329869.1  GI:33807959
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KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3378
CF329946
LOCUS       CF329946                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-H12, mRNA sequence.
ACCESSION   CF329946
VERSION     CF329946.1  GI:33808114
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="NACL--05-H12"
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3379
CF329946/c
LOCUS       CF329946                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-H12, mRNA sequence.
ACCESSION   CF329946
VERSION     CF329946.1  GI:33808114
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3380
CF329988
LOCUS       CF329988                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-I10, mRNA sequence.
ACCESSION   CF329988
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VERSION     CF329988.1  GI:33808198
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3381
CF329988/c
LOCUS       CF329988                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-I10, mRNA sequence.
ACCESSION   CF329988
VERSION     CF329988.1  GI:33808198
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3382
CF330023
LOCUS       CF330023                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-J05.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-J05, mRNA sequence.
ACCESSION   CF330023
VERSION     CF330023.1  GI:33808268
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--05-J05"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3383
CF330023/c
LOCUS       CF330023                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-J05.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-J05, mRNA sequence.
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ACCESSION   CF330023
VERSION     CF330023.1  GI:33808268
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--05-J05"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3384
CF330725
LOCUS       CF330725                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-J01, mRNA sequence.
ACCESSION   CF330725
VERSION     CF330725.1  GI:33809672
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-J01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3385
CF330725/c
LOCUS       CF330725                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-J01, mRNA sequence.
ACCESSION   CF330725
VERSION     CF330725.1  GI:33809672
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-J01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3386
CF331041
LOCUS       CF331041                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza
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            sativa cDNA clone NACL--07-A04, mRNA sequence.
ACCESSION   CF331041
VERSION     CF331041.1  GI:33810299
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /clone="NACL--07-A04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3387
CF331041/c
LOCUS       CF331041                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-A04, mRNA sequence.
ACCESSION   CF331041
VERSION     CF331041.1  GI:33810299
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /clone="NACL--07-A04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3388
CF331266
LOCUS       CF331266                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-F06, mRNA sequence.
ACCESSION   CF331266
VERSION     CF331266.1  GI:33810744
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3389
CF331266/c
LOCUS       CF331266                 13 bp    mRNA    linear   EST 18-AUG-2003
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DEFINITION  NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-F06, mRNA sequence.
ACCESSION   CF331266
VERSION     CF331266.1  GI:33810744
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--07-F06"
                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3390
CF331273
LOCUS       CF331273                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION   CF331273
VERSION     CF331273.1  GI:33810757
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         1 AAAAAAAAAAAAA 13


RESULT 3391
CF331273/c
LOCUS       CF331273                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION   CF331273
VERSION     CF331273.1  GI:33810757
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1


RESULT 3392
CF331903
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LOCUS       CF331903                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-D07, mRNA sequence.
ACCESSION   CF331903
VERSION     CF331903.1  GI:33812027
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-D07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3393
CF331903/c
LOCUS       CF331903                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-D07, mRNA sequence.
ACCESSION   CF331903
VERSION     CF331903.1  GI:33812027
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     with oligoribonucleotides and then used as templates for
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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3394
CF332079
LOCUS       CF332079                 13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-H04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-H04, mRNA sequence.
ACCESSION   CF332079
VERSION     CF332079.1  GI:33812379
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Db          1 TTTTTTTTTTTTT 13


RESULT 3395
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CF332079/c
LOCUS CF332079 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--08-H04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-H04, mRNA sequence.
ACCESSION CF332079
VERSION CF332079.1 GI:33812379
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAA 2798
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Db 13 AAAAAAAAAAAAA 1

RESULT 3396
CF332695
LOCUS CF332695 13 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.
ACCESSION CF332695
VERSION CF332695.1 GI:33813618
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTT 2178
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Db 1 TTTTTTTTTTTTT 13

RESULT 3397
CF332695/c
LOCUS CF332695 13 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.
ACCESSION CF332695
VERSION CF332695.1 GI:33813618
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAA 2798

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Db          13 AAAAAAAAAAAAA 1


RESULT 3398
CF332696
LOCUS       CF332696                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-E21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.
ACCESSION   CF332696
VERSION     CF332696.1  GI:33813620
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

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  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3399
CF332696/c
LOCUS       CF332696                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-E21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.
ACCESSION   CF332696
VERSION     CF332696.1  GI:33813620
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     methyltransferase overexpression line."

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Db          13 TTTTTTTTTTTTT 1


RESULT 3400
CF333486
LOCUS       CF333486                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--02-G11, mRNA sequence.
ACCESSION   CF333486
VERSION     CF333486.1  GI:33815268
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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methyltransferase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
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Db          1 TTTTTTTTTTTTT 13
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DEFINITION JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-G11, mRNA sequence.
ACCESSION CF333486
VERSION CF333486.1 GI:33815268
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         13 AAAAAAAAAAAAA 1
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RESULT 3402
CF333972
LOCUS CF333972 13 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-B12.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.
ACCESSION CF333972
VERSION CF333972.1 GI:33816249
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 TTTTTTTTTTTTT 13
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RESULT 3403
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LOCUS CF333972 13 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-B12.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.
ACCESSION CF333972
VERSION CF333972.1 GI:33816249
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/dev_stage="14 days after germination"
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAA 2798
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Db 13 AAAAAAAAAAAAA 1

RESULT 3404
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LOCUS CF333973 13 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-B12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.
ACCESSION CF333973
VERSION CF333973.1 GI:33816251
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAA 2798
||||||||||||||
Db 1 AAAAAAAAAAAAA 13

RESULT 3405
CF333973/c
LOCUS CF333973 13 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-B12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.
ACCESSION CF333973
VERSION CF333973.1 GI:33816251
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-B12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTT 2178
||||||||||||||
Db 13 TTTTTTTTTTTTT 1

RESULT 3406
CF334347
LOCUS CF334347 13 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-J19.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-J19, mRNA sequence.
ACCESSION CF334347
VERSION CF334347.1 GI:33817022
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers

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    source          1. .13
                    /organism="Oryza sativa"
                    /mol_type="mRNA"
                    /cultivar="Nackdong"
                    /db_xref="taxon:4530"
                    /clone="JMT--03-J19"
                    /tissue_type="leaf"
                    /dev_stage="14 days after germination"
                    /lab_host="E.coli DH10B"
                    /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                    cDNA library (JMT)"
                    /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                    was reverse transcribed and then used for PCR. mRNA was
                    pepared from Arabidopsis Jasmoinate Carboxyl
                    methyltransferase overexpression line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3407
CF334347/c
LOCUS       CF334347                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-J19.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-J19, mRNA sequence.
ACCESSION   CF334347
VERSION     CF334347.1  GI:33817022
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES            Location/Qualifiers
     source         1. .13
                    /organism="Oryza sativa"
                    /mol_type="mRNA"
                    /cultivar="Nackdong"
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                    /clone="JMT--03-J19"
                    /tissue_type="leaf"
                    /dev_stage="14 days after germination"
                    /lab_host="E.coli DH10B"
                    /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                    cDNA library (JMT)"
                    /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                    was reverse transcribed and then used for PCR. mRNA was
                    pepared from Arabidopsis Jasmoinate Carboxyl
                    methyltransferase overexpression line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||

Db          13 AAAAAAAAAAAAA 1


RESULT 3408
CF337022
LOCUS       CF337022                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--07-E22, mRNA sequence.
ACCESSION   CF337022
VERSION     CF337022.1  GI:33822426
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES            Location/Qualifiers
     source         1. .13
                    /organism="Oryza sativa"
                    /mol_type="mRNA"
                    /cultivar="Nackdong"
                    /db_xref="taxon:4530"
                    /clone="JMT--07-E22"
                    /tissue_type="leaf"
                    /dev_stage="14 days after germination"
                    /lab_host="E.coli DH10B"
                    /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                    cDNA library (JMT)"
                    /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                    was reverse transcribed and then used for PCR. mRNA was
                    pepared from Arabidopsis Jasmoinate Carboxyl
                    methyltransferase overexpression line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3409
CF337022/c
LOCUS       CF337022                  13 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--07-E22, mRNA sequence.
ACCESSION   CF337022
VERSION     CF337022.1  GI:33822426
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
```

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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES                Location/Qualifiers
     source             1. .13
                        /organism="Oryza sativa"
                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:4530"
                        /clone="JMT--07-E22"
                        /tissue_type="leaf"
                        /dev_stage="14 days after germination"
                        /lab_host="E.coli DH10B"
                        /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                        cDNA library (JMT)"
                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                        was reverse transcribed and then used for PCR. mRNA was
                        pepared from Arabidopsis Jasmoinate Carboxyl
                        methyltransferase overexpression line."

  Query Match             0.5%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3410
CF327203
LOCUS       CF327203                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-J16, mRNA sequence.
ACCESSION   CF327203
VERSION     CF327203.1  GI:33802665
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES                Location/Qualifiers
     source             1. .14
                        /organism="Oryza sativa"
                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:4530"
                        /clone="NACL--01-J16"
                        /tissue_type="callus"
                        /dev_stage="proliferated callus on 2N6 media for 30 days"
                        /lab_host="E.coli DH10B"
                        /clone_lib="Rice callus plasmid cDNA library (NACL)"
                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 3411
CF327203/c
LOCUS       CF327203                  14 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-J16, mRNA sequence.
ACCESSION   CF327203
VERSION     CF327203.1  GI:33802665
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES                Location/Qualifiers
     source             1. .14
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                        /db_xref="taxon:4530"
                        /clone="NACL--01-J16"
                        /tissue_type="callus"
                        /dev_stage="proliferated callus on 2N6 media for 30 days"
                        /lab_host="E.coli DH10B"
                        /clone_lib="Rice callus plasmid cDNA library (NACL)"
                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

  Query Match             0.5%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 3412
AW251049
LOCUS       AW251049                  16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821507.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821507 3',
            mRNA sequence.
ACCESSION   AW251049
VERSION     AW251049.1  GI:6593995
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
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COMMENT     Other_ESTs: 2821507.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM6  row: P  column: 20
            High quality sequence stop: 10.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821507"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAAC 2189
              |||||||||||||
Db          1 TTTTTTTTTTAAC 13


RESULT 3413
AW251033
LOCUS       AW251033                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821399.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821399 3',
            mRNA sequence.
ACCESSION   AW251033
VERSION     AW251033.1  GI:6593979
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821399.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 17
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 17 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM6  row: L  column: 8
            High quality sequence stop: 17.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821399"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAA 1784
              |||||||||||||
Db          1 TTTTTTTTTTGAA 13


RESULT 3414
AW246451
LOCUS       AW246451                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821637.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821637 3',
            mRNA sequence.
ACCESSION   AW246451
VERSION     AW246451.1  GI:6589444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821637.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
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PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM7 row: F column: 6
High quality sequence stop: 9.

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FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821637"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
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  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAAC 2189
              |||||||||||||
Db             1 TTTTTTTTTTAAC 13
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RESULT 3415
AZ764511
LOCUS       AZ764511                19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0560B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0560B08 R, genomic survey sequence.
ACCESSION   AZ764511
VERSION     AZ764511.1  GI:12879549
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0560  row: B  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0560B08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

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  Query Match             0.5%;  Score 13;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db             1 AAAAAAAAAAAAA 13
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RESULT 3416
AZ764511/c
LOCUS       AZ764511                19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0560B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0560B08 R, genomic survey sequence.
ACCESSION   AZ764511
VERSION     AZ764511.1  GI:12879549
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0560  row: B  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
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/clone="UUGC1M0560B08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1
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RESULT 3417
AZ995149
LOCUS AZ995149 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0280D22R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0280D22 R, genomic survey sequence.
ACCESSION AZ995149
VERSION AZ995149.1 GI:13866376
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0280 row: D column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0280D22"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        606 ACCTGCTGCTGCC 618
              |||||||||||||
Db          2 ACCTGCTGCTGCC 14
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RESULT 3418
AZ479732/c
LOCUS AZ479732 20 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0300A09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0300A09 R, genomic survey sequence.
ACCESSION AZ479732
VERSION AZ479732.1 GI:10639901
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0300 row: A column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0300A09"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAAA 2797
              |||||||||||||
Db         13 GAAAAAAAAAAAA 1
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RESULT 3419
AZ427740/c
LOCUS AZ427740 20 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0209J23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0209J23 R, genomic survey sequence.
ACCESSION AZ427740
VERSION AZ427740.1 GI:10551753
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0209 row: J column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0209J23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2175 TTTTTTTTTTTTA 2187
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Db         13 TTTTTTTTTTTTA 1
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RESULT 3420
AZ506216
LOCUS AZ506216 20 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0347G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0347G11 F, genomic survey sequence.
ACCESSION AZ506216
VERSION AZ506216.1 GI:10687532
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0347 row: G column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0347G11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAA 2798
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Db          1 AAAAAAAAAAAAA 13
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RESULT 3421
AZ506216/c
LOCUS AZ506216 20 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0347G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0347G11 F, genomic survey sequence.
ACCESSION AZ506216
VERSION AZ506216.1 GI:10687532
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0347 row: G column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0347G11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTT 2178
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Db         13 TTTTTTTTTTTTT 1
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RESULT 3422
AZ764514
LOCUS AZ764514 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0560F09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560F09 R, genomic survey sequence.
ACCESSION AZ764514
VERSION AZ764514.1 GI:12879555
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: F column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560F09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13
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RESULT 3423
AZ764514/c
LOCUS       AZ764514                  20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0560F09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0560F09 R, genomic survey sequence.
ACCESSION   AZ764514
VERSION     AZ764514.1  GI:12879555
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0560  row: F  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0560F09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
```

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db         13 TTTTTTTTTTTTT 1
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RESULT 3424
AZ772040
LOCUS       AZ772040                  20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0574G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0574G11 R, genomic survey sequence.
ACCESSION   AZ772040
VERSION     AZ772040.1  GI:12894936
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0574  row: G  column: 11
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0574G11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTT 2177
              |||||||||||||
Db          1 CTTTTTTTTTTTT 13
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RESULT 3425
AZ773905
LOCUS       AZ773905                  20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0001C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0001C15 R, genomic survey sequence.
ACCESSION   AZ773905
VERSION     AZ773905.1  GI:12898761
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0001  row: C  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0001C15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

```
  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          8 TTTTTTTTTTTTT 20
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RESULT 3426
AZ773905/c
LOCUS       AZ773905                  20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0001C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0001C15 R, genomic survey sequence.
ACCESSION   AZ773905
VERSION     AZ773905.1  GI:12898761
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0001  row: C  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0001C15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         20 AAAAAAAAAAAAA 8
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RESULT 3427
AZ834769/c
LOCUS       AZ834769                 20 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0117F08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0117F08 R, genomic survey sequence.
ACCESSION   AZ834769
VERSION     AZ834769.1  GI:13004677
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0117  row: F  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0117F08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
```

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1947 TTGGTTTTTGTGT 1959
              |||||||||||||
Db         18 TTGGTTTTTGTGT 6
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RESULT 3428
AZ589400/c
LOCUS       AZ589400                 21 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0398C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0398C23 F, genomic survey sequence.
ACCESSION   AZ589400
VERSION     AZ589400.1  GI:11711590
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0398  row: C  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0398C23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
```

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.5%;  Score 13;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         21 AAAAAAAAAAAAA 9
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RESULT 3429
AZ346714
LOCUS       AZ346714                21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0082N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0082N05 F, genomic survey sequence.
ACCESSION   AZ346714
VERSION     AZ346714.1  GI:10425951
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0082  row: N  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0082N05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
```

```
  Query Match             0.5%;  Score 13;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 4.2e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              ||  | || | ||||||||||
Db          1 TTACATAATACAAAAAAAAAA 21
```

```
RESULT 3430
CB305256
LOCUS       CB305256                23 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  3'EST-Nfly-071 Drosophila melanogaster cDNA Library Drosophila
            melanogaster cDNA 3', mRNA sequence.
ACCESSION   CB305256
VERSION     CB305256.1  GI:31297660
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Lee,S., Zhou,G., Bao,J., Shapiro,J., Xu,J., Sun,M., Lin,W.,
            Zhang,R., Chen,J., Clark,T., Sun,M., Wang,J., Johnson,D., Tseng,C.,
            Yang,H., Wang,J., Du,W., Wu,C.I., Zhang,X. and Wang,S.M.
  TITLE     Novel SAGE tags represent a significant number of novel genes in
            Drosophila genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Wang SM
            Hem/Onc
            University of Chicago Medical Center
            5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
            Tel: 773-702-6788
            Fax: 773-702-3002
            Email: swang1@midway.uchicago.edu
            This EST was detected from Drosophila melanogaster cDNA Library
            with GLGI technique (Generation of Longer cDNA fragments from SAGE
            tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349,
            2000; A high-throughput GLGI procedure for converting a large
            number of SAGE tag sequences into 3' ESTs, Genes, Chromosomes &
            Cancers 33:252-261, 2002 ), which covers from the 3' end of cDNA
            till the first CATG.
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone_lib="Drosophila melanogaster cDNA Library"
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  Query Match             0.5%;  Score 13;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAA 1784
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Db          1 TTTTTTTTTTGAA 13
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RESULT 3431
AZ615086/c
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LOCUS       AZ615086                 23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0444C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0444C14 F, genomic survey sequence.
ACCESSION   AZ615086
VERSION     AZ615086.1  GI:11737276
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0444  row: C  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0444C14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         23 AAAAAAAAAAAAA 11


RESULT 3432
AZ819376
LOCUS       AZ819376                 23 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0089P23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0089P23 R, genomic survey sequence.
ACCESSION   AZ819376
VERSION     AZ819376.1  GI:12989284
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0089  row: P  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0089P23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 13;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 3433
AA937877
LOCUS       AA937877                 16 bp    mRNA    linear   EST 30-APR-1998
DEFINITION  nw90e06.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1253890
```

```
            similar to TR:Q35989 Q35989 CYTOCHROME C OXIDASE SUBUNIT 1 ;, mRNA
            sequence.
ACCESSION   AA937877
VERSION     AA937877.1  GI:3095988
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
            Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1253890"
                      /sex="male"
                      /tissue_type="metastatic prostate bone lesion"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Pr12"
                      /note="Vector: pAMP10; mRNA made from metastatic prostate
                      lesion of the bone, cDNA made by  oligo-dT priming.
                      Non-directionally cloned.  Size-selected on agarose  gel,
                      average insert size 600 bp.  Library made by D. Krizman,
                      NIH."

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2181
              || ||||||| |||||
Db          1 TTGTTTTTTTATTTTT 16


RESULT 3434
AA937877/c
LOCUS       AA937877                 16 bp    mRNA    linear   EST 30-APR-1998
DEFINITION  nw90e06.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1253890
            similar to TR:Q35989 Q35989 CYTOCHROME C OXIDASE SUBUNIT 1 ;, mRNA
            sequence.
ACCESSION   AA937877
VERSION     AA937877.1  GI:3095988
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
            Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1253890"
                      /sex="male"
                      /tissue_type="metastatic prostate bone lesion"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Pr12"
                      /note="Vector: pAMP10; mRNA made from metastatic prostate
                      lesion of the bone, cDNA made by  oligo-dT priming.
                      Non-directionally cloned.  Size-selected on agarose  gel,
                      average insert size 600 bp.  Library made by D. Krizman,
                      NIH."

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              ||||| ||||||| ||
Db         16 AAAAATAAAAAAACAA 1


RESULT 3435
AW245338/c
LOCUS       AW245338                 16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822905.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822905 3',
            mRNA sequence.
ACCESSION   AW245338
VERSION     AW245338.1  GI:6588331
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822905.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 15
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
```

```
           Plate: LLCM10  row: K  column: 2
           High quality sequence stop: 15.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822905"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||| | ||||||||||
Db         16 GAACACAAAAAAAAAA 1


RESULT 3436
BQ591425
LOCUS       BQ591425                16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012712-024-017-C11-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-C11 3-PRIME, mRNA sequence.
ACCESSION   BQ591425
VERSION     BQ591425.1  GI:26121008
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 17  row: C  column: 11
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188698"
                     /db_xref="taxon:161934"
                     /clone="024-017-C11"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1632 CCTTACTATTTAAAGA 1647
              |||||||||| ||| |
Db          1 CCTTACTATTAAAAAA 16


RESULT 3437
AW247976/c
LOCUS       AW247976                17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820717.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820717 3',
            mRNA sequence.
ACCESSION   AW247976
VERSION     AW247976.1  GI:6591064
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820717.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM4  row: O  column: 22.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820717"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
```

(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2782 ATTGAAAAAAAAAAAA 2797
              ||||  ||||||||||
Db         16 ATTGTTAAAAAAAAAA 1
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RESULT 3438
CF312453
LOCUS CF312453 18 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-D15.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--08-D15, mRNA sequence.
ACCESSION CF312453
VERSION CF312453.1 GI:33684214
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--08-D15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||| ||||||||||| |
Db          1 AAAGAAAAAAAAAACA 16
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RESULT 3439
CF312453/c
LOCUS CF312453 18 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-D15.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--08-D15, mRNA sequence.
ACCESSION CF312453
VERSION CF312453.1 GI:33684214
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--08-D15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTT 2181
              | ||||||||||| |||
Db         16 TGTTTTTTTTTCTTT 1
```

RESULT 3440
AI149192
LOCUS AI149192 19 bp mRNA linear EST 28-OCT-1998
DEFINITION qc76d09.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1715537 3' similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN. ;contains element TAR1 repetitive element ;, mRNA sequence.
ACCESSION AI149192
VERSION AI149192.1 GI:3677661
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 675 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:1715537"
/dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_placenta_8to9weeks_2NbHP8to9W"
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGATTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.5%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        108 TTGGGGGCTGGGGGGA 123
              ||||||| |||||||
Db          4 TTGGGGGGGGGGGGGA 19
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RESULT 3441
AI357421/c
LOCUS AI357421 19 bp mRNA linear EST 06-JAN-1999
DEFINITION qu01c02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:1963490 3' similar to TR:O20200 O20200 ORF54D. ;, mRNA sequence.
ACCESSION AI357421
VERSION AI357421.1 GI:4109042
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1963490"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Co14"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"

Query Match 0.5%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2176 TTTTTTTTTTAACTT 2191
              || |||||||||| ||
Db         19 TTCTTTTTTTAATTT 4
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RESULT 3442
AZ608537
LOCUS AZ608537 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0432N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0432N14 R, genomic survey sequence.
ACCESSION AZ608537
VERSION AZ608537.1 GI:11730727
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0432 row: N column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0432N14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTT 2170
              |||||||| ||| |||
Db          4 TTTTTTTCCCCTCTTT 19


RESULT 3443
AZ786308/c
LOCUS       AZ786308               19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0031B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0031B17 R, genomic survey sequence.
ACCESSION   AZ786308
VERSION     AZ786308.1  GI:12923936
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0031  row: B  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0031B17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 4.4e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        253 CCCCCACCTCTCCTCC 268
```

```
              |||||||||| || ||
Db         17 CCCCCACCTCCCCGCC 2


RESULT 3444
AZ830469
LOCUS       AZ830469               19 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0109C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0109C14 R, genomic survey sequence.
ACCESSION   AZ830469
VERSION     AZ830469.1  GI:13000377
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0109  row: C  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0109C14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 4.4e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        107 CTTGGGGGCTGGGGGG 122
              ||||||  ||||||||
```

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Db          2 CTTGGGACCTGGGGGG 17


RESULT 3445
AZ326642
LOCUS       AZ326642                 22 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0049D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0049D09 R, genomic survey sequence.
ACCESSION   AZ326642
VERSION     AZ326642.1  GI:10384599
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0049  row: D  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0049D09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 22;
  Best Local Similarity   87.5%;  Pred. No. 4.1e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1494 AGAAAATGGAGAAACA 1509
              | ||||||||| ||||
Db          6 AAAAAATGGAGCAACA 21
```

```
RESULT 3446
BG929133/c
LOCUS       BG929133                 25 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC34-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BG929133
VERSION     BG929133.1  GI:14323656
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  MEDLINE   21482651
   PUBMED   11597177
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="cartilage"
                     /lab_host="E.coli DH10 B"
                     /clone_lib="HNC (Human Normal Cartilage)"
                     /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                     Directional"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 25;
  Best Local Similarity   70.8%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   || | || ||| |||||||
Db         25 AAAAAAACACAATAAAGAAAAAAA 2


RESULT 3447
AI745099
LOCUS       AI745099                 25 bp    mRNA    linear   EST 21-JUN-1999
DEFINITION  tr21a09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218936 3'
            similar to TR:Q34096 Q34096 MURF2 PROTEIN. ;contains element L1 L1
            repetitive element ;, mRNA sequence.
ACCESSION   AI745099
VERSION     AI745099.1  GI:5113387
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
```

```
          Emmert-Buck, M.D., Ph.D.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html

          Trace considered overall poor quality
          Seq primer: -40UP from Gibco
          High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2218936"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ov23"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell.  All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"

  Query Match              0.5%;  Score 12.8;  DB 1;  Length 25;
  Best Local Similarity   70.8%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||  |||| | |  | ||||||||
Db          1 AAAAGAAACAGATGAGAAAAAAAA 24


RESULT 3448
AZ785005/c
LOCUS       AZ785005                 28 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0028P24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0028P24 F, genomic survey sequence.
ACCESSION   AZ785005
VERSION     AZ785005.1  GI:12921312
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0028  row: P  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0028P24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.5%;  Score 12.8;  DB 1;  Length 28;
  Best Local Similarity   70.8%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
              | ||   |||||   |||||||||
Db         24 ACAAACCAAAAACGTAAAAAAAAA 1


RESULT 3449
AI371092/c
LOCUS       AI371092                 19 bp    mRNA    linear   EST 16-FEB-1999
DEFINITION  ta07g09.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2043424 3'
            similar to TR:Q26195 Q26195 PVA1 GENE. ;contains L1.b3 L1
            repetitive element ;, mRNA sequence.
ACCESSION   AI371092
VERSION     AI371092.1  GI:4149845
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 536   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2043424"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn23"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| | ||||||  ||||
Db         19 AAAAGAGAAAAAAGGAAAA 1
```

RESULT 3450
AZ408157
LOCUS AZ408157 19 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0179A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0179A16 F, genomic survey sequence.
ACCESSION AZ408157
VERSION AZ408157.1 GI:10532170
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0179 row: A column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0179A16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              | ||||   ||||||||||
Db          1 AAAATTATTAAAAAAAAAA 19
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RESULT 3451
AZ850833/c
LOCUS AZ850833 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0152P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0152P13 R, genomic survey sequence.
ACCESSION AZ850833
VERSION AZ850833.1 GI:13036226
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0152 row: P column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0152P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
              || |||| || ||| ||||
Db         19 TTTAAAATAACAAACAAAA 1
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RESULT 3452
AW246477
LOCUS AW246477 19 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821873.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821873 3', mRNA sequence.
ACCESSION AW246477
VERSION AW246477.1 GI:6589470
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821873.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 18 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: P column: 2
High quality sequence stop: 18.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821873"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

```
  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCA 1789
              ||||||||||  || || |
Db          1 TTTTTTTTTTCCAAGCCAA 19
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RESULT 3453
AW246477/c
LOCUS AW246477 19 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821873.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821873 3', mRNA sequence.
ACCESSION AW246477
VERSION AW246477.1 GI:6589470
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821873.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 18 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: P column: 2
High quality sequence stop: 18.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821873"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

```
  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1971 TTACCTTGAAAAAAAGAAA 1989
              ||  |||| |||||| |||
Db         19 TTGGCTTGGAAAAAAAAAA 1


RESULT 3454
AW246513
LOCUS       AW246513                 19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821739.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821739 3',
            mRNA sequence.
ACCESSION   AW246513
VERSION     AW246513.1  GI:6589506
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821739.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 17
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 19 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: J  column: 12
            High quality sequence stop: 17.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821739"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAACTTTGAA 2195
              |||||||||| |  || ||
Db          1 TTTTTTTTTTCAGGTTCAA 19


RESULT 3455
AW246513/c
LOCUS       AW246513                 19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821739.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821739 3',
            mRNA sequence.
ACCESSION   AW246513
VERSION     AW246513.1  GI:6589506
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821739.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 17
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 19 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: J  column: 12
            High quality sequence stop: 17.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821739"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1970 TTTACCTTGAAAAAAAGAA 1988
              || | | |||||||| ||
Db         19 TTGAACCTGAAAAAAAAAA 1


RESULT 3456
AW248820
LOCUS       AW248820                 19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821008.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821008 3',
            mRNA sequence.
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ACCESSION   AW248820
VERSION     AW248820.1  GI:6591813
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821008.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 19
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 19 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: L  column: 1
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821008"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              ||||||||||    |||||
Db          1 TTTTTTTTTGGGGTTTTT 19


RESULT 3457
AW248820/c
LOCUS       AW248820                 19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821008.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821008 3',
            mRNA sequence.
ACCESSION   AW248820
VERSION     AW248820.1  GI:6591813
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821008.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 19
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 19 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: L  column: 1
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821008"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||    ||||||||||
Db         19 AAAAACCCCAAAAAAAAAA 1


RESULT 3458
BQ593604/c
LOCUS       BQ593604                 19 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012766-024-026-H12-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-026-H12 5-PRIME, mRNA sequence.
ACCESSION   BQ593604
VERSION     BQ593604.1  GI:26123187
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
```

```
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 19   Std Error: 0.00
            Plate: 26  row: H  column: 12
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:193251"
                     /db_xref="taxon:161934"
                     /clone="024-026-H12"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        340 CTACTTTCCCCCTCCCTAC 358
              || || |||||||| ||| |
Db         19 CTTCTCTCCCCCTCTCTTC 1


RESULT 3459
AZ345537/c
LOCUS       AZ345537                 19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080P01 F, genomic survey sequence.
ACCESSION   AZ345537
VERSION     AZ345537.1  GI:10424774
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: P  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080P01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              |||||   |||| ||||||
Db         19 TTTTTAAATTTTATTTTTA 1


RESULT 3460
AZ345792/c
LOCUS       AZ345792                 19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080G12 R, genomic survey sequence.
ACCESSION   AZ345792
VERSION     AZ345792.1  GI:10425029
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: G  column: 12
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            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0080G12"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        294 CGCCACCCCTCTCCCACAC 312
              |||| |||||| ||| | |
Db         19 CGCCCCCCCTCCCCCCCC 1


RESULT 3461
AZ424216
LOCUS       AZ424216                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0203O11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0203O11 R, genomic survey sequence.
ACCESSION   AZ424216
VERSION     AZ424216.1  GI:10548229
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0203  row: O  column: 11
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0203O11"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              | |||| |||| ||| |||
Db          1 ACAAAACAAAACAAACAAA 19


RESULT 3462
AZ424216/c
LOCUS       AZ424216                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0203O11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0203O11 R, genomic survey sequence.
ACCESSION   AZ424216
VERSION     AZ424216.1  GI:10548229
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0203  row: O  column: 11
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
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            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0203O11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              ||| ||| |||| |||| |
Db         19 TTTGTTTGTTTTGTTTTGT 1


RESULT 3463
AZ440413
LOCUS       AZ440413                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0231A01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0231A01 R, genomic survey sequence.
ACCESSION   AZ440413
VERSION     AZ440413.1  GI:10564426
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0231  row: A  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0231A01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTT 2182
              ||||||| | ||| ||| |
Db          1 CCTTTTTCTCTTTCTTTCT 19


RESULT 3464
AZ493581
LOCUS       AZ493581                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0328A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0328A24 F, genomic survey sequence.
ACCESSION   AZ493581
VERSION     AZ493581.1  GI:10667400
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0328  row: A  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCC 307
              |||| |||| |||| | ||
Db          1 CCCCCCGCCCCCCCCCCCC 19


RESULT 3465
AZ595570/c
LOCUS       AZ595570                19 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0408I15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0408I15 F, genomic survey sequence.
ACCESSION   AZ595570
VERSION     AZ595570.1  GI:11717760
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0408  row: I  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
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                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2032 AGGCAAAGGTTCTATCTGC 2050
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Db         19 AGGCAAAGTTTGGAGCTGC 1


RESULT 3466
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DEFINITION  1M0554N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0554N21 F, genomic survey sequence.
ACCESSION   AZ760597
VERSION     AZ760597.1  GI:12868613
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0554  row: N  column: 21
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 290 CCCGCGCCACCCCTCTCCC 308
||| | || |||| |||||
Db 1 CCCCCCCCCCCCCCCTCCC 19

RESULT 3467
AZ761834
LOCUS AZ761834 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0556E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0556E19 F, genomic survey sequence.
ACCESSION AZ761834
VERSION AZ761834.1 GI:12871174
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0556 row: E column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
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/clone="UUGC1M0556E19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 47 GCGCGCGGCGGGGGCGGCG 65
| |||||| ||||| || |
Db 1 GGGCGCGGTGGGGGTGGGG 19

RESULT 3468
AZ775865/c
LOCUS AZ775865 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0009P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0009P05 F, genomic survey sequence.
ACCESSION AZ775865
VERSION AZ775865.1 GI:12902847
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: P column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"

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                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        348 CCCCTCCCTACCAGCAGCT 366
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Db         19 CCCCTCTCTACCACATGCT 1


RESULT 3469
AZ779094
LOCUS       AZ779094                19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0015E02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0015E02 F, genomic survey sequence.
ACCESSION   AZ779094
VERSION     AZ779094.1  GI:12909402
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0015  row: E  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2681 TGGGTGAAATGGAGATTTG 2699
              | ||||||||||| |  |||
Db          1 TTGGTGAAATGGTGTGTTG 19


RESULT 3470
AZ782026
LOCUS       AZ782026                19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0021I23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0021I23 R, genomic survey sequence.
ACCESSION   AZ782026
VERSION     AZ782026.1  GI:12915307
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0021  row: I  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="UUGC2M0021I23"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        792 GTCAGAAGGAGCTGGTGGG 810
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Db          1 GGCAGGAGGTGCGGGTGGG 19
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RESULT 3471
AZ789674
LOCUS AZ789674 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0037L08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0037L08 R, genomic survey sequence.
ACCESSION AZ789674
VERSION AZ789674.1 GI:12930742
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: L column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037L08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db          1 TTTGGTTTGTTTTATTTTT 19
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RESULT 3472
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LOCUS AZ789674 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0037L08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0037L08 R, genomic survey sequence.
ACCESSION AZ789674
VERSION AZ789674.1 GI:12930742
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: L column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037L08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| |||| ||| |||
Db         19 AAAAATAAAACAAACCAAA 1
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RESULT 3473
AZ807440
LOCUS AZ807440 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0070K18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0070K18 F, genomic survey sequence.
ACCESSION AZ807440
VERSION AZ807440.1 GI:12971791
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0070 row: K column: 18
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0070K18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2599 GAAACTCTCTGTTCAGAAA 2617
              ||| | || |||| |||||
Db          1 GAATCGCTGTGTTAAGAAA 19
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RESULT 3474
AZ962769
LOCUS AZ962769 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0231P08R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0231P08 R, genomic survey sequence.
ACCESSION AZ962769
VERSION AZ962769.1 GI:13833996
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0231 row: P column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0231P08"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        289 CCCCGCGCCACCCCTCTCC 307
              |||| | || ||||| |||
Db          1 CCCCCCCCCCCCCCTTTCC 19
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RESULT 3475
AL587630/c
LOCUS AL587630 20 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587630 BP Chicken Brain Library Gallus gallus cDNA clone ROS060A07, mRNA sequence.
ACCESSION AL587630
VERSION AL587630.1 GI:13192664
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murray,F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-
Seq primer: M13F.
FEATURES Location/Qualifiers
source 1. .20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS060A07"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-1)"

Query Match 0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||    |||
Db         20 AAAAAAAAAAAACTGGAAA 2
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RESULT 3476
AU264645
LOCUS AU264645 20 bp mRNA linear EST 10-MAY-2002
DEFINITION AU264645 VS Dictyostelium discoideum cDNA clone VSD846 5', mRNA sequence.
ACCESSION AU264645
VERSION AU264645.1 GI:20523443
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 20)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .20
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSD846"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              | ||||   ||||||||||
Db          2 AAAATTTTAAAAAAAAAA 20
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RESULT 3477
AU267884
LOCUS AU267884 20 bp mRNA linear EST 10-MAY-2002
DEFINITION AU267884 VS Dictyostelium discoideum cDNA clone VSH730 3', mRNA sequence.
ACCESSION AU267884
VERSION AU267884.1 GI:20526682
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 20)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664

```
          Fax: 81-298-53-6614
          Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSH730"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTT 2175
              ||||| | ||||||| | |
Db          2 TTTTTTTGCTTTTTTCTCT 20


RESULT 3478
CF301021
LOCUS       CF301021                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-L10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
ACCESSION   CF301021
VERSION     CF301021.1  GI:33672782
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-L10"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              |||||| |||||||
Db          1 AAAAAATAAAAAAA 14


RESULT 3479
CF301021/c
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LOCUS       CF301021                  14 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-L10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
ACCESSION   CF301021
VERSION     CF301021.1  GI:33672782
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-L10"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||| ||||||
Db         14 TTTTTTTATTTTTT 1


RESULT 3480
CF543203
LOCUS       CF543203                  15 bp    mRNA    linear   EST 22-SEP-2003
DEFINITION  S014679-024-030-D05-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-030-D05 5-PRIME, mRNA sequence.
ACCESSION   CF543203
VERSION     CF543203.1  GI:34891643
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
```

```
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 15   Std Error: 0.00
            Plate: 30  row: D  column: 05
            Seq primer: SP6.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:936579"
                      /db_xref="taxon:161934"
                      /clone="024-030-D05"
                      /tissue_type="leaf"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-leaf"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 3.8e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              | ||||||||||||
Db          2 TCAAAAAAAAAAAA 15


RESULT 3481
AW245585
LOCUS       AW245585                 15 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822740.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822740 3',
            mRNA sequence.
ACCESSION   AW245585
VERSION     AW245585.1  GI:6588578
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822740.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 6 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 15 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM10  row: D  column: 5
            High quality sequence stop: 6.
FEATURES              Location/Qualifiers
     source           1. .15
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2822740"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_7"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 3.8e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTAACT 2190
              |||||||||||| |
Db          1 TTTTTTTTTAATT 14


RESULT 3482
AW245585/c
LOCUS       AW245585                 15 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822740.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822740 3',
            mRNA sequence.
ACCESSION   AW245585
VERSION     AW245585.1  GI:6588578
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822740.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 6 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 15 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM10  row: D  column: 5
            High quality sequence stop: 6.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2822740"
                      /tissue_type="small cell carcinoma"
```

/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2781 AATTGAAAAAAAAA 2794
              |||| |||||||||
Db         14 AATTAAAAAAAAAA 1
```

RESULT 3483
AW246494
LOCUS AW246494 15 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821595.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821595 3', mRNA sequence.
ACCESSION AW246494
VERSION AW246494.1 GI:6589487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 15)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821595.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 14 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: D column: 12
High quality sequence stop: 14.
FEATURES Location/Qualifiers
source 1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821595"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1772 TTTTTTTTTGAAC 1785
              ||||||||||||
Db          1 TTTTTTTTTGATC 14
```

RESULT 3484
AW246551
LOCUS AW246551 15 bp mRNA linear EST 07-JAN-2000
DEFINITION 2822090.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822090 3', mRNA sequence.
ACCESSION AW246551
VERSION AW246551.1 GI:6589544
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 15)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2822090.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 14 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM8 row: I column: 3
High quality sequence stop: 14.
FEATURES Location/Qualifiers
source 1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822090"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.8e+03;

```
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAAC 1785
              ||||||||||  |||
Db          1 TTTTTTTTTTAAAC 14


RESULT 3485
CF299603/c
LOCUS       CF299603                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
ACCESSION   CF299603
VERSION     CF299603.1  GI:33671364
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-L01"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 3.8e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTT 2192
              ||||||||||  |||
Db         15 TTTTTTTTAAATTT 2


RESULT 3486
CF319827
LOCUS       CF319827                 16 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-H16.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.
ACCESSION   CF319827
VERSION     CF319827.1  GI:33691588
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-H16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 4.2e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAA 2794
              ||||  |||||||||
Db          2 AATTAAAAAAAAAA 15


RESULT 3487
AI564678/c
LOCUS       AI564678                 16 bp    mRNA    linear   EST 14-MAY-1999
DEFINITION  tq78g03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2214964 3'
            similar to TR:Q15214 Q15214 SALIVARY PROLINE-RICH PROTEIN 1
            ;contains element MSR1 repetitive element ;, mRNA sequence.
ACCESSION   AI564678
VERSION     AI564678.1  GI:4523135
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 1719   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
```

```
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2214964"
                     /tissue_type="well-differentiated endometrial
                     adenocarcinoma, 7 pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut1"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Life Technologies catalog #:
                     11538-014"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 4.2e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGC 64
              |||| |||||||||
Db         14 GCGGAGGGGGCGGC 1


RESULT 3488
AW246490/c
LOCUS       AW246490                 16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821591.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821591 3',
            mRNA sequence.
ACCESSION   AW246490
VERSION     AW246490.1  GI:6589483
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821591.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 12
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: D  column: 8
            High quality sequence stop: 12.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821591"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 4.2e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAA 2796
              ||| ||||||||||
Db         14 TTGCAAAAAAAAAA 1


RESULT 3489
BQ588093/c
LOCUS       BQ588093                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012336-024-009-A19-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-009-A19 5-PRIME, mRNA sequence.
ACCESSION   BQ588093
VERSION     BQ588093.1  GI:26117675
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 9  row: A  column: 19
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184766"
                     /db_xref="taxon:161934"
                     /clone="024-009-A19"
                     /tissue_type="leaf"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-leaf"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 4.2e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTT 2172
              ||||||| ||||||
```

```
Db         14 TTTCTCCCTTTTTT 1


RESULT 3490
AW245664/c
LOCUS       AW245664                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3',
            mRNA sequence.
ACCESSION   AW245664
VERSION     AW245664.1  GI:6588657
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822994.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence.
            Plate: LLCM10  row: N  column: 19.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822994"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2799
              ||||||||||||| |
Db         17 AAAAAAAAAAAACA 4


RESULT 3491
BM398017/c
LOCUS       BM398017                 18 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-4-D05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398017
VERSION     BM398017.1  GI:18198070
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 4.6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        219 GCCACGACGGGAGC 232
              |||||| |||||||
Db         17 GCCACGGCGGGAGC 4


RESULT 3492
AZ774536
LOCUS       AZ774536                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0004P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0004P01 F, genomic survey sequence.
ACCESSION   AZ774536
VERSION     AZ774536.1  GI:12900089
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0004  row: P  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2783 TTGAAAAAAAAAAA 2796
              || ||||||||||||
Db          4 TTAAAAAAAAAAAA 17
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RESULT 3493
AI648553/c
LOCUS AI648553 19 bp mRNA linear EST 16-DEC-1999
DEFINITION tz55e07.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292516 3' similar to TR:O04216 O04216 EXTENSIN ;, mRNA sequence.
ACCESSION AI648553
VERSION AI648553.1 GI:4729387
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 249 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2292516"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ov35"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; This library represents the normalized version of NCI_CGAP_Ov23. Cloned unidirectionally. Primer: Oligo dT. Average insert size 0.86 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Constructed by Life Technologies."

Query Match 0.4%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        542 CCCCACCTCTCCGG 555
              |||| |||||||||
Db         14 CCCCCCCTCTCCGG 1
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RESULT 3494
AZ369369
LOCUS AZ369369 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0119K19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0119K19 R, genomic survey sequence.
ACCESSION AZ369369
VERSION AZ369369.1 GI:10483069
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0119 row: K column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0119K19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.4%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2673 AGTGTGTGTGGGTG 2686
              ||||||||||||| |
Db             1 AGTGTGTGTGGGGG 14
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RESULT 3495
AZ510143
LOCUS       AZ510143                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0354P21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0354P21 F, genomic survey sequence.
ACCESSION   AZ510143
VERSION     AZ510143.1  GI:10691459
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0354  row: P  column: 21
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0354P21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.4%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        346 TCCCCCTCCCTACC 359
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Db          5 TCCCCCTCCCCACC 18
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RESULT 3496
AZ514586/c
LOCUS       AZ514586                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0361B17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0361B17 F, genomic survey sequence.
ACCESSION   AZ514586
VERSION     AZ514586.1  GI:10695818
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0361  row: B  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0361B17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
```

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.4%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAAC 1785
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Db         17 TTTTTTTTTTGCAC 4
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RESULT 3497
AZ827164
LOCUS       AZ827164                19 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0103M22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0103M22 F, genomic survey sequence.
ACCESSION   AZ827164
VERSION     AZ827164.1  GI:12997072
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0103  row: M  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0103M22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
```

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
  Query Match             0.4%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        831 AGGTCTTCTGCTCA 844
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Db          6 AGGTTTTCTGCTCA 19
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RESULT 3498
CF302637/c
LOCUS       CF302637                20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-F12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-F12, mRNA sequence.
ACCESSION   CF302637
VERSION     CF302637.1  GI:33674398
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-F12"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."
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  Query Match             0.4%;  Score 12.4;  DB 1;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAA 2796
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Db         18 TTTAAAAAAAAAAA 5
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RESULT 3499
AZ772040/c
LOCUS       AZ772040                20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0574G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0574G11 R, genomic survey sequence.
ACCESSION   AZ772040
VERSION     AZ772040.1  GI:12894936
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KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0574  row: G  column: 11
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0574G11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              | ||||||||||||
Db         15 TCAAAAAAAAAAAA 2


RESULT 3500
AZ355624
LOCUS       AZ355624                 22 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0095E22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0095E22 F, genomic survey sequence.
ACCESSION   AZ355624
VERSION     AZ355624.1  GI:10468133
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0095  row: E  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0095E22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   72.7%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2772 TCTTGTTAGAATTGAAAAAAAA 2793
              |||  ||  || | ||||||||
Db          1 TCTCTTTCTAAATTAAAAAAAA 22


RESULT 3501
BH856226/c
LOCUS       BH856226                 25 bp    DNA     linear   GSS 08-JUL-2002
DEFINITION  SALK_083159.52.35.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_083159.52.35.x, genomic
            survey sequence.
ACCESSION   BH856226
VERSION     BH856226.1  GI:21705816
KEYWORDS    GSS.
```

```
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_083159.52.35.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 25;
  Best Local Similarity   72.7%;  Pred. No. 3.6e+03;
  Matches   16;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTAA 2188
              ||   | |||| ||| ||||||
Db         23 TTCACTCTTTTCTTTCTTTTAA 2

RESULT 3502
AW246446/c
LOCUS       AW246446                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821601.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821601 3',
            mRNA sequence.
ACCESSION   AW246446
VERSION     AW246446.1  GI:6589439
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821601.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM7  row: D  column: 18
            High quality sequence stop: 9.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821601"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 4.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              || | | ||||||||||
Db         17 TTAACACAAAAAAAAAA 1

RESULT 3503
AW248779
LOCUS       AW248779                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821015.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821015 3',
            mRNA sequence.
ACCESSION   AW248779
VERSION     AW248779.1  GI:6591772
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821015.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
```

```
           Plate: LLCM5  row: L  column: 8.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821015"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 4.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1773 TTTTTTTTTGAACCCCA 1789
              ||||||||| || || |
Db          1 TTTTTTTTTCAAGCCTA 17


RESULT 3504
AW246528
LOCUS       AW246528                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821879.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821879 3',
            mRNA sequence.
ACCESSION   AW246528
VERSION     AW246528.1  GI:6589521
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821879.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washingtion Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 13
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 17 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: P  column: 8
            High quality sequence stop: 13.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821879"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 4.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTGAACCC 1787
              ||||||||||  || ||
Db          1 TTTTTTTTTAAAAACC 17


RESULT 3505
AZ924200
LOCUS       AZ924200                 18 bp    DNA     linear   GSS 01-APR-2001
DEFINITION  4906.ic27n17.s1 Saccharomyces mikatae IFO 1815 Saccharomyces
            mikatae genomic clone 4906.ic27n17.s1, genomic survey sequence.
ACCESSION   AZ924200
VERSION     AZ924200.1  GI:13495098
KEYWORDS    GSS.
SOURCE      Saccharomyces mikatae
  ORGANISM  Saccharomyces mikatae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cliften,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T.,
            Gish,W.R., Waterston,R.H. and Johnston,M.
  TITLE     Surveying Saccharomyces genomes to identify functional elements by
            comparative DNA sequence analysis
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Johnston M
            Department of Genetics
            Washington University Medical School
            Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
            Tel: 314 362 2735
            Fax: 314 362 7855
            Email: mj@genetics.wustl.edu
            Class: random plasmid subclone.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Saccharomyces mikatae"
                     /mol_type="genomic DNA"
                     /strain="IFO 1815"
                     /db_xref="taxon:114525"
                     /clone="4906.ic27n17.s1"
                     /clone_lib="Saccharomyces mikatae IFO 1815"
                     /note="Random genomic sequence "

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.7e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              || ||| | ||||||||
Db          1 TTAAAAGACAAAAAAAA 17


RESULT 3506
AW246520/c
LOCUS       AW246520                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821787.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821787 3',
            mRNA sequence.
ACCESSION   AW246520
```

```
VERSION     AW246520.1  GI:6589513
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821787.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 16
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 18 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: L  column: 12
            High quality sequence stop: 16.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821787"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.7e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              ||||   ||||||||||
Db         17 TTGAGGCAAAAAAAAAA 1


RESULT 3507
AI476315
LOCUS       AI476315                 19 bp    mRNA    linear   EST 09-MAR-1999
DEFINITION  ta15c09.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2044144 3'
            similar to TR:Q61431 Q61431 PROCOLLAGEN TYPE V ALPHA 2. ;contains
            OFR.b3 MSR1 repetitive element ;, mRNA sequence.
ACCESSION   AI476315
VERSION     AI476315.1  GI:4329360
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mark Raffeld, M.D.
             cDNA Library Preparation: Stratagene, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2044144"
                     /tissue_type="follicular lymphoma"
                     /lab_host="SOLR (Stratagene, kanamycin resistant)"
                     /clone_lib="NCI_CGAP_Lym5"
                     /note="Organ: lymph node; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. Average insert size 1.2 kb. Non-amplified
                     library. ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3'
                     adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 4.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1599 CCCTCCTGGCCTGGGGG 1615
              |||  |||||||  ||||
Db          1 CCCCCCTGGCCCTGGGG 17


RESULT 3508
AI357421
LOCUS       AI357421                 19 bp    mRNA    linear   EST 06-JAN-1999
DEFINITION  qu01c02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:1963490 3'
            similar to TR:O20200 O20200 ORF54D. ;, mRNA sequence.
ACCESSION   AI357421
VERSION     AI357421.1  GI:4109042
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
```

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FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1963490"
                     /tissue_type="moderately-differentiated adenocarcinoma"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Co14"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.7 kb. Life Technologies catalog #:
                     11531-019"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 4.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1972 TACCTTGAAAAAAAGAA 1988
              ||  || ||||||||||
Db          3 TAAATTAAAAAAAAGAA 19


RESULT 3509
AZ608537/c
LOCUS       AZ608537                 19 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0432N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0432N14 R, genomic survey sequence.
ACCESSION   AZ608537
VERSION     AZ608537.1  GI:11730727
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0432  row: N  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0432N14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 4.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAA 2795
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Db         17 AGAGGGGAAAAAAAAAA 1


RESULT 3510
AZ404619
LOCUS       AZ404619                 25 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0173L20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0173L20 F, genomic survey sequence.
ACCESSION   AZ404619
VERSION     AZ404619.1  GI:10528632
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0173  row: L  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0173L20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
```

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.2; DB 1; Length 25;
Best Local Similarity 68.0%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy       2180 TTTTTTTAACTTTGAAAGTTAACTC 2204
              || ||| |  |||||| |   ||||
Db          1 TTATTTGATATTTGAATGGCTACTC 25
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RESULT 3511
BG668943
LOCUS BG668943 12 bp mRNA linear EST 30-APR-2001
DEFINITION DRN03E05 Rat DRG Library Rattus norvegicus cDNA clone DRN03E05 5', mRNA sequence.
ACCESSION BG668943
VERSION BG668943.1 GI:13890865
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 12)
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C., Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D., Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
TITLE Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
MEDLINE 22056133
PUBMED 12060780
COMMENT Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR PRimers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA=No.
FEATURES Location/Qualifiers
source 1. .12
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRN03E05"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAA 2797
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Db          1 AAAAAAAAAAAA 12
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RESULT 3512
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LOCUS BG668943 12 bp mRNA linear EST 30-APR-2001
DEFINITION DRN03E05 Rat DRG Library Rattus norvegicus cDNA clone DRN03E05 5', mRNA sequence.
ACCESSION BG668943
VERSION BG668943.1 GI:13890865
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 12)
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C., Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D., Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
TITLE Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
MEDLINE 22056133
PUBMED 12060780
COMMENT Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR PRimers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA=No.
FEATURES Location/Qualifiers
source 1. .12
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRN03E05"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTT 2177
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Db         12 TTTTTTTTTTTT 1
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RESULT 3513
BQ582536
LOCUS BQ582536 12 bp mRNA linear EST 06-DEC-2002
DEFINITION S013300-024-007-P01-T7 MPIZ-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-007-P01 3-PRIME, mRNA sequence.
ACCESSION BQ582536
VERSION BQ582536.1 GI:26112113

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KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 12   Std Error: 0.00
            Plate: 7  row: P  column: 01
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184167"
                     /db_xref="taxon:161934"
                     /clone="024-007-P01"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3514
BQ582536/c
LOCUS       BQ582536                 12 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013300-024-007-P01-T7 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-007-P01 3-PRIME, mRNA sequence.
ACCESSION   BQ582536
VERSION     BQ582536.1  GI:26112113
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 12   Std Error: 0.00
            Plate: 7  row: P  column: 01
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184167"
                     /db_xref="taxon:161934"
                     /clone="024-007-P01"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3515
BQ588719
LOCUS       BQ588719                 12 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013713-024-014-P24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-014-P24 3-PRIME, mRNA sequence.
ACCESSION   BQ588719
VERSION     BQ588719.1  GI:26118302
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
```

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            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 12   Std Error: 0.00
            Plate: 14  row: P  column: 24
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
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                      /mol_type="mRNA"
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                      /db_xref="GABI:187286"
                      /db_xref="taxon:161934"
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                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-storage root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
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Db          1 TTTTTTTTTTTT 12


RESULT 3516
BQ588719/c
LOCUS       BQ588719                 12 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S013713-024-014-P24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-014-P24 3-PRIME, mRNA sequence.
ACCESSION   BQ588719
VERSION     BQ588719.1  GI:26118302
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 12   Std Error: 0.00
            Plate: 14  row: P  column: 24
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
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                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
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                      /db_xref="taxon:161934"
                      /clone="024-014-P24"
                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-storage root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match              0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
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Db         12 AAAAAAAAAAAA 1


RESULT 3517
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LOCUS       BQ594698                 12 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012404-024-024-E05-T7 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-024-E05 3-PRIME, mRNA sequence.
ACCESSION   BQ594698
VERSION     BQ594698.1  GI:26124281
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 12   Std Error: 0.00
            Plate: 24  row: E  column: 05
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:192159"
                      /db_xref="taxon:161934"
                      /clone="024-024-E05"
                      /tissue_type="developing root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-developing root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12
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RESULT 3518
BQ594698/c
LOCUS BQ594698 12 bp mRNA linear EST 06-DEC-2002
DEFINITION E012404-024-024-E05-T7 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-024-E05 3-PRIME, mRNA sequence.
ACCESSION BQ594698
VERSION BQ594698.1 GI:26124281
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 24 row: E column: 05
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:192159"
/db_xref="taxon:161934"
/clone="024-024-E05"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAA 2797
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Db         12 AAAAAAAAAAAA 1
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RESULT 3519
CF279278
LOCUS CF279278 12 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--05-I10.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-I10, mRNA sequence.
ACCESSION CF279278
VERSION CF279278.1 GI:33656664
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--05-I10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12
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RESULT 3520
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LOCUS CF279278 12 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--05-I10.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-I10, mRNA sequence.
ACCESSION CF279278
VERSION CF279278.1 GI:33656664
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs

```
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--05-I10"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3521
CF291428
LOCUS       CF291428                  12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION   CF291428
VERSION     CF291428.1  GI:33660461
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-N14"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         1 AAAAAAAAAAAA 12


RESULT 3522
CF291428/c
LOCUS       CF291428                  12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION   CF291428
VERSION     CF291428.1  GI:33660461
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-N14"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db         12 TTTTTTTTTTTT 1


RESULT 3523
CF291800
LOCUS       CF291800                  12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G04.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G04, mRNA sequence.
ACCESSION   CF291800
VERSION     CF291800.1  GI:33660833
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-G04"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3524
CF291800/c
LOCUS       CF291800                12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G04.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G04, mRNA sequence.
ACCESSION   CF291800
VERSION     CF291800.1  GI:33660833
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-G04"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3525
CF291801
LOCUS       CF291801                12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G04.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G04, mRNA sequence.
ACCESSION   CF291801
VERSION     CF291801.1  GI:33660834
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-G04"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db          1 AAAAAAAAAAAA 12


RESULT 3526
CF291801/c
LOCUS       CF291801                12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G04.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G04, mRNA sequence.
ACCESSION   CF291801
VERSION     CF291801.1  GI:33660834
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
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  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-G04"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db         12 TTTTTTTTTTTT 1


RESULT 3527
CF291885
LOCUS       CF291885                12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I01.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-I01, mRNA sequence.
ACCESSION   CF291885
VERSION     CF291885.1  GI:33660918
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-I01"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3528
CF291885/c
LOCUS       CF291885                12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I01.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-I01, mRNA sequence.
ACCESSION   CF291885
VERSION     CF291885.1  GI:33660918
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
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Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3529
CF291886
LOCUS       CF291886                12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I01.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-I01, mRNA sequence.
ACCESSION   CF291886
VERSION     CF291886.1  GI:33660919
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db          1 AAAAAAAAAAAA 12


RESULT 3530
CF291886/c
LOCUS       CF291886                  12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-I01.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-I01, mRNA sequence.
ACCESSION   CF291886
VERSION     CF291886.1  GI:33660919
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
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                     /clone="14ROOT--02-I01"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
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                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
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Qy       2166 TTTTTTTTTTTT 2177
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Db          12 TTTTTTTTTTTT 1


RESULT 3531
CF292107
LOCUS       CF292107                  12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-M21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-M21, mRNA sequence.
ACCESSION   CF292107
VERSION     CF292107.1  GI:33661140
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="14ROOT--02-M21"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3532
CF292107/c
LOCUS       CF292107                  12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-M21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-M21, mRNA sequence.
ACCESSION   CF292107
VERSION     CF292107.1  GI:33661140
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-M21"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3533
CF295593
LOCUS       CF295593                  12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-J18.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-J18, mRNA sequence.
ACCESSION   CF295593
VERSION     CF295593.1  GI:33664626
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--05-J18"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3534
CF295593/c
LOCUS       CF295593                  12 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--05-J18.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-J18, mRNA sequence.
ACCESSION   CF295593
VERSION     CF295593.1  GI:33664626
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3535
CF298686
LOCUS       CF298686                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-D15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-D15, mRNA sequence.
ACCESSION   CF298686
VERSION     CF298686.1  GI:33670447
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3536
CF298686/c
LOCUS       CF298686                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-D15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-D15, mRNA sequence.
ACCESSION   CF298686
VERSION     CF298686.1  GI:33670447
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3537
CF298872
LOCUS       CF298872                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-I17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-I17, mRNA sequence.
ACCESSION   CF298872
VERSION     CF298872.1  GI:33670633
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3538
CF298872/c
LOCUS       CF298872                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-I17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-I17, mRNA sequence.
ACCESSION   CF298872
VERSION     CF298872.1  GI:33670633
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
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                     /cultivar="Nackdong"
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3539
CF299343
LOCUS       CF299343                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-F06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-F06, mRNA sequence.
ACCESSION   CF299343
VERSION     CF299343.1  GI:33671104
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-F06"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         1 AAAAAAAAAAAA 12


RESULT 3540
CF299343/c
LOCUS       CF299343                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-F06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-F06, mRNA sequence.
ACCESSION   CF299343
VERSION     CF299343.1  GI:33671104
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-F06"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db         12 TTTTTTTTTTTT 1


RESULT 3541
CF299514
LOCUS       CF299514                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-J03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-J03, mRNA sequence.
ACCESSION   CF299514
VERSION     CF299514.1  GI:33671275
KEYWORDS    EST.
SOURCE      Oryza sativa
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  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-J03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3542
CF299514/c
LOCUS       CF299514                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-J03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-J03, mRNA sequence.
ACCESSION   CF299514
VERSION     CF299514.1  GI:33671275
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-J03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3543
CF300272
LOCUS       CF300272                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-J19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-J19, mRNA sequence.
ACCESSION   CF300272
VERSION     CF300272.1  GI:33672033
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-J19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3544
CF300272/c
LOCUS       CF300272                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-J19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-J19, mRNA sequence.
ACCESSION   CF300272
VERSION     CF300272.1  GI:33672033
KEYWORDS    EST.
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SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3545
CF300420
LOCUS       CF300420                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-M23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-M23, mRNA sequence.
ACCESSION   CF300420
VERSION     CF300420.1  GI:33672181
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /tissue_type="leaf"
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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3546
CF300420/c
LOCUS       CF300420                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-M23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-M23, mRNA sequence.
ACCESSION   CF300420
VERSION     CF300420.1  GI:33672181
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3547
CF300558
LOCUS       CF300558                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-B09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-B09, mRNA sequence.
ACCESSION   CF300558
VERSION     CF300558.1  GI:33672319
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KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="7LEAF--05-B09"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3548
CF300558/c
LOCUS       CF300558                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-B09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-B09, mRNA sequence.
ACCESSION   CF300558
VERSION     CF300558.1  GI:33672319
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3549
CF300881
LOCUS       CF300881                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-I10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-I10, mRNA sequence.
ACCESSION   CF300881
VERSION     CF300881.1  GI:33672642
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3550
CF300881/c
LOCUS       CF300881                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-I10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-I10, mRNA sequence.
ACCESSION   CF300881
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VERSION     CF300881.1  GI:33672642
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
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  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3551
CF301006
LOCUS       CF301006                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-L02, mRNA sequence.
ACCESSION   CF301006
VERSION     CF301006.1  GI:33672767
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="7LEAF--05-L02"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3552
CF301006/c
LOCUS       CF301006                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-L02, mRNA sequence.
ACCESSION   CF301006
VERSION     CF301006.1  GI:33672767
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3553
CF301075
LOCUS       CF301075                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-M15, mRNA sequence.
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ACCESSION   CF301075
VERSION     CF301075.1  GI:33672836
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /clone="7LEAF--05-M15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3554
CF301075/c
LOCUS       CF301075                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-M15, mRNA sequence.
ACCESSION   CF301075
VERSION     CF301075.1  GI:33672836
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3555
CF301489
LOCUS       CF301489                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-G01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-G01, mRNA sequence.
ACCESSION   CF301489
VERSION     CF301489.1  GI:33673250
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--06-G01"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3556
CF301489/c
LOCUS       CF301489                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-G01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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            sativa cDNA clone 7LEAF--06-G01, mRNA sequence.
ACCESSION   CF301489
VERSION     CF301489.1  GI:33673250
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3557
CF301940
LOCUS       CF301940                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-A01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-A01, mRNA sequence.
ACCESSION   CF301940
VERSION     CF301940.1  GI:33673701
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
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  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3558
CF301940/c
LOCUS       CF301940                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-A01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-A01, mRNA sequence.
ACCESSION   CF301940
VERSION     CF301940.1  GI:33673701
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3559
CF302029
LOCUS       CF302029                12 bp    mRNA    linear   EST 15-AUG-2003
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DEFINITION  7LEAF--07-C18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-C18, mRNA sequence.
ACCESSION   CF302029
VERSION     CF302029.1  GI:33673790
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
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            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
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Db          1 TTTTTTTTTTTT 12


RESULT 3560
CF302029/c
LOCUS       CF302029                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-C18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-C18, mRNA sequence.
ACCESSION   CF302029
VERSION     CF302029.1  GI:33673790
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
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                     /db_xref="taxon:4530"
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                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3561
CF302122
LOCUS       CF302122                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-F15, mRNA sequence.
ACCESSION   CF302122
VERSION     CF302122.1  GI:33673883
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3562
CF302122/c
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LOCUS       CF302122                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-F15, mRNA sequence.
ACCESSION   CF302122
VERSION     CF302122.1  GI:33673883
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
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                     /mol_type="mRNA"
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                     /clone="7LEAF--07-F15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3563
CF302289
LOCUS       CF302289                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-K10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-K10, mRNA sequence.
ACCESSION   CF302289
VERSION     CF302289.1  GI:33674050
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-K10"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3564
CF302289/c
LOCUS       CF302289                12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-K10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-K10, mRNA sequence.
ACCESSION   CF302289
VERSION     CF302289.1  GI:33674050
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3565
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CF302486
LOCUS       CF302486                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-B02, mRNA sequence.
ACCESSION   CF302486
VERSION     CF302486.1  GI:33674247
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-B02"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3566
CF302486/c
LOCUS       CF302486                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-B02, mRNA sequence.
ACCESSION   CF302486
VERSION     CF302486.1  GI:33674247
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-B02"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3567
CF308112
LOCUS       CF308112                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-M19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-M19, mRNA sequence.
ACCESSION   CF308112
VERSION     CF308112.1  GI:33679873
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
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Db          1 TTTTTTTTTTTT 12


RESULT 3568
CF308112/c
LOCUS       CF308112                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-M19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-M19, mRNA sequence.
ACCESSION   CF308112
VERSION     CF308112.1  GI:33679873
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3569
CF311835
LOCUS       CF311835                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION   CF311835
VERSION     CF311835.1  GI:33683596
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3570
CF311835/c
LOCUS       CF311835                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION   CF311835
VERSION     CF311835.1  GI:33683596
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
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then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAA 2797
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Db         12 AAAAAAAAAAAA 1
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RESULT 3571
CF311836
LOCUS CF311836 12 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--07-E11.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311836
VERSION CF311836.1 GI:33683597
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db          1 AAAAAAAAAAAA 12
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RESULT 3572
CF311836/c
LOCUS CF311836 12 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--07-E11.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311836
VERSION CF311836.1 GI:33683597
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
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/mol_type="mRNA"
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/clone="ABF--07-E11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTT 2177
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Db         12 TTTTTTTTTTTT 1
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RESULT 3573
CF313356
LOCUS CF313356 12 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--01-H09.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-H09, mRNA sequence.
ACCESSION CF313356
VERSION CF313356.1 GI:33685117
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"

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                     /db_xref="taxon:4530"
                     /clone="HD--01-H09"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3574
CF313356/c
LOCUS       CF313356                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-H09.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-H09, mRNA sequence.
ACCESSION   CF313356
VERSION     CF313356.1  GI:33685117
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3575
CF315565
LOCUS       CF315565                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-I14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--04-I14, mRNA sequence.
ACCESSION   CF315565
VERSION     CF315565.1  GI:33687326
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3576
CF315565/c
LOCUS       CF315565                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-I14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--04-I14, mRNA sequence.
ACCESSION   CF315565
VERSION     CF315565.1  GI:33687326
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
```

```
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           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3577
CF317551
LOCUS       CF317551                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-E16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-E16, mRNA sequence.
ACCESSION   CF317551
VERSION     CF317551.1  GI:33689312
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3578
CF317551/c
LOCUS       CF317551                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-E16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-E16, mRNA sequence.
ACCESSION   CF317551
VERSION     CF317551.1  GI:33689312
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3579
CF317798
LOCUS       CF317798                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-J24.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-J24, mRNA sequence.
ACCESSION   CF317798
VERSION     CF317798.1  GI:33689559
KEYWORDS    EST.
SOURCE      Oryza sativa
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  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
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Db          1 TTTTTTTTTTTT 12


RESULT 3580
CF317798/c
LOCUS       CF317798                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-J24.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
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ACCESSION   CF317798
VERSION     CF317798.1  GI:33689559
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
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Db         12 AAAAAAAAAAAA 1


RESULT 3581
CF320426
LOCUS       CF320426                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-F02.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--11-F02, mRNA sequence.
ACCESSION   CF320426
VERSION     CF320426.1  GI:33692187
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--11-F02"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
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Db          1 TTTTTTTTTTTT 12
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RESULT 3582
CF320426/c
LOCUS       CF320426                  12 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--11-F02.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--11-F02, mRNA sequence.
ACCESSION   CF320426
VERSION     CF320426.1  GI:33692187
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
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            of Bioscience and Bioinformatics, MyongJi University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--11-F02"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3583
CF324793
LOCUS       CF324793                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT1--01-H22.g1 AtJMT-overexpressing transgenic rice lambda phage
            cDNA library (JMT1) Oryza sativa cDNA clone JMT1--01-H22, mRNA
            sequence.
ACCESSION   CF324793
VERSION     CF324793.1  GI:33797867
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT1--01-H22"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli SOLR"
                     /clone_lib="AtJMT-overexpressing transgenic rice lambda
                     phage cDNA library (JMT1)"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
                     end with EcoRI and 3' end with XhoI site. mRNA was
                     prepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3584
CF324793/c
LOCUS       CF324793                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT1--01-H22.g1 AtJMT-overexpressing transgenic rice lambda phage
            cDNA library (JMT1) Oryza sativa cDNA clone JMT1--01-H22, mRNA
            sequence.
ACCESSION   CF324793
VERSION     CF324793.1  GI:33797867
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli SOLR"
                     /clone_lib="AtJMT-overexpressing transgenic rice lambda
                     phage cDNA library (JMT1)"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
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end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         12 AAAAAAAAAAAA 1
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RESULT 3585
CF326913
LOCUS CF326913 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-D01, mRNA sequence.
ACCESSION CF326913
VERSION CF326913.1 GI:33802082
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--01-D01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12
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RESULT 3586
CF326913/c
LOCUS CF326913 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-D01, mRNA sequence.
ACCESSION CF326913
VERSION CF326913.1 GI:33802082
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--01-D01"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1
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RESULT 3587
CF327376
LOCUS CF327376 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-N10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-N10, mRNA sequence.
ACCESSION CF327376
VERSION CF327376.1 GI:33803011
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--01-N10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTT 2177
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Db 1 TTTTTTTTTTTT 12

RESULT 3588
CF327376/c
LOCUS CF327376 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-N10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-N10, mRNA sequence.
ACCESSION CF327376
VERSION CF327376.1 GI:33803011
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--01-N10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAA 2797
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Db 12 AAAAAAAAAAAA 1

RESULT 3589
CF327962
LOCUS CF327962 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-K14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-K14, mRNA sequence.
ACCESSION CF327962
VERSION CF327962.1 GI:33804174
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTT 2177
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Db 1 TTTTTTTTTTTT 12

RESULT 3590
CF327962/c
LOCUS CF327962 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-K14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-K14, mRNA sequence.
ACCESSION CF327962
VERSION CF327962.1 GI:33804174
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAA 2797
||||||||||||
Db 12 AAAAAAAAAAAA 1

RESULT 3591
CF328229
LOCUS CF328229 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-A13.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--03-A13, mRNA sequence.
ACCESSION CF328229
VERSION CF328229.1 GI:33804704
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="NACL--03-A13"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAA 2797
||||||||||||
Db 1 AAAAAAAAAAAA 12

RESULT 3592
CF328229/c
LOCUS CF328229 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-A13.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--03-A13, mRNA sequence.
ACCESSION CF328229
VERSION CF328229.1 GI:33804704
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-A13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTT 2177
||||||||||||
Db 12 TTTTTTTTTTTT 1

RESULT 3593
CF329141
LOCUS CF329141 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-F18, mRNA sequence.
ACCESSION CF329141
VERSION CF329141.1 GI:33806519
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-F18"
/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTT 2177
||||||||||||
Db 1 TTTTTTTTTTTT 12

RESULT 3594
CF329141/c
LOCUS CF329141 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-F18, mRNA sequence.
ACCESSION CF329141
VERSION CF329141.1 GI:33806519
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAA 2797
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Db 12 AAAAAAAAAAAA 1

RESULT 3595
CF329142
LOCUS CF329142 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-F18.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-F18, mRNA sequence.
ACCESSION CF329142
VERSION CF329142.1 GI:33806520
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAA 2797
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Db 1 AAAAAAAAAAAA 12

RESULT 3596
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ACCESSION CF329142
VERSION CF329142.1 GI:33806520
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
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/cultivar="Nackdong"
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                     RT-PCR."

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Qy       2166 TTTTTTTTTTTT 2177
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Db         12 TTTTTTTTTTTT 1


RESULT 3597
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LOCUS       CF329346                 12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-K07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-K07, mRNA sequence.
ACCESSION   CF329346
VERSION     CF329346.1  GI:33806928
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3598
CF329346/c
LOCUS       CF329346                 12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-K07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-K07, mRNA sequence.
ACCESSION   CF329346
VERSION     CF329346.1  GI:33806928
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Db         12 AAAAAAAAAAAA 1


RESULT 3599
CF329872
LOCUS       CF329872                 12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-F19.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-F19, mRNA sequence.
ACCESSION   CF329872
VERSION     CF329872.1  GI:33807965
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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Qy       2166 TTTTTTTTTTTT 2177
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Db          1 TTTTTTTTTTTT 12


RESULT 3600
CF329872/c
LOCUS       CF329872                 12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-F19.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-F19, mRNA sequence.
ACCESSION   CF329872
VERSION     CF329872.1  GI:33807965
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Db         12 AAAAAAAAAAAA 1


RESULT 3601
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LOCUS       CF329929                 12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-H03.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-H03, mRNA sequence.
ACCESSION   CF329929
VERSION     CF329929.1  GI:33808079
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
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Qy       2166 TTTTTTTTTTTT 2177
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Db          1 TTTTTTTTTTTT 12


RESULT 3602
CF329929/c
LOCUS       CF329929                 12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-H03.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-H03, mRNA sequence.
ACCESSION   CF329929
VERSION     CF329929.1  GI:33808079
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Qy       2786 AAAAAAAAAAAA 2797
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Db         12 AAAAAAAAAAAA 1


RESULT 3603
CF331241
LOCUS       CF331241                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-E15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-E15, mRNA sequence.
ACCESSION   CF331241
VERSION     CF331241.1  GI:33810705
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     RT-PCR."

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  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
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Db          1 TTTTTTTTTTTT 12


RESULT 3604
CF331241/c
LOCUS       CF331241                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-E15.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION   CF331241
VERSION     CF331241.1  GI:33810705
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
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Qy       2786 AAAAAAAAAAAA 2797
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Db         12 AAAAAAAAAAAA 1


RESULT 3605
CF331858
LOCUS       CF331858                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-C08.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-C08, mRNA sequence.
ACCESSION   CF331858
VERSION     CF331858.1  GI:33811939
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="NACL--08-C08"
                     /tissue_type="callus"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
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  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db          1 AAAAAAAAAAAA 12


RESULT 3606
CF331858/c
LOCUS       CF331858                 12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-C08.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-C08, mRNA sequence.
ACCESSION   CF331858
VERSION     CF331858.1  GI:33811939
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-C08"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db         12 TTTTTTTTTTTT 1


RESULT 3607
CF331904
LOCUS       CF331904                 12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-D07.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-D07, mRNA sequence.
ACCESSION   CF331904
VERSION     CF331904.1  GI:33812029
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-D07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db          1 AAAAAAAAAAAA 12


RESULT 3608
CF331904/c
LOCUS       CF331904                 12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-D07.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-D07, mRNA sequence.
ACCESSION   CF331904
VERSION     CF331904.1  GI:33812029
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-D07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db         12 TTTTTTTTTTTT 1


RESULT 3609
CF331950
LOCUS       CF331950                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-E07, mRNA sequence.
ACCESSION   CF331950
VERSION     CF331950.1  GI:33812121
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-E07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3610
CF331950/c
LOCUS       CF331950                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-E07, mRNA sequence.
ACCESSION   CF331950
VERSION     CF331950.1  GI:33812121
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3611
CF332993
LOCUS       CF332993                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-L10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--01-L10, mRNA sequence.
ACCESSION   CF332993
VERSION     CF332993.1  GI:33814228
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .12
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3612
CF332993/c
LOCUS       CF332993                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-L10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--01-L10, mRNA sequence.
ACCESSION   CF332993
VERSION     CF332993.1  GI:33814228
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3613
CF333992
LOCUS       CF333992                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-B22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-B22, mRNA sequence.
ACCESSION   CF333992
VERSION     CF333992.1  GI:33816288
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 3614
CF333992/c
LOCUS       CF333992                  12 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-B22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-B22, mRNA sequence.
ACCESSION   CF333992
VERSION     CF333992.1  GI:33816288
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="Oryza sativa"
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                      /db_xref="taxon:4530"
                      /clone="JMT--03-B22"
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                      /dev_stage="14 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                      cDNA library (JMT)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                      was reverse transcribed and then used for PCR. mRNA was
                      pepared from Arabidopsis Jasmoinate Carboxyl
                      methyltransferase overexpression line."

  Query Match             0.4%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         12 AAAAAAAAAAAA 1


RESULT 3615
BQ591949
LOCUS       BQ591949                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012580-024-016-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-016-C15 5-PRIME, mRNA sequence.
ACCESSION   BQ591949
VERSION     BQ591949.1  GI:26121532
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 16  row: C  column: 15
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
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                      /cultivar="KWS2320 (double haploid, monogerm breeding
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                      /db_xref="GABI:188168"
                      /db_xref="taxon:161934"
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                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-storage root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.4%;  Score 12;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          2 TTTTTTTTTTTT 13


RESULT 3616
BQ591949/c
LOCUS       BQ591949                 14 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012580-024-016-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-016-C15 5-PRIME, mRNA sequence.
ACCESSION   BQ591949
VERSION     BQ591949.1  GI:26121532
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 14   Std Error: 0.00
            Plate: 16  row: C  column: 15
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding
                      line)"
                      /db_xref="GABI:188168"
                      /db_xref="taxon:161934"
                      /clone="024-016-C15"
                      /tissue_type="storage root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-storage root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
```

RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         13 AAAAAAAAAAAA 2
```

RESULT 3617
CF291593
LOCUS CF291593 14 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-B10.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-B10, mRNA sequence.
ACCESSION CF291593
VERSION CF291593.1 GI:33660626
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-B10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1771 TTTTTTTTTTTG 1782
              ||||||||||||
Db          1 TTTTTTTTTTTG 12
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RESULT 3618
CF330198
LOCUS CF330198 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-N04.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-N04, mRNA sequence.
ACCESSION CF330198
VERSION CF330198.1 GI:33808624
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-N04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          3 TTTTTTTTTTTT 14
```

RESULT 3619
CF330198/c
LOCUS CF330198 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-N04.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-N04, mRNA sequence.
ACCESSION CF330198
VERSION CF330198.1 GI:33808624
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-N04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAA 2797
             ||||||||||||
Db         14 AAAAAAAAAAAA 3
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RESULT 3620
AW249689/c
LOCUS AW249689 15 bp mRNA linear EST 07-JAN-2000
DEFINITION 2819706.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819706 3', mRNA sequence.
ACCESSION AW249689
VERSION AW249689.1 GI:6592682
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 15)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2819706.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 13 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM2 row: E column: 19
High quality sequence stop: 13.
FEATURES Location/Qualifiers
source 1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819706"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAA 2795
             ||||||||||||
Db         12 TGAAAAAAAAAA 1
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RESULT 3621
AW250976/c
LOCUS AW250976 15 bp mRNA linear EST 07-JAN-2000
DEFINITION 2822229.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822229 3', mRNA sequence.
ACCESSION AW250976
VERSION AW250976.1 GI:6594065
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 15)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2822229.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 11 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM8 row: N column: 22
High quality sequence stop: 11.
FEATURES Location/Qualifiers
source 1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822229"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2784 TGAAAAAAAAAA 2795
             ||||||||||||
Db         12 TGAAAAAAAAAA 1
```

RESULT 3622
AW248540

```
LOCUS       AW248540                 16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820844.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820844 3',
            mRNA sequence.
ACCESSION   AW248540
VERSION     AW248540.1  GI:6591533
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820844.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 15
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: E  column: 5
            High quality sequence stop: 15.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820844"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAA 2188
              ||||||||||||
Db          1 TTTTTTTTTTAA 12


RESULT 3623
AW246518/c
LOCUS       AW246518                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821785.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821785 3',
            mRNA sequence.
ACCESSION   AW246518
VERSION     AW246518.1  GI:6589511
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821785.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 15
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 17 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: L  column: 10
            High quality sequence stop: 15.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821785"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAA 2795
              ||||||||||||
Db         12 TGAAAAAAAAAA 1


RESULT 3624
AW249853/c
LOCUS       AW249853                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821520.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821520 3',
            mRNA sequence.
ACCESSION   AW249853
VERSION     AW249853.1  GI:6592846
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
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COMMENT     Other_ESTs: 2821520.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 18 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM7  row: A  column: 9.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2821520"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_7"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAA 2795
              ||||||||||||
Db         12 TGAAAAAAAAAA 1


RESULT 3625
AW249970
LOCUS       AW249970                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821763.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821763 3',
            mRNA sequence.
ACCESSION   AW249970
VERSION     AW249970.1  GI:6592963
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821763.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 18 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM7  row: K  column: 12
            High quality sequence stop: 9.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2821763"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_7"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12;  DB 1;  Length 18;
  Best Local Similarity   92.3%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAA 1784
              |||||||||| ||
Db          1 TTTTTTTTTTNAA 13


RESULT 3626
AW249970/c
LOCUS       AW249970                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821763.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821763 3',
            mRNA sequence.
ACCESSION   AW249970
VERSION     AW249970.1  GI:6592963
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821763.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 18 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
```

of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: K column: 12
High quality sequence stop: 9.

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FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821763"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12;  DB 1;  Length 18;
  Best Local Similarity   92.3%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAA 2795
              || ||||||||||
Db         13 TTNAAAAAAAAAA 1


RESULT 3627
AW251048
LOCUS        AW251048                  18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION   2821495.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821495 3',
             mRNA sequence.
ACCESSION    AW251048
VERSION      AW251048.1  GI:6593994
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 18)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Other_ESTs: 2821495.5prime
             Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
             Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
             Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
             project Clone distribution: MGC clone distribution information can
             be found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
             Scores: PHRED from University of Washington Genome Center. Vector
             Trimming: cross_match from University of Washington Genome Center
             PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
             Drosophila Genome Project. University of Washington Genome Center:
             http://www.genome.washington.edu Low Quality Sequence: 10
             contiguous PHRED high quality bases following vector sequence. Very
             Low Quality Sequence: Trace file contained 18 contiguous distinct
             peaks following vector sequence. Polyadenylation: Based upon the
             presence of a XhoI site followed by a run of 14 or more T residues
             at the beginning of the sequence, this cDNA insert was
             polyadenylated.
             Plate: LLCM6 row: P column: 8
             High quality sequence stop: 10.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821495"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAA 2188
              ||||||||||||
Db          1 TTTTTTTTTTAA 12


RESULT 3628
AZ772074/c
LOCUS        AZ772074                  20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION   1M0574M10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
             clone UUGC1M0574M10 R, genomic survey sequence.
ACCESSION    AZ772074
VERSION      AZ772074.1  GI:12895006
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 20)
  AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
             Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
             Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
  JOURNAL    Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000  Std Error: 0.00
             Plate: 0574  row: M  column: 10
             Seq primer: CACACAGGAAACAGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0574M10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       1854 ACAGACCCACACACTTAGCC 1873
              ||| || |||||||   |||
Db         20 ACACACACACACACACTGCC 1
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RESULT 3629
CF322590/c
LOCUS CF322590 20 bp mRNA linear EST 18-AUG-2003
DEFINITION HDN--01-I03.g1 OsHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-I03, mRNA sequence.
ACCESSION CF322590
VERSION CF322590.1 GI:33793421
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--01-I03"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2785 GAAAAAAAAAAA 2796
              ||||||||||||
Db         12 GAAAAAAAAAAA 1
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RESULT 3630
AZ427740
LOCUS AZ427740 20 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0209J23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0209J23 R, genomic survey sequence.
ACCESSION AZ427740
VERSION AZ427740.1 GI:10551753
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0209 row: J column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0209J23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAA 2797
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Db          2 AAAAAAAAAAAA 13


RESULT 3631
AZ967472
LOCUS       AZ967472                 21 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0238L20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0238L20 F, genomic survey sequence.
ACCESSION   AZ967472
VERSION     AZ967472.1  GI:13838699
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0238  row: L  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0238L20"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12;  DB 1;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 4.3e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        555 GGCTGGAGGCGGGCGCGGTG 574
              ||  || || |||||||| |
Db          1 GGGGGGGGGGGGGCGCGGGG 20


RESULT 3632
AW248826/c
LOCUS       AW248826                 21 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821056.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821056 3',
            mRNA sequence.
ACCESSION   AW248826
VERSION     AW248826.1  GI:6591819
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821056.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 21
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 21 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM5  row: N  column: 1
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821056"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 12;  DB 1;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 4.3e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAA 2796
              ||||  |   ||||||||||
Db         20 TTAGGGTCCCAAAAAAAAAA 1


RESULT 3633
AZ665864/c
LOCUS       AZ665864                 24 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0547I04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0547I04 R, genomic survey sequence.
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ACCESSION   AZ665864
VERSION     AZ665864.1  GI:11803010
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0547  row: I  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0547I04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 12;  DB 1;  Length 24;
  Best Local Similarity   75.0%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        433 CCTGCACCAGCCGGCGCCCA 452
              | | ||||  ||||| ||||
Db         24 CTTACACCCCCCGGCCCCCA 5


RESULT 3634
CF330669
LOCUS       CF330669                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-H16.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-H16, mRNA sequence.
ACCESSION   CF330669
VERSION     CF330669.1  GI:33809573
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-H16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAA 2793
              | |||| ||||||||
Db          1 AAAATTAAAAAAAAA 15


RESULT 3635
AW246494/c
LOCUS       AW246494                 15 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821595.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821595 3',
            mRNA sequence.
ACCESSION   AW246494
VERSION     AW246494.1  GI:6589487
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821595.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 14
```

contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: D column: 12
High quality sequence stop: 14.

```
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821595"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAA 2798
              |||  ||||||||||
Db         15 TGATCAAAAAAAAAA 1


RESULT 3636
CF299603
LOCUS       CF299603                 15 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-L01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
ACCESSION   CF299603
VERSION     CF299603.1  GI:33671364
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-L01"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAA 2793
              | ||||  ||||||||
Db          1 AAAATTTAAAAAAAA 15


RESULT 3637
BM658732
LOCUS       BM658732                 15 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  LZV602768445.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
            sequence.
ACCESSION   BM658732
VERSION     BM658732.1  GI:18959003
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Porcine ESTs
  JOURNAL   Unpublished (2002)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone_lib="CSEQFXL37 pig adrenal"
                     /note="Organ: adrenal gland; Vector: pBluescript SK+;
                     Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
                     GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     non-normalized library, sequenced 3' with M13R primer."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTT 2172
              |||| || |||||||
Db          1 TTTTTTCGTTTTTTT 15


RESULT 3638
BM658732/c
LOCUS       BM658732                 15 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  LZV602768445.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
            sequence.
ACCESSION   BM658732
VERSION     BM658732.1  GI:18959003
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Porcine ESTs
```

```
  JOURNAL   Unpublished (2002)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone_lib="CSEQFXL37 pig adrenal"
                     /note="Organ: adrenal gland; Vector: pBluescript SK+;
                     Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert
                     (5'-NNN. . .NNNinsert)
                     GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                     the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                     non-normalized library, sequenced 3' with M13R primer."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||| ||||||
Db         15 AAAAAAACGAAAAAA 1


RESULT 3639
CF332179
LOCUS       CF332179                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-J10.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-J10, mRNA sequence.
ACCESSION   CF332179
VERSION     CF332179.1  GI:33812582
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-J10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAA 2796
              ||| | |||||||||
Db          1 ATTTATAAAAAAAAA 15


RESULT 3640
CF332179/c
LOCUS       CF332179                 15 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-J10.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-J10, mRNA sequence.
ACCESSION   CF332179
VERSION     CF332179.1  GI:33812582
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-J10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTAACT 2190
              ||||||||| ||| |
Db         15 TTTTTTTTTATAAAT 1


RESULT 3641
AW245338
LOCUS       AW245338                 16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822905.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822905 3',
            mRNA sequence.
ACCESSION   AW245338
VERSION     AW245338.1  GI:6588331
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822905.5prime
```

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM10 row: K column: 2
High quality sequence stop: 15.

```
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822905"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 4.7e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1922 TTTTTTTTCAGTGTT 1936
              ||||||||  |||||
Db          1 TTTTTTTTTTGTGTT 15


RESULT 3642
AI798250
LOCUS       AI798250                 16 bp    mRNA    linear   EST 06-JUL-1999
DEFINITION  tr32b08.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219991 3'
            similar to TR:O79354 O79354 CYTOCHROME OXIDASE SUBUNIT III. ;, mRNA
            sequence.
ACCESSION   AI798250
VERSION     AI798250.1  GI:5363722
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219991"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ov23"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.35 kb. Tumor types include: mixed
                     Mullerian tumor, papillary serous, clear cell, spindle
                     cell. All are primary tumors, metastasis positive. Life
                     Technologies catalog #: 11534-013"

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 4.7e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              | |||||||||| |||
Db          2 ACAAAAAAAAAGAAA 16


RESULT 3643
AI798250/c
LOCUS       AI798250                 16 bp    mRNA    linear   EST 06-JUL-1999
DEFINITION  tr32b08.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219991 3'
            similar to TR:O79354 O79354 CYTOCHROME OXIDASE SUBUNIT III. ;, mRNA
            sequence.
ACCESSION   AI798250
VERSION     AI798250.1  GI:5363722
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2219991"
                     /tissue_type="tumor, 5 pooled (see description)"
                     /lab_host="DH10B"
```

/clone_lib="NCI_CGAP_Ov23"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"

Query Match 0.4%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              ||| |||||||||| |
Db         16 TTTCTTTTTTTTTGT 2
```

RESULT 3644
AW250449/c
LOCUS AW250449 18 bp mRNA linear EST 07-JAN-2000
DEFINITION 2822458.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822458 3', mRNA sequence.
ACCESSION AW250449
VERSION AW250449.1 GI:6593442
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2822458.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 18 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM9 row: H column: 11
High quality sequence stop: 18.
FEATURES Location/Qualifiers
source 1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822458"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2781 AATTGAAAAAAAAAA 2795
              ||  ||||||||||
Db         15 AAGGGAAAAAAAAAA 1
```

RESULT 3645
AZ323986/c
LOCUS AZ323986 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0045P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0045P09 R, genomic survey sequence.
ACCESSION AZ323986
VERSION AZ323986.1 GI:10379252
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: P column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0045P09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
  Query Match             0.4%;  Score 11.8;  DB 1;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 4.7e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||| ||| ||||||
Db         19 AAAACAAACAAAAAA 5


RESULT 3646
AZ810717/c
LOCUS       AZ810717                  19 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0076N24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0076N24 F, genomic survey sequence.
ACCESSION   AZ810717
VERSION     AZ810717.1  GI:12978242
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0076  row: N  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0076N24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 4.7e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||||||  ||
Db         19 TTTTTTTTTTCCAA 5


RESULT 3647
AZ786781/c
LOCUS       AZ786781                  20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0032C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0032C05 R, genomic survey sequence.
ACCESSION   AZ786781
VERSION     AZ786781.1  GI:12924886
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0032  row: C  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0032C05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 4.5e+03;
```

```
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||| | ||
Db         20 AAAAAAAAAATATAA 6


RESULT 3648
AZ810709
LOCUS       AZ810709                23 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0076M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0076M20 F, genomic survey sequence.
ACCESSION   AZ810709
VERSION     AZ810709.1  GI:12978228
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0076  row: M  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0076M20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 11.8;  DB 1;  Length 23;
  Best Local Similarity   86.7%;  Pred. No. 3.9e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2758 TATAATAAAAGTATT 2772
              ||||||||||| | ||
Db          1 TATAATAAAAATTTT 15


RESULT 3649
AI364573/c
LOCUS       AI364573                19 bp    mRNA    linear   EST 15-FEB-1999
DEFINITION  qw37g03.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:1993300 3'
            similar to TR:Q39835 Q39835 EXTENSIN. ;, mRNA sequence.
ACCESSION   AI364573
VERSION     AI364573.1  GI:4124262
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 1632   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1993300"
                     /tissue_type="serous papillary carcinoma, high grade, 2
                     pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut4"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.48 kb. Life Technologies catalog #:
                     11542-016"

  Query Match             0.4%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 4.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         49 GCGCGGCGGGGGCGGCGG 66
              | | || ||||| |||||
Db         19 GTGGGGGGGGGGTGGCGG 2


RESULT 3650
AW248167
LOCUS       AW248167                19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819811.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819811 5',
            mRNA sequence.
ACCESSION   AW248167
VERSION     AW248167.1  GI:6591160
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819811.3prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 14
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 19 contiguous distinct
            peaks following vector sequence. Possible Inverted Insert: Based
            upon the presence of a XhoI site followed by a run of 14 or more T
            residues at the beginning of the sequence, this clone probably
            contains an inverted cDNA insert. EST# does not reflect transcript
            orientation. Possible Chimera: Based upon the presence of a XhoI
            site followed by a run of 14 or more T residues at the beginning of
            this sequence and at the beginning of the sequence from the 3' read
            of this clone, this cDNA insert appears to be chimeric.
            Plate: LLCM2  row: J  column: 4
            High quality sequence stop: 14.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2819811"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_7"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 4.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1773 TTTTTTTTTGAACCCCAT 1790
              ||||||||||     |||||
Db          1 TTTTTTTTTTCTTCCCAT 18


RESULT 3651
AW249918
LOCUS       AW249918                 19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821753.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821753 3',
            mRNA sequence.
ACCESSION   AW249918
VERSION     AW249918.1  GI:6592911
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821753.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 11
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 19 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: K  column: 2
            High quality sequence stop: 11.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2821753"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_7"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 4.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAA 2188
              |||||||||| |  | ||
Db          1 TTTTTTTTTGTCATCAA 18


RESULT 3652
AZ447864/c
LOCUS       AZ447864                 19 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0245A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0245A14 F, genomic survey sequence.
ACCESSION   AZ447864
VERSION     AZ447864.1  GI:10600087
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: A column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0245A14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2778 TAGAATTGAAAAAAAAAA 2795
              || || |||| | |||||
Db         18 TAAAAATGAATATAAAAA 1
```

RESULT 3653
AZ345537
LOCUS AZ345537 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080P01 F, genomic survey sequence.
ACCESSION AZ345537
VERSION AZ345537.1 GI:10424774
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: P column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 11.6; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||| ||||   |||||
Db          2 AAAAATAAAATTTAAAAA 19
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RESULT 3654
AZ493581/c
LOCUS AZ493581 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0328A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0328A24 F, genomic survey sequence.
ACCESSION AZ493581
VERSION AZ493581.1 GI:10667400
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

```
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000   Std Error: 0.00
          Plate: 0328  row: A  column: 24
          Seq primer: CGTTGTAAAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0328A24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.4%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 4.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         49 GCGCGGCGGGGGCGGCGG 66
              | | || ||||||||| ||
Db         19 GGGGGGGGGGGGCGGGGG 2


RESULT 3655
AZ369369/c
LOCUS       AZ369369                 19 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0119K19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0119K19 R, genomic survey sequence.
ACCESSION   AZ369369
VERSION     AZ369369.1  GI:10483069
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0119  row: K  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0119K19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match              0.4%;  Score 11.6;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 4.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        296 CCACCCCTCTCCCACACT 313
              || |||| | | ||||||
Db         18 CCCCCCCCCACACACACT 1


RESULT 3656
AA888191
LOCUS       AA888191                 22 bp    mRNA    linear   EST 31-MAR-1998
DEFINITION  of82a05.s1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:1436816 3'
            similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ;, mRNA sequence.
ACCESSION   AA888191
VERSION     AA888191.1  GI:3003866
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
```

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            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1436816"
                      /tissue_type="hepatic adenoma"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Li5"
                      /note="Organ: liver; Vector: pCMV-SPORT4; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 0.8 kb."

  Query Match             0.4%;  Score 11.6;  DB 1;  Length 22;
  Best Local Similarity   77.8%;  Pred. No. 4.1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              || |||| |||| || ||
Db          2 AACAAAATAAAAGAAGAA 19


RESULT 3657
CF291593/c
LOCUS       CF291593                 14 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-B10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-B10, mRNA sequence.
ACCESSION   CF291593
VERSION     CF291593.1  GI:33660626
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="14ROOT--02-B10"
                      /tissue_type="root"
                      /dev_stage="14 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.4%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 4.5e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAA 2797
              | ||||||||||||
Db         13 GCAAAAAAAAAAA 1


RESULT 3658
AW246551/c
LOCUS       AW246551                 15 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2822090.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822090 3',
            mRNA sequence.
ACCESSION   AW246551
VERSION     AW246551.1  GI:6589544
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2822090.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 14
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 15 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM8  row: I  column: 3
            High quality sequence stop: 14.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2822090"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_7"
                      /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                      EcoRI; cDNA made by oligo-dT priming.  Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGCACGAG(G).  Size-selected >500bp for average
                      insert size 1.8kb.  Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 4.9e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAA 2795
              || ||||||||||
Db         13 TTTAAAAAAAAAA 1


RESULT 3659
AW249689
LOCUS       AW249689                 15 bp    mRNA    linear   EST 07-JAN-2000
```

```
DEFINITION  2819706.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819706 3',
            mRNA sequence.
ACCESSION   AW249689
VERSION     AW249689.1  GI:6592682
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819706.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 13
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 15 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM2  row: E  column: 19
            High quality sequence stop: 13.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819706"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 4.9e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAAC 2189
              ||||||||||  ||
Db          1 TTTTTTTTTTCAC 13


RESULT 3660
AW246490
LOCUS       AW246490                 16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821591.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821591 3',
            mRNA sequence.
ACCESSION   AW246490
VERSION     AW246490.1  GI:6589483
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821591.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 12
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: D  column: 8
            High quality sequence stop: 12.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821591"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11.4;  DB 1;  Length 16;
  Best Local Similarity   92.3%;  Pred. No. 5e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1772 TTTTTTTTTTGAA 1784
              ||||||||||| |
Db          1 TTTTTTTTTTGCA 13


RESULT 3661
AW248540/c
LOCUS       AW248540                 16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820844.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820844 3',
            mRNA sequence.
ACCESSION   AW248540
VERSION     AW248540.1  GI:6591533
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820844.5prime
```

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM5 row: E column: 5
High quality sequence stop: 15.

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FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820844"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11.4;  DB 1;  Length 16;
  Best Local Similarity   92.3%;  Pred. No. 5e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAA 2795
              || ||||||||||
Db         13 TTTAAAAAAAAAA 1


RESULT 3662
AW251033/c
LOCUS       AW251033                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821399.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821399 3',
            mRNA sequence.
ACCESSION   AW251033
VERSION     AW251033.1  GI:6593979
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821399.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 17
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 17 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM6 row: L column: 8
            High quality sequence stop: 17.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821399"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11.4;  DB 1;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 5e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAA 2795
              || ||||||||||
Db         13 TTCAAAAAAAAAA 1


RESULT 3663
AW246528/c
LOCUS       AW246528                 17 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821879.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821879 3',
            mRNA sequence.
ACCESSION   AW246528
VERSION     AW246528.1  GI:6589521
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821879.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 13
            contiguous PHRED high quality bases following vector sequence. Very
```

Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: P column: 8
High quality sequence stop: 13.

FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821879"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 5e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAA 2795
|| ||||||||||
Db 13 TTTAAAAAAAAAA 1

RESULT 3664
AW246518
LOCUS AW246518 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821785.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821785 3', mRNA sequence.
ACCESSION AW246518
VERSION AW246518.1 GI:6589511
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821785.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: L column: 10
High quality sequence stop: 15.

FEATURES Location/Qualifiers
source 1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821785"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 5e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2177 TTTTTTTTTTAAC 2189
|||||||||| ||
Db 1 TTTTTTTTTTCAC 13

RESULT 3665
AW249853
LOCUS AW249853 18 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821520.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821520 3', mRNA sequence.
ACCESSION AW249853
VERSION AW249853.1 GI:6592846
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821520.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: A column: 9.

FEATURES Location/Qualifiers
source 1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821520"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 18;
Best Local Similarity 92.3%; Pred. No. 4.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2177 TTTTTTTTTTAAC 2189
              ||||||||||  ||
Db          1 TTTTTTTTTCAC 13
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RESULT 3666
AW251048/c
LOCUS AW251048 18 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821495.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821495 3', mRNA sequence.
ACCESSION AW251048
VERSION AW251048.1 GI:6593994
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821495.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 10 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM6 row: P column: 8
High quality sequence stop: 10.

FEATURES Location/Qualifiers
source 1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821495"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 18;
Best Local Similarity 92.3%; Pred. No. 4.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2783 TTGAAAAAAAAAA 2795
              || ||||||||||
Db         13 TTTAAAAAAAAAA 1
```

RESULT 3667
AZ995149/c
LOCUS AZ995149 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0280D22R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0280D22 R, genomic survey sequence.
ACCESSION AZ995149
VERSION AZ995149.1 GI:13866376
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0280 row: D column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0280D22"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.4%; Score 11.4; DB 1; Length 19;
Best Local Similarity 92.3%; Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        458 AGCCAGCAGCAGG 470
              || ||||||||||
Db         15 AGGCAGCAGCAGG 3
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RESULT 3668
AZ514586
LOCUS AZ514586 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0361B17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0361B17 F, genomic survey sequence.
ACCESSION AZ514586
VERSION AZ514586.1 GI:10695818
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: B column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361B17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 11.4; DB 1; Length 19;
Best Local Similarity 92.3%; Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAAA 2796
              || ||||||||||
Db          5 TGCAAAAAAAAAA 17
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RESULT 3669
AZ308410
LOCUS AZ308410 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0011A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0011A24 F, genomic survey sequence.
ACCESSION AZ308410
VERSION AZ308410.1 GI:10348378
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: A column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0011A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.4%;  Score 11.4;  DB 1;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.5e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        110 GGGGGCTGGGGGG 122
              |||||| ||||||
Db          2 GGGGGCGGGGGGG 14
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RESULT 3670
AZ469472/c
LOCUS AZ469472 20 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0283A06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0283A06 F, genomic survey sequence.
ACCESSION AZ469472
VERSION AZ469472.1 GI:10627597
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0283 row: A column: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0283A06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.4%;  Score 11.4;  DB 1;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.5e+03;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAG 1991
              ||||||| |||||
Db         20 AAAAAAACAAAAG 8
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RESULT 3671
AZ303903
LOCUS AZ303903 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0003B18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0003B18 R, genomic survey sequence.
ACCESSION AZ303903
VERSION AZ303903.1 GI:10339339
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: B column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0003B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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  Query Match             0.4%;  Score 11.4;  DB 1;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.5e+03;
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```
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2568 CTGTTCTTGGCTT 2580
              |||||| ||||||
Db          1 CTGTTCCTGGCTT 13


RESULT 3672
BQ583458
LOCUS       BQ583458                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E011979-024-005-J11-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-005-J11 5-PRIME, mRNA sequence.
ACCESSION   BQ583458
VERSION     BQ583458.1  GI:26113035
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 5  row: J  column: 11
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:183240"
                     /db_xref="taxon:161934"
                     /clone="024-005-J11"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.4%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 5.2e+03;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1980 AAAAAAGAAAAGTGTG 1995
              |||||| ||||| | |
Db          1 AAAAAAAAAAAGGGGG 16


RESULT 3673
AZ440413/c
LOCUS       AZ440413                 19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0231A01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0231A01 R, genomic survey sequence.
ACCESSION   AZ440413
VERSION     AZ440413.1  GI:10564426
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0231  row: A  column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0231A01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 11.2;  DB 1;  Length 19;
  Best Local Similarity   81.2%;  Pred. No. 4.7e+03;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              |||| ||| | |||||
Db         18 GAAAGAAAGAGAAAAA 3


RESULT 3674
AZ957966/c
LOCUS       AZ957966                 20 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0225I01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
```

```
            clone UUGC2M0225I01 F, genomic survey sequence.
ACCESSION   AZ957966
VERSION     AZ957966.1  GI:13829193
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0225  row: I  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0225I01"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 11.2;  DB 1;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1980 AAAAAAGAAAAGTGTG 1995
              |||||| ||||| | |
Db         20 AAAAAAAAAAAGGGGG 5


RESULT 3675
D20705
LOCUS       D20705                    22 bp    mRNA    linear   EST 30-JUL-1996
DEFINITION  HUMGS01681 Human promyelocyte Homo sapiens cDNA clone pm2012 3',
            mRNA sequence.
ACCESSION   D20705
VERSION     D20705.1  GI:501801
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y.,
            Yoshinari,H., Arimoto,J. and Matsubara,K.
  TITLE     Gene expression of human promyelocytic cell line HL60 before and
            after induction of differentiation. A new application of 3'directed
            cDNA sequencing
  JOURNAL   Unpublished (1993)
COMMENT     Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y.,
            Yoshinari,H., Arimoto,J. and Matsubara,K.
            Institute for Molecular and Cellular Biology
            Osaka University
            3-1 Yamada-oka,Suita,Osaka 565,Japan.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="pm2012"
                     /clone_lib="Human promyelocyte"
                     /note="Female, adult, cell_line = HL60, cell_type =
                     promyelocyte. "

  Query Match             0.4%;  Score 11.2;  DB 1;  Length 22;
  Best Local Similarity   76.5%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAA 2793
              ||| || | |||| |||
Db          6 TTAAAAGTNAAAATAAA 22


RESULT 3676
CF291636/c
LOCUS       CF291636                  24 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-C09.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-C09, mRNA sequence.
ACCESSION   CF291636
VERSION     CF291636.1  GI:33660669
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-C09"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 11.2; DB 1; Length 24;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy         50 CGCGGCGGGGGCGGCGGCAGACGC 73
              ||| || |  || || || | |||
Db         24 CGCCGCCGCCGCCGCCGCCGCCGC 1
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RESULT 3677
AW250976
LOCUS AW250976 15 bp mRNA linear EST 07-JAN-2000
DEFINITION 2822229.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822229 3', mRNA sequence.
ACCESSION AW250976
VERSION AW250976.1 GI:6594065
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 15)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2822229.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washingtion Genome Center. Vector Trimming: cross_match from University of Washingtion Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion Genome Center: http://www.genome.washington.edu Low Quality Sequence: 11 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM8 row: N column: 22
High quality sequence stop: 11.
FEATURES Location/Qualifiers
source 1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822229"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1922 TTTTTTTTCAG 1932
              ||||||||||
Db          3 TTTTTTTTCAG 13
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RESULT 3678
AW246520
LOCUS AW246520 18 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821787.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821787 3', mRNA sequence.
ACCESSION AW246520
VERSION AW246520.1 GI:6589513
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821787.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washingtion Genome Center. Vector Trimming: cross_match from University of Washingtion Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion Genome Center: http://www.genome.washington.edu Low Quality Sequence: 16 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: L column: 12
High quality sequence stop: 16.
FEATURES Location/Qualifiers
source 1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821787"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1772 TTTTTTTTTTG 1782
              ||||||||||
Db          1 TTTTTTTTTTG 11
```

```
RESULT 3679
AZ328922/c
LOCUS       AZ328922                19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0052L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0052L22 R, genomic survey sequence.
ACCESSION   AZ328922
VERSION     AZ328922.1  GI:10389127
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0052  row: L  column: 22
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0052L22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 11;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 4.8e+03;
  Matches   14;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              || || ||||  | |||||
Db         19 AAGAAGAAAAGTAGAAAAA 1


RESULT 3680
AW248934/c
LOCUS       AW248934                19 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819262.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819262 3',
            mRNA sequence.
ACCESSION   AW248934
VERSION     AW248934.1  GI:6591927
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819262.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 19 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM1  row: C  column: 7
            High quality sequence stop: 8.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819262"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.4%;  Score 11;  DB 1;  Length 19;
  Best Local Similarity   73.7%;  Pred. No. 4.8e+03;
  Matches   14;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||||     ||||||||||
Db         19 GAAAGTCCCAAAAAAAAAA 1


RESULT 3681
CF317946/c
LOCUS       CF317946                20 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-N06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-N06, mRNA sequence.
ACCESSION   CF317946
VERSION     CF317946.1  GI:33689707
KEYWORDS    EST.
SOURCE      Oryza sativa
```

```
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--07-N06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.4%;  Score 11;  DB 1;  Length 20;
  Best Local Similarity   73.7%;  Pred. No. 4.5e+03;
  Matches   14;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        432 CCCTGCACCAGCCGGCGCC 450
              | ||||  | |||| ||||
Db         20 CGCTGCCGCCGCCGCCGCC 2


RESULT 3682
AZ512414/c
LOCUS       AZ512414                20 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0357J21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0357J21 R, genomic survey sequence.
ACCESSION   AZ512414
VERSION     AZ512414.1  GI:10693730
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0357  row: J  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0357J21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 11;  DB 1;  Length 20;
  Best Local Similarity   73.7%;  Pred. No. 4.5e+03;
  Matches   14;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        471 CCTGGCCCGGCCGCCAGAG 489
              || | ||| ||||||  ||
Db         19 CCCGCCCCCGCCGCCCCAG 1


RESULT 3683
AZ331046/c
LOCUS       AZ331046                21 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0056K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0056K08 R, genomic survey sequence.
ACCESSION   AZ331046
VERSION     AZ331046.1  GI:10393185
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0056  row: K  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
```

```
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0056K08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 11;  DB 1;  Length 21;
  Best Local Similarity   73.7%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2736 ATTGTTGTGTGTATGATAC 2754
              ||   ||| ||||| ||||
Db         21 ATATATGTATGTATAATAC 3


RESULT 3684
TA181E11P
LOCUS       TA181E11P                22 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 181e11, forward sequence,
            genomic survey sequence.
ACCESSION   AL474328
VERSION     AL474328.1  GI:11839616
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="181e11"

  Query Match             0.4%;  Score 11;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAA 2796
              |||||||||||
Db          9 AAAAAAAAAAA 19


RESULT 3685
AW251049/c
LOCUS       AW251049                 16 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821507.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821507 3',
            mRNA sequence.
ACCESSION   AW251049
VERSION     AW251049.1  GI:6593995
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821507.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washingtion Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 10
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 16 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM6  row: P  column: 20
            High quality sequence stop: 10.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821507"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
```

(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 5.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAAAA 2797
              || |||||||||
Db         14 TGTTAAAAAAAAAA 1
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RESULT 3686
BQ588093
LOCUS BQ588093 16 bp mRNA linear EST 06-DEC-2002
DEFINITION E012336-024-009-A19-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-009-A19 5-PRIME, mRNA sequence.
ACCESSION BQ588093
VERSION BQ588093.1 GI:26117675
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 9 row: A column: 19
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:184766"
/db_xref="taxon:161934"
/clone="024-009-A19"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 5.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1494 AGAAAATGGAGAAA 1507
              | |||| |||||||
Db          1 AAAAAAGGGAGAAA 14
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RESULT 3687
AW246451/c
LOCUS AW246451 18 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821637.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821637 3', mRNA sequence.
ACCESSION AW246451
VERSION AW246451.1 GI:6589444
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821637.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 9 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: F column: 6
High quality sequence stop: 9.
FEATURES Location/Qualifiers
source 1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821637"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 10.8; DB 1; Length 18;
Best Local Similarity 85.7%; Pred. No. 5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2784 TGAAAAAAAAAAAA 2797
              || |||||||||
Db         14 TGTTAAAAAAAAAA 1
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RESULT 3688
AZ803756/c
LOCUS AZ803756 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0064M15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0064M15 F, genomic survey sequence.
ACCESSION AZ803756
VERSION AZ803756.1 GI:12956079

```
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0064  row: M  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0064M15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 10.8;  DB 1;  Length 19;
  Best Local Similarity   85.7%;  Pred. No. 4.8e+03;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2026 GGTAGGAGGCAAAG 2039
              || | |||||||||
Db         15 GGAACGAGGCAAAG 2

RESULT 3689
AZ786308
LOCUS       AZ786308                 19 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0031B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0031B17 R, genomic survey sequence.
ACCESSION   AZ786308
VERSION     AZ786308.1  GI:12923936
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0031  row: B  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0031B17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 10.8;  DB 1;  Length 19;
  Best Local Similarity   85.7%;  Pred. No. 4.8e+03;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        110 GGGGGCTGGGGGGA 123
              ||| | ||||||||
Db          6 GGGAGGTGGGGGGA 19

RESULT 3690
AZ595570
LOCUS       AZ595570                 19 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0408I15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0408I15 F, genomic survey sequence.
ACCESSION   AZ595570
VERSION     AZ595570.1  GI:11717760
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
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  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0408  row: I  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0408I15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.4%;  Score 10.8;  DB 1;  Length 19;
  Best Local Similarity   85.7%;  Pred. No. 4.8e+03;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1710 ATCTCCTAACTTTG 1723
              | |||| |||||||
Db          3 AGCTCCAAACTTTG 16


RESULT 3691
AU257221/c
LOCUS       AU257221                 20 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU257221 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0010046 3', mRNA sequence.
ACCESSION   AU257221
VERSION     AU257221.1  GI:20321628
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="BED0010046"
                     /tissue_type="brain"
                     /clone_lib="3'-directed mouse cDNA library"

  Query Match             0.4%;  Score 10.8;  DB 1;  Length 20;
  Best Local Similarity   85.7%;  Pred. No. 4.5e+03;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1515 AATAAAATTGGAAC 1528
              ||| |||||||| |
Db         14 AATCAAATTGGATC 1


RESULT 3692
AZ789280
LOCUS       AZ789280                 20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0037A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0037A08 F, genomic survey sequence.
ACCESSION   AZ789280
VERSION     AZ789280.1  GI:12930134
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0037  row: A  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0037A08"
                     /sex="Male"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 10.8; DB 1; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2782 ATTGAAAAAAAAAA 2795
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Db          5 ATTAAAAAAAAATA 18
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RESULT 3693
AZ629111/c
LOCUS AZ629111 21 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0481D22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0481D22 R, genomic survey sequence.
ACCESSION AZ629111
VERSION AZ629111.1 GI:11751301
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0481 row: D column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0481D22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 10.8; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1854 ACAGACCCACACAC 1867
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Db         15 ACACACACACACAC 2
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RESULT 3694
BH791022
LOCUS BH791022 25 bp DNA linear GSS 02-APR-2002
DEFINITION SALK_058381.35.95.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_058381.35.95.x, genomic survey sequence.
ACCESSION BH791022
VERSION BH791022.1 GI:19884432
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 25)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g36950.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .25
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_058381.35.95.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

Query Match 0.4%; Score 10.8; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1825 AGAATCTTTTAAAT 1838
              ||||| |||||| |
Db         10 AGAATATTTTAATT 23
```

RESULT 3695
AA878744
LOCUS AA878744 19 bp mRNA linear EST 25-MAR-1998
DEFINITION of85a08.s1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:1437110 3' similar to TR:Q67633 Q67633 ECO Q PROTEIN. [1] ;contains TAR1.t2 TAR1 repetitive element ;, mRNA sequence.
ACCESSION AA878744
VERSION AA878744.1 GI:2987709
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1437110"
/tissue_type="hepatic adenoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Li5"
/note="Organ: liver; Vector: pCMV-SPORT4; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 0.8 kb."

Query Match 0.4%; Score 10.6; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       1660 TCTGCATCACCCGCCCC 1676
              ||||| | ||| ||||
Db          2 TCTGCCCCCCCCCCCCC 18
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RESULT 3696
AZ782026/c
LOCUS AZ782026 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0021I23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0021I23 R, genomic survey sequence.
ACCESSION AZ782026
VERSION AZ782026.1 GI:12915307
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0021 row: I column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0021I23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 10.6; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        618 CCCACGCACACGCCCTG 634
              ||||| | |||  ||||
Db         19 CCCACCCGCACCTCCTG 3
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RESULT 3697
AZ828826
LOCUS AZ828826 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0106O01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0106O01 F, genomic survey sequence.
ACCESSION AZ828826
VERSION AZ828826.1 GI:12998734
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

```
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0106  row: O  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC2M0106O01"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."

  Query Match             0.4%;  Score 10.6;  DB 1;  Length 20;
  Best Local Similarity   76.5%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1913 AACAATACCTTTTTTTT 1929
              || |||||| ||| | |
Db          1 AATAATACCATTTATAT 17


RESULT 3698
AZ387816
LOCUS       AZ387816                 20 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0147B22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0147B22 R, genomic survey sequence.
ACCESSION   AZ387816
VERSION     AZ387816.1  GI:10501524
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0147  row: B  column: 22
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0147B22"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."

  Query Match             0.4%;  Score 10.6;  DB 1;  Length 20;
  Best Local Similarity   76.5%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1784 ACCCCATTCTTTCCTTC 1800
              || ||||| | |||| |
Db          4 ACTCCATTTTCTCCTCC 20


RESULT 3699
BQ591425/c
LOCUS       BQ591425                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012712-024-017-C11-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-C11 3-PRIME, mRNA sequence.
ACCESSION   BQ591425
VERSION     BQ591425.1  GI:26121008
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
```

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          fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 17  row: C  column: 11
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188698"
                     /db_xref="taxon:161934"
                     /clone="024-017-C11"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.4%;  Score 10.4;  DB 1;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2467 TTTTAATATTAA 2478
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Db         14 TTTTAATAGTAA 3


Search completed: June 10, 2004, 13:03:18
Job time : 93 secs
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Db          16 GAAAAAAAAAAA 5


RESULT 3696
US-10-362-262-2/c
; Sequence 2, Application US/10362262
; Publication No. US20040014636A1
; GENERAL INFORMATION:
;  APPLICANT: Brodin et al.
;  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING A MODULATOR OF ADAMTS-1
;  FILE REFERENCE: ASZD-P01-138
;  CURRENT APPLICATION NUMBER: US/10/362,262
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: PCT/GB01/03650
;  PRIOR FILING DATE: 2001-08-16
;  PRIOR APPLICATION NUMBER: SE 0002973-6
;  PRIOR FILING DATE: 2000-08-22
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PCR primer
US-10-362-262-2

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
                ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 3697
US-10-362-607-4/c
; Sequence 4, Application US/10362607
; Publication No. US20040096842A1
; GENERAL INFORMATION:
;  APPLICANT: Brodin , Peter
;  APPLICANT:  Thelin, Anders Lars
;  TITLE OF INVENTION: MOLECULES INVOLVED IN THE REGULATION OF
;  TITLE OF INVENTION:  INSULIN RESISTANCE SYNDROME (IRS)
;  FILE REFERENCE: 06275-339US1
;  CURRENT APPLICATION NUMBER: US/10/362,607
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: PCT/GB01/03828
;  PRIOR FILING DATE: 2001-08-23
;  PRIOR APPLICATION NUMBER: US 60/228,117
;  PRIOR FILING DATE: 2000-08-28
;  PRIOR APPLICATION NUMBER: US 60/282,496
;  PRIOR FILING DATE: 2000-04-10
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: H-T11-C primer
US-10-362-607-4

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
                ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 3698
US-10-432-803-4/c
; Sequence 4, Application US/10432803
; Publication No. US20040029199A1
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jin Woo
;  TITLE OF INVENTION: HUMAN CERVICAL CANCER 2 PROTOONCOGENE AND PROTEIN ENCODED THEREIN
;  FILE REFERENCE: KJW-0613
;  CURRENT APPLICATION NUMBER: US/10/432,803
;  CURRENT FILING DATE:  2003-05-23
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: KOPATIN 1.5
; SEQ ID NO 4
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: H-T11G anchored oligo-dT primer
US-10-432-803-4

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
                ||||||||||||
Db         15 AAAAAAAAAAAA 4


RESULT 3699
US-10-338-777-262/c
; Sequence 262, Application US/10338777
; Publication No. US20030188343A1
; GENERAL INFORMATION:
;  APPLICANT: Lynx Therapeutics, Inc.
;  APPLICANT:  United States Department of Agriculture
;  APPLICANT:  Bowen, Benjamin A
;  APPLICANT:  Haudenschild, Christian D
;  APPLICANT:  Buckler, Edward S
;  TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants
;  FILE REFERENCE: 37-000510US
;  CURRENT APPLICATION NUMBER: US/10/338,777
;  CURRENT FILING DATE:  2003-01-07
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 262
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-338-777-262

  Query Match             0.4%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
                ||||||||||||
Db         17 AAAAAAAAAAAA 6


Search completed: June 10, 2004, 12:49:50
Job time : 100 secs
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Db         16 GAAAAAAAAAAA 5


RESULT 3692
US-10-432-803-5/c
; Sequence 5, Application US/10432803
; Publication No. US20040029199A1
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jin Woo
;  TITLE OF INVENTION: HUMAN CERVICAL CANCER 2 PROTOONCOGENE AND PROTEIN ENCODED THEREIN
;  FILE REFERENCE: KJW-0613
;  CURRENT APPLICATION NUMBER: US/10/432,803
;  CURRENT FILING DATE:  2003-05-23
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: KOPATIN 1.5
; SEQ ID NO 5
;    LENGTH: 16
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: H-T11C anchored oligo-dT primer
US-10-432-803-5

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 3693
US-10-291-808-58/c
; Sequence 58, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
;  APPLICANT: McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE: P-PH 3457
;  CURRENT APPLICATION NUMBER: US/10/291,808
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: US/09/300,958
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/083,331
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: 60/098,070
;  PRIOR FILING DATE: 1998-08-27
;  PRIOR APPLICATION NUMBER: 60/118,624
;  PRIOR FILING DATE: 1999-02-04
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
;    LENGTH: 16
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-58

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 3694
US-10-291-808-84/c
; Sequence 84, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
;  APPLICANT: McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE: P-PH 3457
;  CURRENT APPLICATION NUMBER: US/10/291,808
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: US/09/300,958
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/083,331
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: 60/098,070
;  PRIOR FILING DATE: 1998-08-27
;  PRIOR APPLICATION NUMBER: 60/118,624
;  PRIOR FILING DATE: 1999-02-04
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
;    LENGTH: 16
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-84

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 3695
US-10-431-304-17/c
; Sequence 17, Application US/10431304
; Publication No. US20030182690A1
; GENERAL INFORMATION:
;  APPLICANT: Clendennen, Stephanie K.
;  APPLICANT:  Kellogg, Jill A.
;  APPLICANT:  Phan, Chau B.
;  APPLICANT:  Mathews, Helena V.
;  APPLICANT:  Webb, Nancy M.
;  TITLE OF INVENTION: Banana and Melon Promoters for
;  TITLE OF INVENTION:  Expression of Transgenes in Plants
;  FILE REFERENCE: 4257-0019.30
;  CURRENT APPLICATION NUMBER: US/10/431,304
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: US/09/527,972
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/125,310
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-19
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;    LENGTH: 16
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: oligonucleotide primer
US-10-431-304-17

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
```

RESULT 3688
US-09-924-946-8/c
; Sequence 8, Application US/09924946
; Patent No. US20020102645A1
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corporation
; APPLICANT: Evans, Mark
; APPLICANT: Scicchitano, Marshall
; APPLICANT: Bapat, Ashok
; APPLICANT: Beer, Eric
; APPLICANT: Bhat, Ramesh
; APPLICANT: Ferris, Elissa
; APPLICANT: Mastroeni, Rob
; APPLICANT: Zhang, Jianxiong
; APPLICANT: Karathanasis, Sotirios K.
; TITLE OF INVENTION: A No. US20020102645A1el Member of the Lysyl Oxidase Gene Family
; FILE REFERENCE: 0630/1G703-US2
; CURRENT APPLICATION NUMBER: US/09/924,946
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/223,763
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/255,838
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-924-946-8

Query Match 0.4%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAA 2796
||||||||||||
Db 15 GAAAAAAAAAAA 4

RESULT 3689
US-09-811-093-22/c
; Sequence 22, Application US/09811093
; Patent No. US20020133850A1
; GENERAL INFORMATION:
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Kellogg, Jill A.
; TITLE OF INVENTION: MELON PROMOTERS FOR EXPRESSION OF
; TITLE OF INVENTION: TRANSGENES IN PLANTS
; FILE REFERENCE: 4257-0025.30
; CURRENT APPLICATION NUMBER: US/09/811,093
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/190,414
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-811-093-22

Query Match 0.4%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAA 2796
||||||||||||
Db 16 GAAAAAAAAAAA 5

RESULT 3690
US-09-997-672-31/c
; Sequence 31, Application US/09997672
; Publication No. US20030061632A1
; GENERAL INFORMATION:
; APPLICANT: Weterings, Koen
; APPLICANT: Apuya, Nestor R.
; APPLICANT: Tatarinova, Tatiana
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; APPLICANT: Ceres, Inc.
; TITLE OF INVENTION: Polynucleotides Useful for Modulationg Transcription
; FILE REFERENCE: 02307O-115810US
; CURRENT APPLICATION NUMBER: US/09/997,672
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,672
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anchor/reverse
; OTHER INFORMATION: primer C primer
US-09-997-672-31

Query Match 0.4%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAA 2796
||||||||||||
Db 16,GAAAAAAAAAAA 5

RESULT 3691
US-10-362-711-8/c
; Sequence 8, Application US/10362711
; Publication No. US20040029141A1
; GENERAL INFORMATION:
; APPLICANT: Brodin, Peter
; APPLICANT: Thelin, Anders Lars
; TITLE OF INVENTION: HUMAN AND MOUSE E2-PROTEIN, NUCLEIC
; TITLE OF INVENTION: ACIDS CODING THEREFOR AND USES THEREOF
; FILE REFERENCE: 06275-340US1
; CURRENT APPLICATION NUMBER: US/10/362,711
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/GB01/03807
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 60/228,118
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: H-T11-C primer
US-10-362-711-8

Query Match 0.4%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAA 2796
||||||||||||

```
;                       EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
;                       THEREOF
;       NUMBER OF SEQUENCES: 37
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Cooper & Dunham LLP
;            STREET: 1185 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: U.S.A
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/809,920
;            FILING DATE: 16-Mar-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/156,191
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: White, John P.
;            REGISTRATION NUMBER: 28,678
;            REFERENCE/DOCKET NUMBER: 0575/51902
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 278-0400
;            TELEFAX: (212) 391-0525
;   INFORMATION FOR SEQ ID NO: 35:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 22 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-809-920-35

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        790 CTGTCAGAAGGAGCTGG 806
              ||||||| |  ||||||
Db          5 CTGTCAGTATTAGCTGG 21


RESULT 3686
US-10-127-890-58
; Sequence 58, Application US/10127890
; Publication No. US20030166196A1
;   GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 173
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/127,890
;            FILING DATE: 23-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,360
;            FILING DATE: 13-MAY-1996
;            APPLICATION NUMBER: PCT/US94/05348
;            FILING DATE: 12-MAY-1994
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
;            TELEFAX: 312/707-9155
;            TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 58:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 22 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-127-890-58

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 3687
US-09-964-261-301
; Sequence 301, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
;  APPLICANT: De Canck, Ilse
;  APPLICANT:  Rombout, Annelles
;  APPLICANT:  Rossau, Rudi
;  TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
;  FILE REFERENCE: IGJ-002
;  CURRENT APPLICATION NUMBER: US/09/964,261
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: EP 99870068.6
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: US 60/138,614
;  PRIOR FILING DATE: 1999-06-11
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 301
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-964-261-301

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 23;
  Best Local Similarity   66.7%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        959 GTTCTCAGAAGAGCCAAATCG 979
              :|||||| | :| || || |
Db          1 RTTCTCAGGATRGTCACATGG 21
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mouse origin
US-10-056-790-67

Query Match 0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1036 GGCCGGGAGGCGGAAAG 1052
|| ||||||| |||||
Db 4 GGAAGGGAGGCTGAAAG 20

RESULT 3681
US-10-728-509-34/c
; Sequence 34, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-34

Query Match 0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1920 CCTTTTTTTTCAGTGTT 1936
|||||| ||||| |||
Db 18 CCTTTTGCTTCAGGGTT 2

RESULT 3682
US-10-728-509-35/c
; Sequence 35, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-35

Query Match 0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1920 CCTTTTTTTTCAGTGTT 1936
|||||| ||||| |||
Db 19 CCTTTTGCTTCAGGGTT 3

RESULT 3683
US-10-303-635-44/c
; Sequence 44, Application US/10303635
; Publication No. US20040102621A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
; FILE REFERENCE: RTS-0418
; CURRENT APPLICATION NUMBER: US/10/303,635
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 257
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-635-44

Query Match 0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 500 GCGGGGCTGCCCTCGCA 516
|| |||| |||| ||||
Db 17 GCAGGGCAGCCCGCGCA 1

RESULT 3684
US-10-227-001-16
; Sequence 16, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
; APPLICANT: Dempcy, Robert O.
; APPLICANT: Afonina, Irina Aleksandrovna
; APPLICANT: Vermeulen, Nicolaas M.J.
; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: Hybridization-Triggered Fluorescent
; TITLE OF INVENTION: Detection of Nucleic Acids
; FILE REFERENCE: 17682A-004210US
; CURRENT APPLICATION NUMBER: US/10/227,001
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 09/428,236
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mismatched target sequence
US-10-227-001-16

Query Match 0.4%; Score 12.2; DB 1; Length 21;
Best Local Similarity 82.4%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2157 TTTTTCTCCTTTTTTTT 2173
| ||||| ||||| |||
Db 1 TCTTTCTTCTTTTCTTT 17

RESULT 3685
US-09-809-920-35
; Sequence 35, Application US/09809920
; Publication No. US20030139584A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING

```
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-949-428-228

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        683 CAGATGGACGAGGTGCA 699
              || ||||| || |||||
Db         20 CAAATGGAAGAAGTGCA 4


RESULT 3677
US-09-824-322B-54/c
; Sequence 54, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Butler, Madeline M.
;  APPLICANT:  Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALP
;  TITLE OF INVENTION:  ALPHA) EXPRESSION
;  FILE REFERENCE: ISPH-0501
;  CURRENT APPLICATION NUMBER: US/09/824,322B
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 09/313,932
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: US 09/166,186
;  PRIOR FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-824-322B-54

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1494 AGAAAATGGAGAAACAC 1510
              | || |||||||||  ||
Db         18 AAAACATGGAGAAAGAC 2


RESULT 3678
US-09-908-147-34/c
; Sequence 34, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
;  FILE REFERENCE: RTS-0185
;  CURRENT APPLICATION NUMBER: US/09/908,147
;  CURRENT FILING DATE:  2001-07-17
;  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-34

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1920 CCTTTTTTTTCAGTGTT 1936
              ||||||  ||||| |||
Db         18 CCTTTTGCTTCAGGGTT 2


RESULT 3679
US-09-908-147-35/c
; Sequence 35, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
;  FILE REFERENCE: RTS-0185
;  CURRENT APPLICATION NUMBER: US/09/908,147
;  CURRENT FILING DATE:  2001-07-17
;  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-35

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1920 CCTTTTTTTTCAGTGTT 1936
              ||||||  ||||| |||
Db         19 CCTTTTGCTTCAGGGTT 3


RESULT 3680
US-10-056-790-67
; Sequence 67, Application US/10056790
; Publication No. US20030165497A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF
;  FILE REFERENCE: RRPCIP2002
;  CURRENT APPLICATION NUMBER: US/10/056,790
;  CURRENT FILING DATE:  2002-01-23
;  PRIOR APPLICATION NUMBER: US 09/908,419
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/219,289
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: US 60/277,487
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: US 60/277,471
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: US 60/304,863
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: US 60/296,076
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/305,017
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: US 60/328,605
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/328,491
;  PRIOR FILING DATE: 2001-10-10
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
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```
; SEQ ID NO 15
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide
US-10-265-689-15

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 4.1e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1787 CCATTCTTTCCTTCTCT 1803
              || | ||| ||||||||
Db         19 CCCTCCTTCCCTTCTCT 3


RESULT 3673
US-10-023-782A-24
; Sequence 24, Application US/10023782A
; Publication No. US20030147863A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TFAP2C EXPRESSION
;  FILE REFERENCE: RTS-0343
;  CURRENT APPLICATION NUMBER: US/10/023,782A
;  CURRENT FILING DATE:  2001-12-17
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-023-782A-24

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         59 GGCGGCGGCAGACGCCT 75
              |||||||||  |||| |
Db          1 GGCGGCGGCGTACGCTT 17


RESULT 3674
US-10-349-143-5201
; Sequence 5201, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5201
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: upstream amplification primer 99-22490 for SEQ 1267,
US-10-349-143-5201

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1626 TACCTACCTTACTATTT 1642
              | ||| |||| ||||||
Db          2 TTCCTTCCTTCCTATTT 18


RESULT 3675
US-09-949-427-228/c
; Sequence 228, Application US/09949427
; Publication No. US20030054418A1
; GENERAL INFORMATION:
;  APPLICANT: Bodnar, Jackie S.
;  APPLICANT:  Castellani, Lawrence W.
;  APPLICANT:  Chatterjee, Aurobindo
;  APPLICANT:  de Jong, Pieter
;  APPLICANT:  Lusis, Aldons J.
;  APPLICANT:  Ohmen, Jeff
;  APPLICANT:  Ross, David
;  APPLICANT:  Tafuri, Sherrie
;  APPLICANT:  Wu, Chenyan
;  TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
;  FILE REFERENCE: 02810.0014.NPUS02
;  CURRENT APPLICATION NUMBER: US/09/949,427
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: 60/231,322
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-949-427-228

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        683 CAGATGGACGAGGTGCA 699
              || ||||| || |||||
Db         20 CAAATGGAAGAAGTGCA 4


RESULT 3676
US-09-949-428-228/c
; Sequence 228, Application US/09949428
; Publication No. US20030064372A1
; GENERAL INFORMATION:
;  APPLICANT: Bodnar, Jackie S.
;  APPLICANT:  Castellani, Lawrence W.
;  APPLICANT:  Chatterjee, Aurobindo
;  APPLICANT:  de Jong, Pieter
;  APPLICANT:  Lusis, Aldons J.
;  APPLICANT:  Ohmen, Jeff
;  APPLICANT:  Ross, David
;  APPLICANT:  Tafuri, Sherrie
;  APPLICANT:  Wu, Chenyan
;  TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder
;  FILE REFERENCE: 02810.0014.NPUS01
;  CURRENT APPLICATION NUMBER: US/09/949,428
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: 60/231,322
;  PRIOR FILING DATE: 2000-09-08
```

```
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-47

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db          1 AAAAAAAAAAAAGGGGG 17


RESULT 3670
US-10-209-608-43/c
; Sequence 43, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-43

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db          1 AAAAAAAAAAAAGGGGG 17


RESULT 3671
US-10-209-608-47
; Sequence 47, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-47

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db          1 AAAAAAAAAAAAGGGGG 17


RESULT 3672
US-10-265-689-15/c
; Sequence 15, Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
;  APPLICANT: SURWIT, RICHARD S.
;  APPLICANT:  COLLINS, SHEILA A.
;  APPLICANT:  WARDEN, CRAIG H.
;  APPLICANT:  SELDIN, MICHAEL F.
;  APPLICANT:  RICQUIER, DANIEL
;  APPLICANT:  BOUILLAUD, FREDERIC
;  TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
;  FILE REFERENCE: 1579-376
;  CURRENT APPLICATION NUMBER: US/10/265,689
;  CURRENT FILING DATE:  2002-10-08
;  PRIOR APPLICATION NUMBER: US/09/353,645
;  PRIOR FILING DATE: 1999-07-15
;  PRIOR APPLICATION NUMBER: PCT/US97/06864
;  PRIOR FILING DATE: 1997-04-22
;  PRIOR APPLICATION NUMBER: 60/034,960
;  PRIOR FILING DATE: 1997-01-15
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn Ver. 2.1
```

```
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1080
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-1080

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   11.8%;  Pred. No. 3.8e+03;
  Matches    2;  Conservative   12;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACT 2190
              ::::::::::::  || :
Db          1 UUUUUUUUUUUCCAAAU 17


RESULT 3666
US-10-287-949A-1080
; Sequence 1080, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1080
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1080

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   11.8%;  Pred. No. 3.8e+03;
  Matches    2;  Conservative   12;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACT 2190
              ::::::::::::  || :
Db          1 UUUUUUUUUUUCCAAAU 17


RESULT 3667
US-09-891-517-43/c
; Sequence 43, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-43

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db         18 AAAAAAAAAAAAGGGGG 2


RESULT 3668
US-10-683-386-43/c
; Sequence 43, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-43

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db         18 AAAAAAAAAAAAGGGGG 2


RESULT 3669
US-10-683-386-47
; Sequence 47, Application US/10683386
; Publication No. US20040063137A1
```

```
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: MBHB00,918-A 400/027
;  CURRENT APPLICATION NUMBER: US/09/930,423
;  CURRENT FILING DATE:  2001-08-15
;  NUMBER OF SEQ ID NOS: 4553
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-09-930-423-1448

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||||  | ||||
Db          1 AAAAAAAAACUAGAAAA 17


RESULT 3661
US-09-745-237A-284
; Sequence 284, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: 400/007 (MBHB00-918-A)
;  CURRENT APPLICATION NUMBER: US/09/745,237A
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 4550
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-745-237A-284

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||  | |||||||
Db          1 AAAAAACUAGAAAAAA 17


RESULT 3662
US-09-745-237A-959
; Sequence 959, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: 400/007 (MBHB00-918-A)
;  CURRENT APPLICATION NUMBER: US/09/745,237A
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 4550
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 959
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-745-237A-959

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||  | ||||||
Db          1 AAAAAAACUAGAAAAA 17


RESULT 3663
US-09-745-237A-1448
; Sequence 1448, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: 400/007 (MBHB00-918-A)
;  CURRENT APPLICATION NUMBER: US/09/745,237A
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 4550
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-745-237A-1448

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||||  | ||||
Db          1 AAAAAAAAACUAGAAAA 17


RESULT 3664
US-10-238-700-3359/c
; Sequence 3359, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels
;  FILE REFERENCE: 400/057  (MBHB01-1158-A)
;  CURRENT APPLICATION NUMBER: US/10/238,700
;  CURRENT FILING DATE:  2002-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 02/16840
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/318,471
;  PRIOR FILING DATE: 2001-09-10
;  NUMBER OF SEQ ID NOS: 4666
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3359
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-238-700-3359

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1544 GAGTAGGGAAGGAACAG 1560
              |||| ||| |||| |||
Db         17 GAGTGGGGCAGGAGCAG 1


RESULT 3665
US-10-138-674-1080
; Sequence 1080, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-144-140-14

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        360 AGCAGCTGGCCTAC 373
              ||||||||||||  |
Db         14 AGCAGCTGGCCTGC 1


RESULT 3656
US-09-780-533A-237
; Sequence 237, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 237
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-237

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||  |  ||  ||||
Db          1 AAAAAAAUAGAAGAAAA 17


RESULT 3657
US-09-780-533A-2172
; Sequence 2172, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2172
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-2172

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||  |  ||  ||
Db          1 AAAAAAAUAGAAGAAAA 17


RESULT 3658
US-09-930-423-284
; Sequence 284, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: MBHB00,918-A 400/027
;  CURRENT APPLICATION NUMBER: US/09/930,423
;  CURRENT FILING DATE:  2001-08-15
;  NUMBER OF SEQ ID NOS: 4553
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-09-930-423-284

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||  | |||||||
Db          1 AAAAAACUAGAAAAAAA 17


RESULT 3659
US-09-930-423-959
; Sequence 959, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: MBHB00,918-A 400/027
;  CURRENT APPLICATION NUMBER: US/09/930,423
;  CURRENT FILING DATE:  2001-08-15
;  NUMBER OF SEQ ID NOS: 4553
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 959
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-09-930-423-959

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||  | ||||||
Db          1 AAAAAACUAGAAAAAAA 17


RESULT 3660
US-09-930-423-1448
; Sequence 1448, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
```

```
Db         17 AAAAAAAAAAAAGT 4


RESULT 3651
US-10-287-949A-1070/c
; Sequence 1070, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1070
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1070

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGT 1992
              ||||||| ||||||
Db         17 AAAAAAAAAAAAGT 4


RESULT 3652
US-10-041-856-35
; Sequence 35, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
;  APPLICANT: SLAUGENHAUPT, SUSAN
;  APPLICANT:  GUSELLA, JAMES F.
;  TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
;  TITLE OF INVENTION:  DYSAUTONOMIA
;  FILE REFERENCE: 1829-4004US1
;  CURRENT APPLICATION NUMBER: US/10/041,856
;  CURRENT FILING DATE:  2002-07-08
;  PRIOR APPLICATION NUMBER: 60/260,080
;  PRIOR FILING DATE: 2001-01-06
;  NUMBER OF SEQ ID NOS: 88
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Mus sp.
US-10-041-856-35

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTA 2187
              ||||||||||||| |
Db          1 TTTTTTTTTTTCA 14


RESULT 3653
US-10-239-912-6
; Sequence 6, Application US/10239912
; Publication No. US20030212012A1
; GENERAL INFORMATION:
;  APPLICANT: Henry, James L
;  APPLICANT:  Fundytus, Marian E
;  APPLICANT:  Vaudreuil, Terrasse
;  TITLE OF INVENTION: Oligonucleotide For Metabotropic Glutamate Receptor
;  TITLE OF INVENTION:  Type 1 (MGLUR1)
;  FILE REFERENCE: 457-107PCT
;  CURRENT APPLICATION NUMBER: US/10/239,912
;  CURRENT FILING DATE:  2002-09-26
;  PRIOR APPLICATION NUMBER: 60/144,004
;  PRIOR FILING DATE: 1999-07-15
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-239-912-6

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 3.8e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||| ||||
Db          1 GAAAAAAAACAAAA 14


RESULT 3654
US-09-828-034-15
; Sequence 15, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
;  APPLICANT: Zhong, Weidong
;  APPLICANT:  Hong, Zhi
;  APPLICANT:  Ferrari, Eric
;  TITLE OF INVENTION: HCV REPLICASE COMPLEXES
;  FILE REFERENCE: IN01165
;  CURRENT APPLICATION NUMBER: US/09/828,034
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: U.S. 60/195,852
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-15

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 3.8e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              |||||||||||| |
Db          1 AAAAAAAAAAAACA 14


RESULT 3655
US-10-144-140-14/c
; Sequence 14, Application US/10144140
; Publication No. US20030211606A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DYRK4 EXPRESSION
;  FILE REFERENCE: RTS-0362
;  CURRENT APPLICATION NUMBER: US/10/144,140
;  CURRENT FILING DATE:  2002-05-10
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
```

```
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-257-294-102

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 21;
  Best Local Similarity   78.9%;  Pred. No. 4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||| ||| ||| ||| |||
Db         21 AAATAAATAAATAAATAAA 3


RESULT 3647
US-10-344-093A-33/c
; Sequence 33, Application US/10344093A
; Publication No. US20040076969A1
; GENERAL INFORMATION:
;  APPLICANT: CAILLOUX, Fabrice
;  APPLICANT:  GOBRON, Stephane
;  TITLE OF INVENTION: Method for detecting known mutations in tube
;  FILE REFERENCE: D19019 - 344 339
;  CURRENT APPLICATION NUMBER: US/10/344,093A
;  CURRENT FILING DATE:  2003-10-21
;  PRIOR APPLICATION NUMBER: PCT/FR 01/02 574
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: FR 00/104 25
;  PRIOR FILING DATE: 2000-08-08
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Primer for the detection of the mutations associated
;   OTHER INFORMATION: with mucoviscidosis.
US-10-344-093A-33

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 24;
  Best Local Similarity   78.9%;  Pred. No. 4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | |||||| |||| || ||
Db         24 GCAAAAAAGAAAAGAAGAA 6


RESULT 3648
US-10-309-775A-4/c
; Sequence 4, Application US/10309775A
; Publication No. US20040006032A1
; GENERAL INFORMATION:
;  APPLICANT: LOPEZ, Ricardo A.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND USES THEREOF
;  FILE REFERENCE: 2901/0M327
;  CURRENT APPLICATION NUMBER: US/10/309,775A
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: CA 2,388,049
;  PRIOR FILING DATE: 2002-05-30
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR primer
US-10-309-775A-4

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 24;
  Best Local Similarity   78.9%;  Pred. No. 4e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||| | ||||| | |||||
Db         24 AAAGACAAAAAGACAAAAA 6


RESULT 3649
US-10-343-710-146/c
; Sequence 146, Application US/10343710
; Publication No. US20040087478A1
; GENERAL INFORMATION:
;  APPLICANT: GILLEN, Clemens
;  APPLICANT:  WETZELS, Ingrid
;  APPLICANT:  WNENDT, Stephan
;  APPLICANT:  WEIHE, E.
;  APPLICANT:  SCHAEFER, M., K.-H.
;  TITLE OF INVENTION: SCREENING METHOD
;  FILE REFERENCE: 029310.52022US
;  CURRENT APPLICATION NUMBER: US/10/343,710
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/EP01/09011
;  PRIOR FILING DATE: 2001-08-03
;  NUMBER OF SEQ ID NOS: 157
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer
US-10-343-710-146

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAA 2796
              || ||||||||||||
Db         14 TTAAAAAAAAAAAA 1


RESULT 3650
US-10-138-674-1070/c
; Sequence 1070, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1070
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-1070

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGT 1992
              ||||||| ||||||
```

; Sequence 11, Application US/10165216
; Publication No. US20030228675A1
; GENERAL INFORMATION:
; APPLICANT: Otterness, Diane M.
; APPLICANT: Abraham, Robert T.
; TITLE OF INVENTION: ATM Related Kinase ATX, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; FILE REFERENCE: P-LJ 5222
; CURRENT APPLICATION NUMBER: US/10/165,216
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-165-216-11

Query Match 0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1292 AGCAGGCTCGCCCCAGTCT 1310
|||| |||| | || ||||
Db 1 AGCAAGCTCCCTCCTGTCT 19

RESULT 3643
US-10-688-706-2086
; Sequence 2086, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2086
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2086

Query Match 0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAA 2801
|| ||||| |||| | |||
Db 1 TTTAAAAACAAAACAGAAA 19

RESULT 3644
US-10-117-955B-3/c
; Sequence 3, Application US/10117955B
; Publication No. US20030199453A1
; GENERAL INFORMATION:
; APPLICANT: Giordano, Tony
; APPLICANT: Sturgess, Michael A.
; TITLE OF INVENTION: Small Molecule Inhibitors of Secretion
; TITLE OF INVENTION: of Proteins Encoded by ARE-mRNAs
; FILE REFERENCE: 50093/018002
; CURRENT APPLICATION NUMBER: US/10/117,955B
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/282,974
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus motif
US-10-117-955B-3

Query Match 0.4%; Score 12.6; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||| ||| ||| ||| |||
Db 20 AAATAAATAAATAAATAAA 2

RESULT 3645
US-10-257-294-44/c
; Sequence 44, Application US/10257294
; Publication No. US20040023231A1
; GENERAL INFORMATION:
; APPLICANT: Abu-Khabar, Khalid
; APPLICANT: Williams, Bryan
; APPLICANT: Frevel, Mathias
; APPLICANT: Silverman, Robert
; TITLE OF INVENTION: System for Identifying and Analyzing Expression of ARE-Containing
; FILE REFERENCE: 26473/04185
; CURRENT APPLICATION NUMBER: US/10/257,294
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11993
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/198,870
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-294-44

Query Match 0.4%; Score 12.6; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||| ||| ||| ||| |||
Db 20 AAATAAATAAATAAATAAA 2

RESULT 3646
US-10-257-294-102/c
; Sequence 102, Application US/10257294
; Publication No. US20040023231A1
; GENERAL INFORMATION:
; APPLICANT: Abu-Khabar, Khalid
; APPLICANT: Williams, Bryan
; APPLICANT: Frevel, Mathias
; APPLICANT: Silverman, Robert
; TITLE OF INVENTION: System for Identifying and Analyzing Expression of ARE-Containing
; FILE REFERENCE: 26473/04185
; CURRENT APPLICATION NUMBER: US/10/257,294
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11993
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/198,870
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 109

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;  CURRENT APPLICATION NUMBER: US/10/159,834
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-834-58

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1339 TCATTTCAGCCTGATTACC 1357
              ||||||||  ||| || ||
Db         19 TCATTTCAAACTGTTTTCC 1


RESULT 3638
US-10-159-834-117
; Sequence 117, Application US/10159834
; Publication No. US20030228688A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ISOPRENYLCYSTEINE CARBOXYL METHYLTRANSFER
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0299
;  CURRENT APPLICATION NUMBER: US/10/159,834
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 117
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-159-834-117

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1339 TCATTTCAGCCTGATTACC 1357
              ||||||||  ||| || ||
Db          2 TCATTTCAAACTGTTTTCC 20


RESULT 3639
US-10-688-706-2467
; Sequence 2467, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2467
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2467

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| |||| | ||| ||
Db          2 AAAAACAAAACAGAAACAA 20


RESULT 3640
US-10-688-706-2843
; Sequence 2843, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2843
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2843

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| |||| | ||| |||
Db          1 AAAACAAAACAGAAACAAA 19


RESULT 3641
US-10-688-706-2908
; Sequence 2908, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2908
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2908

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| |||| | ||| |||
Db          2 AAAACAAAACAGAAACAAA 20


RESULT 3642
US-10-165-216-11
```

```
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02014
US-10-367-470-11

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                 |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 3634
US-10-367-470-12
; Sequence 12, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Complement DNA oligo AGT02009
US-10-367-470-12

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                 |||||||||    ||||||
Db          1 AAAAAAAAATTTTAAAAAA 19


RESULT 3635
US-10-367-470-14
; Sequence 14, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02021
US-10-367-470-14

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                 |||||||||    ||||||
Db          1 AAAAAAAAATTGTAAAAAA 19


RESULT 3636
US-10-367-470-17
; Sequence 17, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02024
US-10-367-470-17

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                 |||||||||    ||||||
Db          1 AAAAAAAAATTCTAAAAAA 19


RESULT 3637
US-10-159-834-58/c
; Sequence 58, Application US/10159834
; Publication No. US20030228688A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ISOPRENYLCYSTEINE CARBOXYL METHYLTRANSFERA
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0299
```

Query Match 0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1449 TGAACCCTGGAGACCAGAG 1467
              || |  |||||||||||  |
Db         19 TGGAATCTGGAGACCAGGG 1
```

RESULT 3629
US-09-984-637-7/c
; Sequence 7, Application US/09984637
; Publication No. US20040048246A1
; GENERAL INFORMATION:
; APPLICANT: Tosoh Corporation
; TITLE OF INVENTION: OLIGONUCLEOTIDE FOR DETECTION OF HIV-1 AND DETECTION METHOD
; FILE REFERENCE: PA211-0315
; CURRENT APPLICATION NUMBER: US/09/984,637
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide hybridizable with a specific site of HIV-1 RNA
US-09-984-637-7

Query Match 0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| ||||  || |||||
Db         20 AAAACAAAAGTAAGAAAAA 2
```

RESULT 3630
US-10-367-470-8/c
; Sequence 8, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02008
US-10-367-470-8

Query Match 0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2
```

RESULT 3631
US-10-367-470-9/c
; Sequence 9, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02012
US-10-367-470-9

Query Match 0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2
```

RESULT 3632
US-10-367-470-10/c
; Sequence 10, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02013
US-10-367-470-10

Query Match 0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2
```

RESULT 3633
US-10-367-470-11/c
; Sequence 11, Application US/10367470

```
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Oligonucleotide AGT02014
US-09-823-647B-11

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||     ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 3625
US-09-823-647B-12
; Sequence 12, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Complement DNA oligo AGT02009
US-09-823-647B-12

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||     ||||||
Db          1 AAAAAAAAATTTTAAAAAA 19


RESULT 3626
US-09-823-647B-14
; Sequence 14, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Oligo AGT02021
US-09-823-647B-14

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||     ||||||
Db          1 AAAAAAAAATTGTAAAAAA 19


RESULT 3627
US-09-823-647B-17
; Sequence 17, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Oligo AGT02024
US-09-823-647B-17

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||     ||||||
Db          1 AAAAAAAAATTCTAAAAAA 19


RESULT 3628
US-09-824-322B-217/c
; Sequence 217, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Butler, Madeline M.
;  APPLICANT:  Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPH
;  TITLE OF INVENTION:  ALPHA) EXPRESSION
;  FILE REFERENCE: ISPH-0501
;  CURRENT APPLICATION NUMBER: US/09/824,322B
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 09/313,932
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: US 09/166,186
;  PRIOR FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 217
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic
US-09-824-322B-217
```

```
              |||||||||    ||||||
Db          1 AAAAAAAAATTGTAAAAAA 19


RESULT 3620
US-09-823-634A-17
; Sequence 17, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02024
US-09-823-634A-17

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTCTAAAAAA 19


RESULT 3621
US-09-823-647B-8/c
; Sequence 8, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02008
US-09-823-647B-8

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 3622
US-09-823-647B-9/c
; Sequence 9, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02012
US-09-823-647B-9

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 3623
US-09-823-647B-10/c
; Sequence 10, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02013
US-09-823-647B-10

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 3624
US-09-823-647B-11/c
; Sequence 11, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
```

```
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02012
US-09-823-634A-9

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                  |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 3616
US-09-823-634A-10/c
; Sequence 10, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02013
US-09-823-634A-10

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                  |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 3617
US-09-823-634A-11/c
; Sequence 11, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02014
US-09-823-634A-11

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                  |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 3618
US-09-823-634A-12
; Sequence 12, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Complement DNA oligo AGT02009
US-09-823-634A-12

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                  |||||||||    ||||||
Db          1 AAAAAAAAATTTTAAAAAA 19


RESULT 3619
US-09-823-634A-14
; Sequence 14, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02021
US-09-823-634A-14

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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```
;              COMPUTER: IBM PS/2
;              OPERATING SYSTEM: WINDOWS 95
;              SOFTWARE: WORDPERFECT 6.1
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/430,196
;              FILING DATE: 05-May-2003
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/923,517A
;              FILING DATE: 07-Aug-2001
;              APPLICATION NUMBER: 09/364,416
;              FILING DATE: 1999-07-30
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Jane Massey Licata
;              REGISTRATION NUMBER: 32,257
;              REFERENCE/DOCKET NUMBER: ISPH-0209
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (609) 810-1515
;              TELEFAX: (609) 810-1454
;    INFORMATION FOR SEQ ID NO: 38:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 20
;              TYPE: Nucleic Acid
;              STRANDEDNESS: Single
;              TOPOLOGY: Linear
;         ANTI-SENSE: Yes
;         SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-430-196-38

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1000 GCGGGAGAAGTTGGACAAG 1018
              ||||  |||||||| | ||
Db         19 GCGGCTGAAGTTGGGCGAG 1


RESULT 3612
US-09-465-589-7/c
; Sequence 7, Application US/09465589
; Patent No. US20020031764A1
; GENERAL INFORMATION:
;  APPLICANT: KOCH, Jorn Erland
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMPLIFYING MULTIPLE TANDEM REPETITIO
;  TITLE OF INVENTION:  OLIGONUCLEOTIDE UNIT (AS AMENDED)
;  FILE REFERENCE: 4305/1E293-US2
;  CURRENT APPLICATION NUMBER: US/09/465,589
;  CURRENT FILING DATE:  1999-12-17
;  PRIOR APPLICATION NUMBER: US 09/091,146
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: PCT/DK96/00513
;  PRIOR FILING DATE: 1996-12-05
;  PRIOR APPLICATION NUMBER: DK 1379/95
;  PRIOR FILING DATE: 1995-12-05
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide with internal repetitions
US-09-465-589-7

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              ||| ||| ||| ||| |||
Db         20 TTTCTTTCTTTCTTTCTTT 2


RESULT 3613
US-09-465-589-8/c
; Sequence 8, Application US/09465589
; Patent No. US20020031764A1
; GENERAL INFORMATION:
;  APPLICANT: KOCH, Jorn Erland
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMPLIFYING MULTIPLE TANDEM REPETITIO
;  TITLE OF INVENTION:  OLIGONUCLEOTIDE UNIT (AS AMENDED)
;  FILE REFERENCE: 4305/1E293-US2
;  CURRENT APPLICATION NUMBER: US/09/465,589
;  CURRENT FILING DATE:  1999-12-17
;  PRIOR APPLICATION NUMBER: US 09/091,146
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: PCT/DK96/00513
;  PRIOR FILING DATE: 1996-12-05
;  PRIOR APPLICATION NUMBER: DK 1379/95
;  PRIOR FILING DATE: 1995-12-05
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide with internal repetitions
US-09-465-589-8

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||| ||| ||| ||| |||
Db         20 AAAGAAAGAAAGAAAGAAA 2


RESULT 3614
US-09-823-634A-8/c
; Sequence 8, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02008
US-09-823-634A-8

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 3615
US-09-823-634A-9/c
; Sequence 9, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
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  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||     ||||||
Db          1 AAAAAAAAATTTGAAAAAA 19


RESULT 3609
US-09-784-674-557/c
; Sequence 557, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,674
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: No. US20030054346A1 available
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/021,701
;             FILING DATE: 10-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Choi, Wendy A.
;             REGISTRATION NUMBER: 36,697
;             REFERENCE/DOCKET NUMBER: 10971464-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-236-2386
;             TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 557:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 557:
US-09-784-674-557

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              ||  ||  ||||| ||||||
Db         20 AGGGTTAAAAAAGAAAAAA 2


RESULT 3610
US-09-923-517-38/c
; Sequence 38, Application US/09923517
; Publication No. US20020039741A1
;   GENERAL INFORMATION:
;        APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
;                   Miraglia; Brenda F. Baker
;        TITLE OF INVENTION: Antisense Oligonucleotide
;                            Compositions and Methods for the Modulation of
;                            Activating Protein 1
;        NUMBER OF SEQUENCES: 139
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Law Offices of Jane Massey Licata
;             STREET: 66 East Main Street
;             CITY: Marlton
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08053
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: WINDOWS 95
;             SOFTWARE: WORDPERFECT 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/923,517
;             FILING DATE: 07-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/364,416
;             FILING DATE: 1999-07-30
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jane Massey Licata
;             REGISTRATION NUMBER: 32,257
;             REFERENCE/DOCKET NUMBER: ISPH-0209
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (609) 810-1515
;             TELEFAX: (609) 810-1454
;   INFORMATION FOR SEQ ID NO: 38:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20
;             TYPE: Nucleic Acid
;             STRANDEDNESS: Single
;             TOPOLOGY: Linear
;        ANTI-SENSE: Yes
;        SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-923-517-38

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1000 GCGGGAGAAGTTGGACAAG 1018
              ||||  |||||||| | ||
Db         19 GCGGCTGAAGTTGGGCGAG 1


RESULT 3611
US-10-430-196-38/c
; Sequence 38, Application US/10430196
; Publication No. US20030194738A1
;   GENERAL INFORMATION:
;        APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
;                   Miraglia; Brenda F. Baker
;        TITLE OF INVENTION: Antisense Oligonucleotide
;                            Compositions and Methods for the Modulation of
;                            Activating Protein 1
;        NUMBER OF SEQUENCES: 139
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Law Offices of Jane Massey Licata
;             STREET: 66 East Main Street
;             CITY: Marlton
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08053
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
```

```
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02020
US-09-823-634A-13

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTTGAAAAAA 19


RESULT 3606
US-09-823-647B-13
; Sequence 13, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02020
US-09-823-647B-13

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTTGAAAAAA 19


RESULT 3607
US-09-784-674-558/c
; Sequence 558, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,674
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: No. US20030054346A1 available
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/021,701
;             FILING DATE: 10-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Choi, Wendy A.
;             REGISTRATION NUMBER: 36,697
;             REFERENCE/DOCKET NUMBER: 10971464-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-236-2386
;             TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 558:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 558:
US-09-784-674-558

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2797
              ||  || ||||| ||||||
Db         19 AGGGTTAAAAAAGAAAAAA 1


RESULT 3608
US-10-367-470-13
; Sequence 13, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02020
US-10-367-470-13
```

```
Qy       2179 TTTTTTTTAACTTTGAAAG 2197
              |||||||||| | | | ||
Db         19 TTTTTTTTAATTATAAGAG 1


RESULT 3601
US-10-126-704-105/c
; Sequence 105, Application US/10126704
; Publication No. US20030170647A1
; GENERAL INFORMATION:
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
;  TITLE OF INVENTION:  AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
;  FILE REFERENCE: 44.US5.DIV
;  CURRENT APPLICATION NUMBER: US/10/126,704
;  CURRENT FILING DATE:  2002-04-20
;  PRIOR APPLICATION NUMBER: US 60/091,315
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/111,909
;  PRIOR FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: Patent.pm
; SEQ ID NO 105
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: potential microsequencing oligo for 5-129-144.mis1
US-10-126-704-105

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGAAAG 2197
              |||||||||| | | | ||
Db         19 TTTTTTTTAATTATAAGAG 1


RESULT 3602
US-09-823-634A-16
; Sequence 16, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02023
US-09-823-634A-16

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATGTGAAAAAA 19


RESULT 3603
US-09-823-647B-16
; Sequence 16, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02023
US-09-823-647B-16

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATGTGAAAAAA 19


RESULT 3604
US-10-367-470-16
; Sequence 16, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02023
US-10-367-470-16

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATGTGAAAAAA 19


RESULT 3605
US-09-823-634A-13
; Sequence 13, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
```

```
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Boldog, Ference L.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Eisen, Andrew J.
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-216
;  CURRENT APPLICATION NUMBER: US/10/231,913
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/251,660
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 60/255,029
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: 60/260,326
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/263,800
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/269,942
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/286,183
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: 60/313,627
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/318,712
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 292
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: CHEMICALLY
;   OTHER INFORMATION: SYNTHESIZED
US-10-231-913-179

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 23;
  Best Local Similarity   87.5%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1398 CCCTGCAGAACTACAT 1413
              ||||||| || ||||
Db          5 CCCTGCAGCACCACAT 20


RESULT 3598
US-10-629-453-20/c
; Sequence 20, Application US/10629453
; Publication No. US20040096878A1
; GENERAL INFORMATION:
;  APPLICANT: Keene, Jack  D.
;  APPLICANT:  Carson, Craig C.
;  APPLICANT:  Tenenbaum, Scott A.
;  TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
;  TITLE OF INVENTION:  complexes
;  FILE REFERENCE: RBN-001DV
;  CURRENT APPLICATION NUMBER: US/10/629,453
;  CURRENT FILING DATE:  2003-07-29
;  PRIOR APPLICATION NUMBER: US 09/750,401
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: US 60/173,338
;  PRIOR FILING DATE: 1999-12-28
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 3 -UTR sequence of Neuronal-Cadherin
US-10-629-453-20

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 23;
  Best Local Similarity   87.5%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||  ||||||
Db         23 AAAAAAAATTAAAAAA 8


RESULT 3599
US-10-098-263B-27520/c
; Sequence 27520, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27520
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-27520

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 25;
  Best Local Similarity   70.8%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1882 GTCAAATTGATGTGCCCTAGATCA 1905
              |||   |||||||| | || || |
Db         25 GTCCTTTTGATGTGTCTTATATTA 2


RESULT 3600
US-10-071-179-105/c
; Sequence 105, Application US/10071179
; Publication No. US20030108882A1
; GENERAL INFORMATION:
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
;  TITLE OF INVENTION:  AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
;  FILE REFERENCE: GENSET.031A
;  CURRENT APPLICATION NUMBER: US/10/071,179
;  CURRENT FILING DATE:  2002-02-07
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/345,882
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/091,315
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/111,909
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: Patent.pm
; SEQ ID NO 105
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: potential microsequencing oligo for 5-129-144.mis1
US-10-071-179-105

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-161-229-99

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 3594
US-10-349-143-9728/c
; Sequence 9728, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9728
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..21
;   OTHER INFORMATION: downstream amplification primer 99-6979 for SEQ 1863, in compleme
US-10-349-143-9728

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              |||  ||||||||||||
Db         21 GAAGGAAAAAAAAAAA 6


RESULT 3595
US-10-309-788-20/c
; Sequence 20, Application US/10309788
; Publication No. US20030211466A1
; GENERAL INFORMATION:
;  APPLICANT: Keene, Jack  D.
;  APPLICANT:  Tenenbaum, Scott A.
;  APPLICANT:  Carson, Craig C.
;  APPLICANT:  Phelps, William C.
;  TITLE OF INVENTION: Method for Identifying Functionally Related Genes and Drug Target
;  FILE REFERENCE: RBN-001CP
;  CURRENT APPLICATION NUMBER: US/10/309,788
;  CURRENT FILING DATE:  2003-06-18
;  PRIOR APPLICATION NUMBER: US 60/173,338
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: US 09/750,401
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 3'-UTR consensus sequence of Neuronal-Cadherin
US-10-309-788-20

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 23;
  Best Local Similarity   87.5%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||  ||||||
Db         23 AAAAAAAATTAAAAAA 8


RESULT 3596
US-10-238-306B-20/c
; Sequence 20, Application US/10238306B
; Publication No. US20030235830A1
; GENERAL INFORMATION:
;  APPLICANT: Keene, Jack  D.
;  APPLICANT:  Tenenbaum, Scott A.
;  APPLICANT:  Carson, Craig C.
;  TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
;  TITLE OF INVENTION:  complexes
;  FILE REFERENCE: RBN-001CN
;  CURRENT APPLICATION NUMBER: US/10/238,306B
;  CURRENT FILING DATE:  2002-09-10
;  PRIOR APPLICATION NUMBER: US 09/750,401
;  PRIOR FILING DATE: 2001-12-28
;  PRIOR APPLICATION NUMBER: US 60/173,338
;  PRIOR FILING DATE: 1999-12-28
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 3'-UTR sequence of Neuronal-Cadherin
US-10-238-306B-20

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 23;
  Best Local Similarity   87.5%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||  ||||||
Db         23 AAAAAAAATTAAAAAA 8


RESULT 3597
US-10-231-913-179
; Sequence 179, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia S.
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Edinger, Schlomit
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Stone, David J.
```

```
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-776

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 3590
US-10-314-578-776/c
; Sequence 776, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Schetter, Christian
;  APPLICANT:  Vollmer, Jorg
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids
;  FILE REFERENCE: C1039/7035 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/314,578
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 60/156,113
;  PRIOR FILING DATE: 1999-09-25
;  PRIOR APPLICATION NUMBER: US 60/156,135
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: US 60/227,436
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 1145
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-314-578-776

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 3591
US-10-112-653-749/c
; Sequence 749, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 749
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-749

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 3592
US-10-017-995-776/c
; Sequence 776, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-776

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 3593
US-10-161-229-99/c
; Sequence 99, Application US/10161229
; Publication No. US20030100527A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules for
;  TITLE OF INVENTION:  Activating Dendritic Cells
;  FILE REFERENCE: C01039/70061
;  CURRENT APPLICATION NUMBER: US/10/161,229
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: US 09/191,170
;  PRIOR FILING DATE: 1998-11-13
;  PRIOR APPLICATION NUMBER: US 08/960,774
;  PRIOR FILING DATE: 1997-10-30
;  PRIOR APPLICATION NUMBER: US 08/738,652
;  PRIOR FILING DATE: 1996-10-30
;  PRIOR APPLICATION NUMBER: US 08/386,063
;  PRIOR FILING DATE: 1995-02-07
;  PRIOR APPLICATION NUMBER: US 08/276,358
;  PRIOR FILING DATE: 1994-07-15
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
;   LENGTH: 20
```

```
US-10-206-839-28
; Sequence 28, Application US/10206839
; Publication No. US20030099977A1
; GENERAL INFORMATION:
;  APPLICANT: Guida, Marco
;  APPLICANT:  Kurth, Janice
;  TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
;  TITLE OF INVENTION:  (STP2)
;  FILE REFERENCE: 4389-6 (formerly SEQ-16P)
;  CURRENT APPLICATION NUMBER: US/10/206,839
;  CURRENT FILING DATE:  2002-07-26
;  PRIOR APPLICATION NUMBER: 09/328,174
;  PRIOR FILING DATE: 1999-06-08
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 28
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: H. sapiens
US-10-206-839-28

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||  ||
Db          3 GAAAAAAAAAAAGGAA 18


RESULT 3586
US-10-007-814-29/c
; Sequence 29, Application US/10007814
; Publication No. US20020160479A1
; GENERAL INFORMATION:
;  APPLICANT: Wojnowski, Leszek
;  APPLICANT:  Gellner, Klaus
;  APPLICANT:  Eiselt, Regina
;  TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
;  TITLE OF INVENTION:  (CYP3A) GENE FAMILY: CYP3AX
;  FILE REFERENCE: 310115.401D1
;  CURRENT APPLICATION NUMBER: US/10/007,814
;  CURRENT FILING DATE:  2001-11-09
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-007-814-29

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        757 CATTTCCATGACCAAG 772
              |||||||||| | |||
Db         20 CATTTCCATGGCAAAG 5


RESULT 3587
US-09-888-326-9/c
; Sequence 9, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
;  TITLE OF INVENTION:  Cell Lysis and Treating Cancer
;  FILE REFERENCE: C1039/7052 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/888,326
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: US 60/213,346
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
;   OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-9

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 3588
US-09-776-479-776/c
; Sequence 776, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-776

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 3589
US-09-776-479-776/c
; Sequence 776, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
```

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;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  PRIOR APPLICATION NUMBER: 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: 60/083,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  NUMBER OF SEQ ID NOS: 1558
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 558
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-825-805-558

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||| |||| |||
Db         16 AAAAAAACAAAACAAA 1


RESULT 3581
US-10-675-685-483/c
; Sequence 483, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: PB0114
;  CURRENT APPLICATION NUMBER: US/10/675,685
;  CURRENT FILING DATE:  2003-09-30
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 483
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-675-685-483

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTT 2178
              | |||| |||||||||
Db         17 TTCTTTCTTTTTTTTT 2


RESULT 3582
US-10-163-552-984/c
; Sequence 984, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
;  TITLE OF INVENTION:  HER2
;  FILE REFERENCE: MBHB01-1653-A (400/014)
;  CURRENT APPLICATION NUMBER: US/10/163,552
;  CURRENT FILING DATE:  2002-06-06
;  NUMBER OF SEQ ID NOS: 1997
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 984
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-163-552-984

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||| |||| |||||||
Db         17 AAACAAAACAAAAAAA 2


RESULT 3583
US-10-163-552-985/c
; Sequence 985, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
;  TITLE OF INVENTION:  HER2
;  FILE REFERENCE: MBHB01-1653-A (400/014)
;  CURRENT APPLICATION NUMBER: US/10/163,552
;  CURRENT FILING DATE:  2002-06-06
;  NUMBER OF SEQ ID NOS: 1997
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 985
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-163-552-985

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||| |||| |||
Db         16 AAAAAAACAAAACAAA 1


RESULT 3584
US-10-156-306-1646/c
; Sequence 1646, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of IKK-Gamma and PKR
;  FILE REFERENCE: MBHB01-664-A (400/050)
;  CURRENT APPLICATION NUMBER: US/10/156,306
;  CURRENT FILING DATE:  2002-05-28
;  NUMBER OF SEQ ID NOS: 8013
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1646
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-156-306-1646

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||| || |||
Db         17 AAAAAAAAAGAATAAA 2


RESULT 3585
```

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;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-1079

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   12.5%;  Pred. No. 3.2e+03;
  Matches    2;  Conservative   12;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAA 2188
              ::::::::::::  ||
Db          1 UUUUUUUUUUUUCCAA 16


RESULT 3577
US-10-287-949A-1079
; Sequence 1079, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1079

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   12.5%;  Pred. No. 3.2e+03;
  Matches    2;  Conservative   12;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAA 2188
              ::::::::::::  ||
Db          1 UUUUUUUUUUUUCCAA 16


RESULT 3578
US-09-827-998-483/c
; Sequence 483, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 483
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-483

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2178
              | |||| |||||||||
Db         17 TTCTTTCTTTTTTTT 2


RESULT 3579
US-09-825-805-557/c
; Sequence 557, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka Matulic
;  APPLICANT:  Sweedler, Dave
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti
;  FILE REFERENCE: MBHB00-831-F (400/009)
;  CURRENT APPLICATION NUMBER: US/09/825,805
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: 09/578,223
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 09/476,387
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: 09/474,432
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  PRIOR APPLICATION NUMBER: 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: 60/083,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  NUMBER OF SEQ ID NOS: 1558
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 557
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-825-805-557

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.2e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              ||| |||| |||||||
Db         17 AAACAAAACAAAAAAA 2


RESULT 3580
US-09-825-805-558/c
; Sequence 558, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka Matulic
;  APPLICANT:  Sweedler, Dave
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti
;  FILE REFERENCE: MBHB00-831-F (400/009)
;  CURRENT APPLICATION NUMBER: US/09/825,805
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: 09/578,223
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 09/476,387
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: 09/474,432
```

```
 ;  APPLICANT:  FURUSHO, KENTA
 ;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
 ;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
 ;  TITLE OF INVENTION:  THE METHOD
 ;  FILE REFERENCE: 199953US0XDIV
 ;  CURRENT APPLICATION NUMBER: US/10/209,608
 ;  CURRENT FILING DATE:  2002-08-01
 ;  PRIOR APPLICATION NUMBER: US/09/725,265
 ;  PRIOR FILING DATE: 2000-11-29
 ;  PRIOR APPLICATION NUMBER: US 09/556,127
 ;  PRIOR FILING DATE: 2000-04-20
 ;  PRIOR APPLICATION NUMBER: JP 1999-111601
 ;  PRIOR FILING DATE: 1999-04-20
 ;  NUMBER OF SEQ ID NOS: 70
 ;  SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 48
 ;   LENGTH: 18
 ;   TYPE: DNA
 ;   ORGANISM: ARTIFICIAL SEQUENCE
 ;   FEATURE:
 ;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-48

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAA 2797
              |||||||||||||
Db         13 GAAAAAAAAAAAA 1


RESULT 3574
US-10-349-143-8908/c
; Sequence 8908, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
 ;  APPLICANT: Cohen, Daniel
 ;  APPLICANT:  Blumenfeld, Marta
 ;  APPLICANT:  Chumakov, Ilya
 ;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 ;  FILE REFERENCE: GENSET.020CP1
 ;  CURRENT APPLICATION NUMBER: US/10/349,143
 ;  CURRENT FILING DATE:  2003-01-21
 ;  PRIOR APPLICATION NUMBER: US/09/422,978
 ;  PRIOR FILING DATE: 1999-10-20
 ;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
 ;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
 ;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
 ;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
 ;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
 ;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
 ;  NUMBER OF SEQ ID NOS: 11796
 ; SEQ ID NO 8908
 ;   LENGTH: 20
 ;   TYPE: DNA
 ;   ORGANISM: Homo Sapiens
 ;   FEATURE:
 ;   NAME/KEY: primer_bind
 ;   LOCATION: 1..20
 ;   OTHER INFORMATION: downstream amplification primer 99-1997 for SEQ 1043, in compleme
US-10-349-143-8908

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1096 TGTTCATTTGGCT 1108
              |||||||||||||
Db         13 TGTTCATTTGGCT 1


RESULT 3575
US-10-173-509-1/c
; Sequence 1, Application US/10173509
; Publication No. US20030017490A1
;  GENERAL INFORMATION:
;       APPLICANT: Belyavsky et al.
;       TITLE OF INVENTION: Method Of Identification And
;                           Cloning Differentially Expressed
;                           Messenger RNAs
;       NUMBER OF SEQUENCES: 5
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Hoffmann & Baron
;            STREET: 350 Jericho Turnpike
;            CITY: Jericho
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 11753
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
;            COMPUTER: IBM compatible
;            OPERATING SYSTEM: MS-DOS
;            SOFTWARE: WordPerfect
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/173,509
;            FILING DATE: 18-Jun-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/664,534
;            FILING DATE: 18-Sep-2000
;            APPLICATION NUMBER: US/08/499,899
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: O'Dea, Sean W.
;            REGISTRATION NUMBER: 37690
;            REFERENCE/DOCKET NUMBER: 454-8
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (516) 822-3550
;            TELEFAX: (516) 822-3582
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 22 nucleotides
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-173-509-1

  Query Match             0.5%;  Score 13;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         22 AAAAAAAAAAAAA 10


RESULT 3576
US-10-138-674-1079
; Sequence 1079, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
 ;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ;  APPLICANT:  Pavco, Pam
 ;  APPLICANT:  McSwiggen, Jim
 ;  APPLICANT:  Stinchcomb, Dan
 ;  APPLICANT:  Escobedo, Jaime
 ;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
 ;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
 ;  FILE REFERENCE: MBHB00-876-N (400/049)
 ;  CURRENT APPLICATION NUMBER: US/10/138,674
 ;  CURRENT FILING DATE:  2002-05-03
 ;  NUMBER OF SEQ ID NOS: 20822
 ;  SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1079
```

```
;  TITLE OF INVENTION:  METHOD OF INTRODUCING WATER-STRESS TOLERANCE
;  FILE REFERENCE: 3097-4009
;  CURRENT APPLICATION NUMBER: US/10/109,363
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Camellia sinensis
US-10-109-363-16

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 3570
US-10-109-363-18/c
; Sequence 18, Application US/10109363
; Publication No. US20030196214A1
; GENERAL INFORMATION:
;  APPLICANT: SHARMA, PRITI
;  APPLICANT:  KUMAR, SANJAY
;  APPLICANT:  AHUJA, PARAMVIR SINGH
;  TITLE OF INVENTION: NOVEL GENES FROM DROUGHT STRESS TOLERANT TEA PLANT AND A
;  TITLE OF INVENTION:  METHOD OF INTRODUCING WATER-STRESS TOLERANCE
;  FILE REFERENCE: 3097-4009
;  CURRENT APPLICATION NUMBER: US/10/109,363
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Camellia sinensis
US-10-109-363-18

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 3571
US-09-891-517-44
; Sequence 44, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-44

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAA 2797
              |||||||||||||
Db          6 GAAAAAAAAAAAA 18


RESULT 3572
US-10-683-386-48/c
; Sequence 48, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-48

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAA 2797
              |||||||||||||
Db         13 GAAAAAAAAAAAA 1


RESULT 3573
US-10-209-608-48/c
; Sequence 48, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
```

```
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1071

  Query Match             0.5%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 3565
US-09-823-887C-5/c
; Sequence 5, Application US/09823887C
; Publication No. US20030180723A1
; GENERAL INFORMATION:
;  APPLICANT: Kumar, Sanjay
;  APPLICANT:  Lal, Lakhvir
;  APPLICANT:  Ahuja, Paramvir
;  TITLE OF INVENTION: Cloning of No. US20030180723A1el Gene Sequences Expressed and Rep
;  TITLE OF INVENTION:  Dormancy in the Apical Buds of Tea (Camellia Sinensis L. (O.) Ku
;  FILE REFERENCE: HO53916.0001US0
;  CURRENT APPLICATION NUMBER: US/09/823,887C
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer_bind
US-09-823-887C-5

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 3566
US-09-823-887C-7/c
; Sequence 7, Application US/09823887C
; Publication No. US20030180723A1
; GENERAL INFORMATION:
;  APPLICANT: Kumar, Sanjay
;  APPLICANT:  Lal, Lakhvir
;  APPLICANT:  Ahuja, Paramvir
;  TITLE OF INVENTION: Cloning of No. US20030180723A1el Gene Sequences Expressed and Rep
;  TITLE OF INVENTION:  Dormancy in the Apical Buds of Tea (Camellia Sinensis L. (O.) Ku
;  FILE REFERENCE: HO53916.0001US0
;  CURRENT APPLICATION NUMBER: US/09/823,887C
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer_bind
US-09-823-887C-7

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 3567
US-10-106-799-1/c
; Sequence 1, Application US/10106799
; Publication No. US20030140379A1
; GENERAL INFORMATION:
;  APPLICANT: Council of Scientific and Industrial Research
;  TITLE OF INVENTION: No. US20030140379A1el DNA sequence in plants Caragana jubata with
;  TITLE OF INVENTION:  method thereof
;  FILE REFERENCE: US 673
;  CURRENT APPLICATION NUMBER: US/10/106,799
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: T11A anchored primers for differential display
US-10-106-799-1

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 3568
US-10-106-799-3/c
; Sequence 3, Application US/10106799
; Publication No. US20030140379A1
; GENERAL INFORMATION:
;  APPLICANT: Council of Scientific and Industrial Research
;  TITLE OF INVENTION: No. US20030140379A1el DNA sequence in plants Caragana jubata with
;  TITLE OF INVENTION:  method thereof
;  FILE REFERENCE: US 673
;  CURRENT APPLICATION NUMBER: US/10/106,799
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: T11G (anchored) primer for differential display
US-10-106-799-3

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 3569
US-10-109-363-16/c
; Sequence 16, Application US/10109363
; Publication No. US20030196214A1
; GENERAL INFORMATION:
;  APPLICANT: SHARMA, PRITI
;  APPLICANT:  KUMAR, SANJAY
;  APPLICANT:  AHUJA, PARAMVIR SINGH
;  TITLE OF INVENTION: NOVEL GENES FROM DROUGHT STRESS TOLERANT TEA PLANT AND A
```

```
  Best Local Similarity   83.3%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1970 TTTACCTTGAAAAAAAGA 1987
              |||||  ||||||||| |
Db         18 TTTACACTGAAAAAAAAA 1


RESULT 3561
US-10-080-797-17/c
; Sequence 17, Application US/10080797
; Publication No. US20020183253A1
; GENERAL INFORMATION:
;  APPLICANT: Campochiaro, Peter A.
;  APPLICANT:  Dixon, Katharine H.
;  APPLICANT:  Brazzell, Romulus K.
;  TITLE OF INVENTION: METHOD FOR TREATING OCULAR
;  TITLE OF INVENTION:  NEOVASCULARIZATION
;  FILE REFERENCE: 4-31881A
;  CURRENT APPLICATION NUMBER: US/10/080,797
;  CURRENT FILING DATE:  2002-02-21
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR Primer
US-10-080-797-17

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 23;
  Best Local Similarity   83.3%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1970 TTTACCTTGAAAAAAAGA 1987
              |||||  ||||||||| |
Db         18 TTTACACTGAAAAAAAAA 1


RESULT 3562
US-10-301-844-23/c
; Sequence 23, Application US/10301844
; Publication No. US20030100747A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruddy, David A.
;                   Wolff, Roger K.
;        TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
;                            HEMOCHROMATOSIS GENE
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds, LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/301,844
;             FILING DATE: 20-No. US20030100747A1-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/852,495C
;             FILING DATE: 07-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-0057-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 23:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 14 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-301-844-23

  Query Match             0.5%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         14 AAAAAAAAAAAAA 2


RESULT 3563
US-10-138-674-1071/c
; Sequence 1071, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1071
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-1071

  Query Match             0.5%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 3564
US-10-287-949A-1071/c
; Sequence 1071, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1071
;   LENGTH: 17
```

```
;  APPLICANT: Batra, Surinder K.
;  APPLICANT:  Brandt, Randall E.
;  APPLICANT:  Ringel, J"erg
;  APPLICANT:  Faulmann, Grit
;  APPLICANT:  L"hr, Matthias
;  APPLICANT:  Varshney, Grish C.
;  APPLICANT:  University of Nebraska Board of Regents
;  TITLE OF INVENTION: Specific Mucin Expression as a Marker
;  TITLE OF INVENTION:  for Pancreatic Cancer
;  FILE REFERENCE: UNMC 63155
;  CURRENT APPLICATION NUMBER: US/10/279,454
;  CURRENT FILING DATE:  2002-10-24
;  PRIOR APPLICATION NUMBER: US/09/733,444
;  PRIOR FILING DATE: 2000-12-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-279-454-13

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        718 CCTGTTGCTGCACGATCA 735
              |||| ||||| | |||||
Db         18 CCTGCTGCTGGATGATCA 1


RESULT 3558
US-10-213-329-3/c
; Sequence 3, Application US/10213329
; Publication No. US20030083465A1
; GENERAL INFORMATION:
;  APPLICANT: Zimrin, Ann B.
;  APPLICANT:  Maciag, Thomas
;  APPLICANT:  Wong, Michael K.K.
;  APPLICANT:  Pepper, Michael S.
;  APPLICANT:  Montesano, Roberto
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
;  TITLE OF INVENTION:  BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: 0036-1U1
;  CURRENT APPLICATION NUMBER: US/10/213,329
;  CURRENT FILING DATE:  2002-08-06
;  PRIOR APPLICATION NUMBER: US/09/199,865
;  PRIOR FILING DATE: 1998-11-25
;  PRIOR APPLICATION NUMBER: 60/018,841
;  PRIOR FILING DATE: 1996-05-31
;  PRIOR APPLICATION NUMBER: PCT/US97/09407
;  PRIOR FILING DATE: 1997-05-30
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: 3' reverse
;   OTHER INFORMATION: transcription primer
US-10-213-329-3

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              |||||||| |||||  ||
Db         21 GAAAAAAAAAAAAGCTTG 4


RESULT 3559
US-09-263-959-614/c
; Sequence 614, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  614:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-614

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||| |||| ||| ||||
Db         22 AAAACAAAACAAACAAAA 5


RESULT 3560
US-09-373-938-13/c
; Sequence 13, Application US/09373938
; Publication No. US20020115202A1
; GENERAL INFORMATION:
;  APPLICANT: Hallenbeck, Paul
;  APPLICANT:  Chen, Cheauyun Theresa
;  TITLE OF INVENTION: ADENOVIRAL VECTORS INCLUDING DNA SEQUENCES ENCODING ANGIOGENIC INH
;  FILE REFERENCE: 4-30899P1
;  CURRENT APPLICATION NUMBER: US/09/373,938
;  CURRENT FILING DATE:  1999-08-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-373-938-13

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 23;
```

```
RESULT 3553
US-10-085-906-446
; Sequence 446, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
;  APPLICANT: Ying, Vincent
;  APPLICANT:  Wu, Paul
;  APPLICANT:  Gray, Gary S.
;  TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
;  TITLE OF INVENTION:  COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
;  FILE REFERENCE: GNN-5343CP2
;  CURRENT APPLICATION NUMBER: US/10/085,906
;  CURRENT FILING DATE:  2002-02-27
;  PRIOR APPLICATION NUMBER: US 60/126,215
;  PRIOR FILING DATE: 1999-03-25
;  PRIOR APPLICATION NUMBER: US 09/534,061
;  PRIOR FILING DATE: 2000-03-24
;  PRIOR APPLICATION NUMBER: PCT/US00/07938
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 545
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 446
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-085-906-446

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||||||| |||  ||
Db          1 AAAAAAAAAATAAAGGAA 18


RESULT 3554
US-10-380-584-123/c
; Sequence 123, Application US/10380584
; Publication No. US20040014088A1
; GENERAL INFORMATION:
;  APPLICANT: Utermohlen, Joseph
;  APPLICANT:  Connaughton, John
;  TITLE OF INVENTION: Oligonucleotide Sequence Formula for Labeling Oligonucleotide Prc
;  TITLE OF INVENTION:  Proteins for In Situ Analysis
;  FILE REFERENCE: 355/001/PCT
;  CURRENT APPLICATION NUMBER: US/10/380,584
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/233,177
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide probe
US-10-380-584-123

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||| ||||| | |||||
Db         21 AAAAGAAAAATAGAAAAA 4


RESULT 3555
US-10-085-906-465
; Sequence 465, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
;  APPLICANT: Ying, Vincent
;  APPLICANT:  Wu, Paul
;  APPLICANT:  Gray, Gary S.
;  TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
;  TITLE OF INVENTION:  COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
;  FILE REFERENCE: GNN-5343CP2
;  CURRENT APPLICATION NUMBER: US/10/085,906
;  CURRENT FILING DATE:  2002-02-27
;  PRIOR APPLICATION NUMBER: US 60/126,215
;  PRIOR FILING DATE: 1999-03-25
;  PRIOR APPLICATION NUMBER: US 09/534,061
;  PRIOR FILING DATE: 2000-03-24
;  PRIOR APPLICATION NUMBER: PCT/US00/07938
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 545
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 465
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-085-906-465

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||   |||||||||
Db          2 AAAAAATTTAAAAAAAAA 19


RESULT 3556
US-09-733-444-13/c
; Sequence 13, Application US/09733444
; Patent No. US20020150894A1
; GENERAL INFORMATION:
;  APPLICANT: Batra, Surinder K.
;  APPLICANT:  Brandt, Randall E.
;  APPLICANT:  Ringel, J"erg
;  APPLICANT:  Faulmann, Grit
;  APPLICANT:  L"hr, Matthias
;  APPLICANT:  Varshney, Grish C.
;  APPLICANT:  University of Nebraska Board of Regents
;  TITLE OF INVENTION: Specific Mucin Expression as a Marker
;  TITLE OF INVENTION:  for Pancreatic Cancer
;  FILE REFERENCE: UNMC 63155
;  CURRENT APPLICATION NUMBER: US/09/733,444
;  CURRENT FILING DATE:  2000-12-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-733-444-13

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        718 CCTGTTGCTGCACGATCA 735
              |||| ||||| | |||||
Db         18 CCTGCTGCTGGATGATCA 1


RESULT 3557
US-10-279-454-13/c
; Sequence 13, Application US/10279454
; Publication No. US20030134343A1
; GENERAL INFORMATION:
```

```
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1724
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-1724

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        894 CAGTGGCTGAAGTACAGA 911
              ||| | ||| ||||||||
Db         18 CAGAGACTGGAGTACAGA 1


RESULT 3549
US-10-688-706-1855
; Sequence 1855, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1855
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-1855

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1824 TAGAATCTTTTAAATACA 1841
              ||||||||||    |||||
Db          3 TAGAATCTTTCTGATACA 20


RESULT 3550
US-10-688-706-2086/c
; Sequence 2086, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2086
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2086

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAA 2188
              ||| | |||| |||||||
Db         19 TTTCTGTTTTGTTTTAA 2


RESULT 3551
US-10-688-706-2139
; Sequence 2139, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2139
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2139

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1824 TAGAATCTTTTAAATACA 1841
              ||||||||||    |||||
Db          2 TAGAATCTTTCTGATACA 19


RESULT 3552
US-10-688-706-2365
; Sequence 2365, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2365
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2365

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1824 TAGAATCTTTTAAATACA 1841
              ||||||||||    |||||
Db          1 TAGAATCTTTCTGATACA 18
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              || |||||||||||  |||
Db         18 AAGCCAGTGGCAGTGTAT 1


RESULT 3544
US-10-688-706-441/c
; Sequence 441, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 441
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-441

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        896 GTGGCTGAAGTACAGAGG 913
              | | ||| ||||||||||
Db         20 GAGACTGGAGTACAGAGG 3


RESULT 3545
US-10-688-706-475/c
; Sequence 475, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 475
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-475

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1148 AAACCAGTGGCAGAATAT 1165
              || |||||||||||  |||
Db         20 AAGCCAGTGGCAGTGTAT 3


RESULT 3546
US-10-688-706-1639
; Sequence 1639, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1639
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-1639

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2226 AATGACATGTTCCCTTAA 2243
              ||| |||| ||| |||||
Db          1 AATCACATCTTCTCTTAA 18


RESULT 3547
US-10-688-706-1698
; Sequence 1698, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1698
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-1698

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2225 AAATGACATGTTCCCTTA 2242
              |||| |||| ||| ||||
Db          3 AAATCACATCTTCTCTTA 20


RESULT 3548
US-10-688-706-1724/c
; Sequence 1724, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
```

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;  APPLICANT: Susan M. Freier
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF SQUALENE SYNTHASE EXPRESSION
;  FILE REFERENCE: PTS-0056
;  CURRENT APPLICATION NUMBER: US/10/304,125
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 68
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-125-68

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1059 ATGTGACTCTCCTGACAT 1076
              ||||||||  ||  |||  ||
Db         18 ATGTGACTGTCATGAGAT 1


RESULT 3540
US-10-304-125-126
; Sequence 126, Application US/10304125
; Publication No. US20040102405A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF SQUALENE SYNTHASE EXPRESSION
;  FILE REFERENCE: PTS-0056
;  CURRENT APPLICATION NUMBER: US/10/304,125
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 126
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-304-125-126

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1740 GTGACAAGTACTGGCTCT 1757
              | ||||||||||| | ||
Db          3 GGGACAAGTACTGCCACT 20


RESULT 3541
US-10-304-125-135
; Sequence 135, Application US/10304125
; Publication No. US20040102405A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF SQUALENE SYNTHASE EXPRESSION
;  FILE REFERENCE: PTS-0056
;  CURRENT APPLICATION NUMBER: US/10/304,125
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 135
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-304-125-135

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1059 ATGTGACTCTCCTGACAT 1076
              ||||||||  ||  |||  ||
Db          3 ATGTGACTGTCATGAGAT 20


RESULT 3542
US-10-688-706-331/c
; Sequence 331, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 331
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-331

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1148 AAACCAGTGGCAGAATAT 1165
              ||  ||||||||||  |||
Db         19 AAGCCAGTGGCAGTGTAT 2


RESULT 3543
US-10-688-706-341/c
; Sequence 341, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 341
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-341

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1148 AAACCAGTGGCAGAATAT 1165
```

```
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF HEPATOCYTE GROWTH FACTOR RECEPTOR EXPRESSION
;  FILE REFERENCE: PTS-0043
;  CURRENT APPLICATION NUMBER: US/10/304,019
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 147
; SEQ ID NO 38
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-019-38

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1139 TTTCCTAGTAAACCAGTG 1156
              | ||||| |||| |||||
Db          2 TGTCCTATTAAAGCAGTG 19


RESULT 3535
US-10-304-019-109/c
; Sequence 109, Application US/10304019
; Publication No. US20040102622A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF HEPATOCYTE GROWTH FACTOR RECEPTOR EXPRESSION
;  FILE REFERENCE: PTS-0043
;  CURRENT APPLICATION NUMBER: US/10/304,019
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 147
; SEQ ID NO 109
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-304-019-109

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1139 TTTCCTAGTAAACCAGTG 1156
              | ||||| |||| |||||
Db         19 TGTCCTATTAAAGCAGTG 2


RESULT 3536
US-10-304-113-71/c
; Sequence 71, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
;  FILE REFERENCE: RTS-0415
;  CURRENT APPLICATION NUMBER: US/10/304,113
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 71
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-113-71

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        701 AATGTCGACGACCAGCAC 718
              |||||| |  ||||||||
Db         20 AATGTCAAATACCAGCAC 3


RESULT 3537
US-10-304-113-145
; Sequence 145, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
;  FILE REFERENCE: RTS-0415
;  CURRENT APPLICATION NUMBER: US/10/304,113
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 145
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-304-113-145

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        701 AATGTCGACGACCAGCAC 718
              |||||| |  ||||||||
Db          1 AATGTCAAATACCAGCAC 18


RESULT 3538
US-10-304-125-59/c
; Sequence 59, Application US/10304125
; Publication No. US20040102405A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF SQUALENE SYNTHASE EXPRESSION
;  FILE REFERENCE: PTS-0056
;  CURRENT APPLICATION NUMBER: US/10/304,125
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 59
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-125-59

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1740 GTGACAAGTACTGGCTCT 1757
              | |||||||||||| | ||
Db         18 GGGACAAGTACTGCCACT 1


RESULT 3539
US-10-304-125-68/c
; Sequence 68, Application US/10304125
; Publication No. US20040102405A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Donna T. Ward
;  APPLICANT:  Alexander H. Borchers
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF GLUCOSE TRANSPORTER-4 EXPRESSION
;  FILE REFERENCE: RTS-0426
;  CURRENT APPLICATION NUMBER: US/10/303,266
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 103
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-303-266-103

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1165 TTTAACCAGACCTCATCT 1182
              ||| |||||| |||| ||
Db          1 TTTGACCAGATCTCAGCT 18


RESULT 3530
US-10-303-327-44
; Sequence 44, Application US/10303327
; Publication No. US20040102396A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF BCL2-ASSOCIATED ATHANOGENE 5 EXPRESSION
;  FILE REFERENCE: HTS-0004
;  CURRENT APPLICATION NUMBER: US/10/303,327
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 44
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-327-44

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1086 AAGGTGAAGCTGTTCATT 1103
              ||||| || ||| |||||
Db          3 AAGGTCAATCTGATCATT 20


RESULT 3531
US-10-303-327-75/c
; Sequence 75, Application US/10303327
; Publication No. US20040102396A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF BCL2-ASSOCIATED ATHANOGENE 5 EXPRESSION
;  FILE REFERENCE: HTS-0004
;  CURRENT APPLICATION NUMBER: US/10/303,327
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 75
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-303-327-75

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1086 AAGGTGAAGCTGTTCATT 1103
              ||||| || ||| |||||
Db         18 AAGGTCAATCTGATCATT 1


RESULT 3532
US-10-303-420-167/c
; Sequence 167, Application US/10303420
; Publication No. US20040102398A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF B7H EXPRESSION
;  FILE REFERENCE: RTS-0417
;  CURRENT APPLICATION NUMBER: US/10/303,420
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 271
; SEQ ID NO 167
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-420-167

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        794 CAGAAGGAGCTGGTGGGG 811
              || ||||||| | |||||
Db         19 CACAAGGAGCAGTTGGGG 2


RESULT 3533
US-10-303-635-44
; Sequence 44, Application US/10303635
; Publication No. US20040102621A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
;  FILE REFERENCE: RTS-0418
;  CURRENT APPLICATION NUMBER: US/10/303,635
;  CURRENT FILING DATE:  2002-11-21
;  NUMBER OF SEQ ID NOS: 257
; SEQ ID NO 44
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-635-44

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1388 GCGGTGTCTGCCCTGCAG 1405
              |||  | ||||||||||||
Db          2 GCGCGGGCTGCCCTGCAG 19


RESULT 3534
US-10-304-019-38
; Sequence 38, Application US/10304019
; Publication No. US20040102622A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
```

```
US-10-300-288-16
; Sequence 16, Application US/10300288
; Publication No. US20040097449A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF KIAA0415 EXPRESSION
;  FILE REFERENCE: HTS-0120
;  CURRENT APPLICATION NUMBER: US/10/300,288
;  CURRENT FILING DATE:  2002-11-19
;  NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-300-288-16

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1398 CCCTGCAGAACTACATCA 1415
                ||||||||||||  || |
Db          3 CCCTGCAGAACTGGATGA 20


RESULT 3525
US-10-300-288-52/c
; Sequence 52, Application US/10300288
; Publication No. US20040097449A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF KIAA0415 EXPRESSION
;  FILE REFERENCE: HTS-0120
;  CURRENT APPLICATION NUMBER: US/10/300,288
;  CURRENT FILING DATE:  2002-11-19
;  NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 52
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-300-288-52

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1398 CCCTGCAGAACTACATCA 1415
                ||||||||||||  || |
Db         18 CCCTGCAGAACTGGATGA 1


RESULT 3526
US-10-301-832-24/c
; Sequence 24, Application US/10301832
; Publication No. US20040102390A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF NOTCH3 EXPRESSION
;  FILE REFERENCE: RTS-0414
;  CURRENT APPLICATION NUMBER: US/10/301,832
;  CURRENT FILING DATE:  2002-11-21
;  NUMBER OF SEQ ID NOS: 155
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-301-832-24

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        480 GCCGCCAGAGCCAGGAGG 497
                 || || |||||||||  ||
Db         18 GCTGCGAGAGCCAGGTGG 1


RESULT 3527
US-10-301-832-101
; Sequence 101, Application US/10301832
; Publication No. US20040102390A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF NOTCH3 EXPRESSION
;  FILE REFERENCE: RTS-0414
;  CURRENT APPLICATION NUMBER: US/10/301,832
;  CURRENT FILING DATE:  2002-11-21
;  NUMBER OF SEQ ID NOS: 155
; SEQ ID NO 101
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-301-832-101

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        480 GCCGCCAGAGCCAGGAGG 497
                 || || |||||||||  ||
Db          3 GCTGCGAGAGCCAGGTGG 20


RESULT 3528
US-10-303-266-26/c
; Sequence 26, Application US/10303266
; Publication No. US20040101848A1
; GENERAL INFORMATION:
;  APPLICANT: Donna T. Ward
;  APPLICANT:  Alexander H. Borchers
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF GLUCOSE TRANSPORTER-4 EXPRESSION
;  FILE REFERENCE: RTS-0426
;  CURRENT APPLICATION NUMBER: US/10/303,266
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-266-26

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1165 TTTAACCAGACCTCATCT 1182
                 ||| |||||| |||| ||
Db         20 TTTGACCAGATCTCAGCT 3


RESULT 3529
US-10-303-266-103
; Sequence 103, Application US/10303266
; Publication No. US20040101848A1
; GENERAL INFORMATION:
```

```
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2704 TGAACTCTCTGCCTGTAA 2721
              |||  |||||| ||||||
Db         18 TGAGATCTCTGGCTGTAA 1


RESULT 3519
US-10-300-236-45/c
; Sequence 45, Application US/10300236
; Publication No. US20040097448A1
; GENERAL INFORMATION:
;  APPLICANT: Andrew T. Watt
;  TITLE OF INVENTION: MODULATION OF CD24 EXPRESSION
;  FILE REFERENCE: RTS-0178
;  CURRENT APPLICATION NUMBER: US/10/300,236
;  CURRENT FILING DATE:  2002-11-19
;  NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 45
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-10-300-236-45

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2696 TTTGGAATTGAACTCTCT 2713
              || |||| ||||||| ||
Db         19 TTGGGAACTGAACTCACT 2


RESULT 3520
US-10-300-236-116
; Sequence 116, Application US/10300236
; Publication No. US20040097448A1
; GENERAL INFORMATION:
;  APPLICANT: Andrew T. Watt
;  TITLE OF INVENTION: MODULATION OF CD24 EXPRESSION
;  FILE REFERENCE: RTS-0178
;  CURRENT APPLICATION NUMBER: US/10/300,236
;  CURRENT FILING DATE:  2002-11-19
;  NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 116
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: H. sapiens
;    FEATURE:
US-10-300-236-116

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2696 TTTGGAATTGAACTCTCT 2713
              || |||| ||||||| ||
Db          2 TTGGGAACTGAACTCACT 19


RESULT 3521
US-10-300-263-23
; Sequence 23, Application US/10300263
; Publication No. US20040096834A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF HIP-1 PROTEIN INTERACTOR EXPRESSION
;  FILE REFERENCE: RTS-0431
;  CURRENT APPLICATION NUMBER: US/10/300,263
;  CURRENT FILING DATE:  2002-11-19
;  NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 23
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-10-300-263-23

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1264 CAGCCAAGACCGGACACC 1281
              |||||| ||||||  |||
Db          1 CAGCCACGACCGGTTACC 18


RESULT 3522
US-10-300-263-29/c
; Sequence 29, Application US/10300263
; Publication No. US20040096834A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF HIP-1 PROTEIN INTERACTOR EXPRESSION
;  FILE REFERENCE: RTS-0431
;  CURRENT APPLICATION NUMBER: US/10/300,263
;  CURRENT FILING DATE:  2002-11-19
;  NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 29
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-10-300-263-29

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1082 GTAGAAGGTGAAGCTGTT 1099
              | |||||  |||||||| |
Db         18 GGAGAAGCTGAAGCTGCT 1


RESULT 3523
US-10-300-263-104
; Sequence 104, Application US/10300263
; Publication No. US20040096834A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF HIP-1 PROTEIN INTERACTOR EXPRESSION
;  FILE REFERENCE: RTS-0431
;  CURRENT APPLICATION NUMBER: US/10/300,263
;  CURRENT FILING DATE:  2002-11-19
;  NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 104
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: H. sapiens
;    FEATURE:
US-10-300-263-104

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1082 GTAGAAGGTGAAGCTGTT 1099
              | |||||  |||||||| |
Db          3 GGAGAAGCTGAAGCTGCT 20


RESULT 3524
```

```
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: US/09/908,147
;  PRIOR FILING DATE: 2001-07-17
;  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-34

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1485 AAACCCTGGAGAAAATGG 1502
              |||||||| || ||| ||
Db          1 AAACCCTGAAGCAAAAGG 18


RESULT 3515
US-10-728-509-35
; Sequence 35, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
;  FILE REFERENCE: RTS-0185
;  CURRENT APPLICATION NUMBER: US/10/728,509
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: US/09/908,147
;  PRIOR FILING DATE: 2001-07-17
;  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-35

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1485 AAACCCTGGAGAAAATGG 1502
              |||||||| || ||| ||
Db          2 AAACCCTGAAGCAAAAGG 19


RESULT 3516
US-10-280-183A-393/c
; Sequence 393, Application US/10280183A
; Publication No. US20040081964A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Bachmanov, Alexander A
;  APPLICANT:  Beauchamp, Gary K.
;  APPLICANT:  Chatterjee, Aurobindo
;  APPLICANT:  De  Jong, Pieter J.
;  APPLICANT:  Li, Shanru
;  APPLICANT:  Li, Xia
;  APPLICANT:  Ohmen, Jeffrey D
;  APPLICANT:  Reed, Danielle R.
;  APPLICANT:  Ross, David
;  APPLICANT:  Tordoff, Michael G.
;  TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
;  TITLE OF INVENTION:  CARBOHYDRATE COMPOUNDS AND OTHER SWEETNERS
;  FILE REFERENCE: PC18306A
;  CURRENT APPLICATION NUMBER: US/10/280,183A
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: 60/200,794
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 652
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 393
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Mouse
US-10-280-183A-393

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1571 ATCCTTCTCCACCGCACA 1588
              |||||| |||||| || |
Db         20 ATCCTTTTCCACCCCAAA 3


RESULT 3517
US-10-643-432-75
; Sequence 75, Application US/10643432
; Publication No. US20040087536A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF KOX 1 EXPRESSION
;  FILE REFERENCE: RTS-0359
;  CURRENT APPLICATION NUMBER: US/10/643,432
;  CURRENT FILING DATE:  2003-08-19
;  PRIOR APPLICATION NUMBER: US/10/173,817
;  PRIOR FILING DATE: 2002-06-17
;  NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 75
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-432-75

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2704 TGAACTCTCTGCCTGTAA 2721
              |||  |||||| ||||||
Db          3 TGAGATCTCTGGCTGTAA 20


RESULT 3518
US-10-643-432-127/c
; Sequence 127, Application US/10643432
; Publication No. US20040087536A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF KOX 1 EXPRESSION
;  FILE REFERENCE: RTS-0359
;  CURRENT APPLICATION NUMBER: US/10/643,432
;  CURRENT FILING DATE:  2003-08-19
;  PRIOR APPLICATION NUMBER: US/10/173,817
;  PRIOR FILING DATE: 2002-06-17
;  NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 127
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-643-432-127

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-628-841-87

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1063 GACTCTCCTGACATCCTT 1080
              |||||| |||||| || |
Db         19 GACTCTGCTGACAGCCCT 2


RESULT 3510
US-10-272-461-49/c
; Sequence 49, Application US/10272461
; Publication No. US20040076959A1
; GENERAL INFORMATION:
;  APPLICANT: Srinivasan, Subha
;  APPLICANT:  Bingham, Jonathan
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR POLYNUCLEOTIDE DETECTION
;  FILE REFERENCE: 37087-8002 US 01
;  CURRENT APPLICATION NUMBER: US/10/272,461
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/343,298
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-272-461-49

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2679 TGTGGGTGAAATGGAGAT 2696
              ||||| |||||||| | |
Db         20 TGTGGTTGAAATGGTGCT 3


RESULT 3511
US-10-272-810-29
; Sequence 29, Application US/10272810
; Publication No. US20040077568A1
; GENERAL INFORMATION:
;  APPLICANT: Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH (DROSOPHILA) HOMOLOG 4 EXPRESSION
;  FILE REFERENCE: RTS-0263
;  CURRENT APPLICATION NUMBER: US/10/272,810
;  CURRENT FILING DATE:  2002-10-16
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-272-810-29

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        722 TTGCTGCACGATCAGACA 739
              ||||||  | ||||||||
Db          3 TTGCTGGGCCATCAGACA 20


RESULT 3512
US-10-273-070-29
; Sequence 29, Application US/10273070
; Publication No. US20040077569A1
; GENERAL INFORMATION:
;  APPLICANT: Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH (DROSOPHILA) HOMOLOG 4 EXPRESSION
;  FILE REFERENCE: RTS-0231
;  CURRENT APPLICATION NUMBER: US/10/273,070
;  CURRENT FILING DATE:  2002-10-16
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-273-070-29

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        722 TTGCTGCACGATCAGACA 739
              ||||||  | ||||||||
Db          3 TTGCTGGGCCATCAGACA 20


RESULT 3513
US-10-703-864-62/c
; Sequence 62, Application US/10703864
; Publication No. US20040077580A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  Susan Murray
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Nicholas M. Dean
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PI3K P85 EXPRESSION
;  FILE REFERENCE: ISIS0057-102 (ISPH-0519)
;  CURRENT APPLICATION NUMBER: US/10/703,864
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: US/09/715,983
;  PRIOR FILING DATE: 2000-11-20
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 62
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-703-864-62

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        452 ACAGGCAGCCAGCAGCAG 469
              | || ||||||||| |||
Db         20 AGAGACAGCCAGCACCAG 3


RESULT 3514
US-10-728-509-34
; Sequence 34, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
;  FILE REFERENCE: RTS-0185
;  CURRENT APPLICATION NUMBER: US/10/728,509
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```
US-10-210-723-116

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1675 CCTGGACTTCTTAGTTGT 1692
              ||||||  ||| ||||||
Db         19 CCTGGAGCTCTGAGTTGT 2


RESULT 3505
US-10-210-723-121/c
; Sequence 121, Application US/10210723
; Publication No. US20040023382A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION
;  FILE REFERENCE: PTS-0028
;  CURRENT APPLICATION NUMBER: US/10/210,723
;  CURRENT FILING DATE:  2002-07-31
;  NUMBER OF SEQ ID NOS: 141
; SEQ ID NO 121
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-723-121

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2074 ATCTGACACACTCTAAAC 2091
              ||  ||||||||||| ||
Db         20 ATAAGACACACTCTATAC 3


RESULT 3506
US-10-210-838-60
; Sequence 60, Application US/10210838
; Publication No. US20040023905A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Sanjay Bhanot
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LAR EXPRESSION
;  FILE REFERENCE: PTS-0013
;  CURRENT APPLICATION NUMBER: US/10/210,838
;  CURRENT FILING DATE:  2002-07-31
;  NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 60
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-838-60

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1640 TTTAAAGAGCCTTCACTG 1657
              ||  |||||| |||||||
Db          2 TTGGAAGAGCTTTCACTG 19


RESULT 3507
US-10-212-993-24
; Sequence 24, Application US/10212993
; Publication No. US20040023385A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF REQUIEM EXPRESSION
;  FILE REFERENCE: PTS-0031
;  CURRENT APPLICATION NUMBER: US/10/212,993
;  CURRENT FILING DATE:  2002-08-05
;  NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-212-993-24

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        460 CCAGCAGCAGGCCTGGCC 477
              | ||| || |||||||||
Db          3 CGAGCTGCTGGCCTGGCC 20


RESULT 3508
US-10-212-993-91/c
; Sequence 91, Application US/10212993
; Publication No. US20040023385A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF REQUIEM EXPRESSION
;  FILE REFERENCE: PTS-0031
;  CURRENT APPLICATION NUMBER: US/10/212,993
;  CURRENT FILING DATE:  2002-08-05
;  NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 91
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-212-993-91

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        460 CCAGCAGCAGGCCTGGCC 477
              | ||| || |||||||||
Db         18 CGAGCTGCTGGCCTGGCC 1


RESULT 3509
US-10-628-841-87/c
; Sequence 87, Application US/10628841
; Publication No. US20040023918A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION
;  FILE REFERENCE: RTS-0191
;  CURRENT APPLICATION NUMBER: US/10/628,841
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: US/09/972,607
;  PRIOR FILING DATE: 2001-10-06
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 87
```

```
US-10-179-940-533/c
; Sequence 533, Application US/10179940
; Publication No. US20040018618A1
;   GENERAL INFORMATION:
;        APPLICANT: Abrams, Mark A.
;                   Bauer, S. C.
;                   Braford-Goldberg, Sarah R.
;                   Caparon, Maire H.
;                   Easton, Alan M.
;                   Klein, Barbara K.
;                   McKearn, John P.
;                   Olins, Peter O.
;                   Paik, Kumnan
;                   Polazzi, Joseph O.
;        TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
;        NUMBER OF SEQUENCES: 549
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol M. Nielsen, Gardere Wynne Sewell LLP,
;             STREET: 1601 Elm Street, Suite 3000
;             CITY: Dallas
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 75201-4761
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/179,940
;             FILING DATE: 19-Jun-2002
;             CLASSIFICATION: Unknown
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 07/981044
;             FILING DATE: 24-NOV-1992
;             APPLICATION NUMBER: PCT/US93/11198
;             FILING DATE: 22-NOV-1993
;             APPLICATION NUMBER: US 08/411796
;             FILING DATE: 09-APR-1995
;             APPLICATION NUMBER: US 08/559390
;             FILING DATE: 15-NOV-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Carol M. Nielsen
;             REGISTRATION NUMBER: 37,676
;             REFERENCE/DOCKET NUMBER: 126181-1056 (C2713/1)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713)276-5383
;             TELEFAX: (713)276-5555
;   INFORMATION FOR SEQ ID NO: 533:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (synthetic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 533:
US-10-179-940-533

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1241 TGTAAAGAATTCACAGAA 1258
              ||| |||| || ||||||
Db         18 TGTCAAGAGTTTACAGAA 1


RESULT 3502
US-10-210-723-47
; Sequence 47, Application US/10210723
; Publication No. US20040023382A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION
;  FILE REFERENCE: PTS-0028
;  CURRENT APPLICATION NUMBER: US/10/210,723
;  CURRENT FILING DATE:  2002-07-31
;  NUMBER OF SEQ ID NOS: 141
; SEQ ID NO 47
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-723-47

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1675 CCTGGACTTCTTAGTTGT 1692
              ||||||  ||| ||||||
Db          2 CCTGGAGCTCTGAGTTGT 19


RESULT 3503
US-10-210-723-53
; Sequence 53, Application US/10210723
; Publication No. US20040023382A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION
;  FILE REFERENCE: PTS-0028
;  CURRENT APPLICATION NUMBER: US/10/210,723
;  CURRENT FILING DATE:  2002-07-31
;  NUMBER OF SEQ ID NOS: 141
; SEQ ID NO 53
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-723-53

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2074 ATCTGACACACTCTAAAC 2091
              ||  |||||||||| ||
Db          1 ATAAGACACACTCTATAC 18


RESULT 3504
US-10-210-723-116/c
; Sequence 116, Application US/10210723
; Publication No. US20040023382A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION
;  FILE REFERENCE: PTS-0028
;  CURRENT APPLICATION NUMBER: US/10/210,723
;  CURRENT FILING DATE:  2002-07-31
;  NUMBER OF SEQ ID NOS: 141
; SEQ ID NO 116
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-131-827-8899

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        455 GGCAGCCAGCAGCAGGCC 472
              | ||| ||||||||| ||
Db         20 GACAGACAGCAGCAGACC 3


RESULT 3497
US-10-131-827-8991/c
; Sequence 8991, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
;  TITLE OF INVENTION:  CHRONIC INFLAMMATORY DISEASES
;  FILE REFERENCE: 506612000120
;  CURRENT APPLICATION NUMBER: US/10/131,827
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9090
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8991
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-131-827-8991

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2131 GTAGAAACGAAGCCTGCT 2148
              |||||||| |  ||||||
Db         19 GTAGAAACCACCCCTGCT 2


RESULT 3498
US-10-199-199-85
; Sequence 85, Application US/10199199
; Publication No. US20040014047A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOMAIN KINASE 1 EXPRESSION
;  FILE REFERENCE: RTS-0375
;  CURRENT APPLICATION NUMBER: US/10/199,199
;  CURRENT FILING DATE:  2002-07-18
;  NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 85
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-199-199-85

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2656 AGGTGAGTGTGCAGTACA 2673
              ||||||||||||   ||
Db          3 AGGTGAGTGTGCAAGGCA 20


RESULT 3499
US-10-199-199-143/c
; Sequence 143, Application US/10199199
; Publication No. US20040014047A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOMAIN KINASE 1 EXPRESSION
;  FILE REFERENCE: RTS-0375
;  CURRENT APPLICATION NUMBER: US/10/199,199
;  CURRENT FILING DATE:  2002-07-18
;  NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 143
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-199-199-143

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2656 AGGTGAGTGTGCAGTACA 2673
              ||||||||||||   ||
Db         18 AGGTGAGTGTGCAAGGCA 1


RESULT 3500
US-10-435-696-204
; Sequence 204, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
;  APPLICANT: Wirtz, Ralph
;  APPLICANT:  Munnes, Marc
;  APPLICANT:  Kallabis, Harald
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS,
;  TITLE OF INVENTION:  PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
;  FILE REFERENCE: LeA 36 108
;  CURRENT APPLICATION NUMBER: US/10/435,696
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: EP03003112.4
;  PRIOR FILING DATE: 2003-02-13
;  PRIOR APPLICATION NUMBER: EP02010291.9
;  PRIOR FILING DATE: 2002-05-21
;  NUMBER OF SEQ ID NOS: 314
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: ORMDL3
US-10-435-696-204

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        505 GCTGCCCTCGCACCACGG 522
              |||||||  || ||||||
Db          2 GCTGCCCCAGCTCCACGG 19


RESULT 3501
```

```
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-5130

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        625 ACACGCCCTGGATGCCGC 642
              ||||||||| ||   |||
Db         18 ACACGCCCTGAATATCGC 1


RESULT 3492
US-10-289-762-6118
; Sequence 6118, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6118
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-6118

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1318 GAACATACAGAACTGCTT 1335
              ||||||| |||||| | |
Db          2 GAACATAGAGAACTCCAT 19


RESULT 3493
US-10-289-762-6292
; Sequence 6292, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6292
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-6292

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        762 CCATGACCAAGAACCCTC 779
              |||| || |||| |||||
Db          1 CCATCACAAAGACCCCTC 18


RESULT 3494
US-10-289-762-6579/c
; Sequence 6579, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6579
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-6579

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        495 AGGGAGCGGGGCTGCCCT 512
              | || |||||||||| |||
Db         20 ATGGTGCGGGGCTGGCCT 3


RESULT 3495
US-10-289-762-6757/c
; Sequence 6757, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6757
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-6757

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1068 TCCTGACATCCTTAGTAG 1085
              ||||| ||  ||||||||
Db         20 TCCTGGCAATCTTAGTAG 3


RESULT 3496
US-10-131-827-8899/c
; Sequence 8899, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
;  APPLICANT: Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
;  TITLE OF INVENTION:  CHRONIC INFLAMMATORY DISEASES
;  FILE REFERENCE: 506612000120
;  CURRENT APPLICATION NUMBER: US/10/131,827
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 10/006,290
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/296,764
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 9090
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8899
;   LENGTH: 20
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;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2313
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-2313

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2046 TCTGCTTAGCAACTAGTT 2063
              ||||||||| |||| | |
Db          3 TCTGCTTAGGAACTTGCT 20


RESULT 3487
US-10-289-762-2530/c
; Sequence 2530, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2530
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-2530

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2551 TAAGAGGATGCTGGGCTC 2568
              || ||||| ||||||| |
Db         20 TATGAGGAGGCTGGGCCC 3


RESULT 3488
US-10-289-762-2581/c
; Sequence 2581, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2581
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-2581

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        686 ATGGACGAGGTGCAGAAT 703
              ||| |||||||||| || |
Db         20 ATGTACGAGGTGCTGACT 3


RESULT 3489
US-10-289-762-4019
; Sequence 4019, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prever
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4019
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-4019

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1479 CTAACAAAACCCTGGAGA 1496
              | | ||||| ||||||||
Db          1 CCACCAAAAACCTGGAGA 18


RESULT 3490
US-10-289-762-5039/c
; Sequence 5039, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prever
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5039
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-5039

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2127 ACTTGTAGAAACGAAGCC 2144
              |||| || | |||||||||
Db         18 ACTTCTAAAGACGAAGCC 1


RESULT 3491
US-10-289-762-5130/c
; Sequence 5130, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prever
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5130
;   LENGTH: 20
;   TYPE: DNA
```

; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10558
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-14228 for SEQ 2693, in complem
US-10-349-143-10558

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2688 AATGGAGATTTGGAATTG 2705
|| ||| ||||| |||||
Db 19 AAGGGAAATTTGAAATTG 2

RESULT 3482
US-10-188-883-84
; Sequence 84, Application US/10188883
; Publication No. US20040006005A1
; GENERAL INFORMATION:
; APPLICANT: Bhanot, Sanjay
; TITLE OF INVENTION: USE OF INTEGRIN-LINKED KINASE INHIBITORS FOR TREATING INSULIN RES
; TITLE OF INVENTION: HYPERGLYCEMIA AND DIABETES
; FILE REFERENCE: ISPH-0687
; CURRENT APPLICATION NUMBER: US/10/188,883
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide.
US-10-188-883-84

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1461 ACCAGAGTCCAGCTGATT 1478
||||||| || |||| ||
Db 3 ACCAGAGGCCTGCTGCTT 20

RESULT 3483
US-10-189-267-101/c
; Sequence 101, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 101
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-101

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1830 CTTTTAAATACATTCCCT 1847
|||||||| |||| | ||
Db 18 CTTTTAAAAACATGCACT 1

RESULT 3484
US-10-289-762-1828/c
; Sequence 1828, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1828
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1828

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2658 GTGAGTGTGCAGTACAGT 2675
| |||||||| ||| |||
Db 20 GAGAGTGTGCTGTAAAGT 3

RESULT 3485
US-10-289-762-2037
; Sequence 2037, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2037
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2037

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 750 AAGGTCCCATTTCCATGA 767
|||||| ||| |||| ||
Db 3 AAGGTCTCATATCCAGGA 20

RESULT 3486
US-10-289-762-2313
; Sequence 2313, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999

```
Qy       1681 CTTCTTAGTTGTTTCTCT 1698
              ||||  |||||||| |||
Db         20 CTTCCAAGTTGTTTTTCT 3


RESULT 3478
US-10-349-143-4188/c
; Sequence 4188, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4188
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: upstream amplification primer 99-13861 for SEQ 254,
US-10-349-143-4188

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1240 GTGTAAAGAATTCACAGA 1257
              ||||||| || ||| |||
Db         19 GTGTAAAAAACTCAAAGA 2


RESULT 3479
US-10-349-143-4995/c
; Sequence 4995, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4995
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: upstream amplification primer 99-20074 for SEQ 1061,
US-10-349-143-4995

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        424 CATCAACCCCCTGCACCA 441
              | ||||||||||||| | |
Db         20 CTTCAACCCCCTGCCCAA 3


RESULT 3480
US-10-349-143-7152
; Sequence 7152, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7152
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: upstream amplification primer 99-24966 for SEQ 3218,
US-10-349-143-7152

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        770 AAGAACCCTCTGAACCTC 787
              | |||||| |||||| ||
Db          1 AGGAACCCCCTGAACTTC 18


RESULT 3481
US-10-349-143-10558/c
; Sequence 10558, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
```

```
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
;  FILE REFERENCE: RTS-0373
;  CURRENT APPLICATION NUMBER: US/10/188,646
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 138
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-188-646-138

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2561 CTGGGCTCTGTTCTTGGC 2578
                ||||  ||  ||||||  |||
Db          2 CTGGACTGTGTTCTGGGC 19


RESULT 3474
US-10-188-779A-111/c
; Sequence 111, Application US/10188779A
; Publication No. US20040005567A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN-DEPENDENT KINASE 4 EXPRESSION
;  FILE REFERENCE: PTS-0042
;  CURRENT APPLICATION NUMBER: US/10/188,779A
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 282
; SEQ ID NO 111
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-779A-111

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        799 GGAGCTGGTGGGGGCCGT 816
                | ||||||  |||||||  |
Db         20 GCAGCTGGAGGGGGCCTT 3


RESULT 3475
US-10-188-779A-240
; Sequence 240, Application US/10188779A
; Publication No. US20040005567A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN-DEPENDENT KINASE 4 EXPRESSION
;  FILE REFERENCE: PTS-0042
;  CURRENT APPLICATION NUMBER: US/10/188,779A
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 282
; SEQ ID NO 240
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: M. musculus
US-10-188-779A-240

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        799 GGAGCTGGTGGGGGCCGT 816
                | ||||||  |||||||  |
Db          1 GCAGCTGGAGGGGGCCTT 18


RESULT 3476
US-10-189-268-47/c
; Sequence 47, Application US/10189268
; Publication No. US20040005570A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GERANYLGERANYL DIPHOSPHATE SYNTHASE 1 EXP
;  FILE REFERENCE: PTS-0021
;  CURRENT APPLICATION NUMBER: US/10/189,268
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 47
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-268-47

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1824 TAGAATCTTTTAAATACA 1841
                |||  ||||||  ||||||
Db         19 TAGGTTCTTTTGAATACA 2


RESULT 3477
US-10-349-143-4087/c
; Sequence 4087, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4087
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: upstream amplification primer 99-13229 for SEQ 153,
US-10-349-143-4087

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
; Sequence 61, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Hong Zhang
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
;  FILE REFERENCE: RTS-0370
;  CURRENT APPLICATION NUMBER: US/10/177,554
;  CURRENT FILING DATE:  2002-06-20
;  NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 61
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-554-61

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        470 GCCTGGCCCGGCCGCCAG 487
              |||||| |||| | ||||
Db         20 GCCTGGGCCGGGCTCCAG 3


RESULT 3469
US-10-177-554-188
; Sequence 188, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Hong Zhang
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
;  FILE REFERENCE: RTS-0370
;  CURRENT APPLICATION NUMBER: US/10/177,554
;  CURRENT FILING DATE:  2002-06-20
;  NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 188
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-177-554-188

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2674 GTGTGTGTGGGTGAAATG 2691
              ||| ||||| ||||| ||
Db          1 GTGCGTGTGTGTGAAGTG 18


RESULT 3470
US-10-177-798-25/c
; Sequence 25, Application US/10177798
; Publication No. US20030235912A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ORPHAN G-PROTEIN COUPLED RECEPTOR GPRC5B
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: PTS-0047
;  CURRENT APPLICATION NUMBER: US/10/177,798
;  CURRENT FILING DATE:  2002-06-19
;  NUMBER OF SEQ ID NOS: 70
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-798-25

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1175 CCTCATCTTGGAGGACGA 1192
              | |||||  |||||||||
Db         19 CATCATCCAGGAGGACGA 2


RESULT 3471
US-10-187-659A-143/c
; Sequence 143, Application US/10187659A
; Publication No. US20040002152A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF P2X4 EXPRESSION
;  FILE REFERENCE: RTS-0379
;  CURRENT APPLICATION NUMBER: US/10/187,659A
;  CURRENT FILING DATE:  2002-07-01
;  NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 143
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-187-659A-143

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1026 TGAATCTTCCGGCCGGGA 1043
              |||||| ||| |||| ||
Db         19 TGAATCGTCCAGCCGCGA 2


RESULT 3472
US-10-188-646-74/c
; Sequence 74, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
;  FILE REFERENCE: RTS-0373
;  CURRENT APPLICATION NUMBER: US/10/188,646
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 74
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-646-74

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2561 CTGGGCTCTGTTCTTGGC 2578
              |||| || |||||| |||
Db         19 CTGGACTGTGTTCTGGGC 2


RESULT 3473
US-10-188-646-138
; Sequence 138, Application US/10188646
; Publication No. US20040005565A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Marcusson, Eric G.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: Phosphatidylinositol-4 Phosphate 5-Kinase, Type 11 Beta
;  TITLE OF INVENTION:  Inhibitors For Inhibiting Angiogenesis
;  FILE REFERENCE: ISPH-0727
;  CURRENT APPLICATION NUMBER: US/10/348,073A
;  CURRENT FILING DATE:  2003-01-16
;  PRIOR APPLICATION NUMBER: 10/175,627
;  PRIOR FILING DATE: 2002-06-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-348-073A-62

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2686 GAAATGGAGATTTGGAAT 2703
                ||| ||| ||||||| ||
Db          1 GAACTGGGGATTTGGGAT 18


RESULT 3465
US-10-448-914A-162
; Sequence 162, Application US/10448914A
; Publication No. US20030235856A1
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
;  APPLICANT:  KIM, Cheol Min
;  APPLICANT:  PARK, Hee Kyung
;  TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
;  FILE REFERENCE: PP05020/PCT
;  CURRENT APPLICATION NUMBER: US/10/448,914A
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019631
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019632
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019633
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019634
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019635
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-2000-0018189
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 243
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 162
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium smegmatis
US-10-448-914A-162

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        104 CCGCTTGGGGGCTGGGGG 121
                ||  |||||||| |||||
Db          2 CCCGTTGGGGGCGGGGGG 19


RESULT 3466
US-10-448-914A-239
; Sequence 239, Application US/10448914A
; Publication No. US20030235856A1
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
;  APPLICANT:  KIM, Cheol Min
;  APPLICANT:  PARK, Hee Kyung
;  TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
;  FILE REFERENCE: PP05020/PCT
;  CURRENT APPLICATION NUMBER: US/10/448,914A
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019631
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019632
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019633
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019634
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019635
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-2000-0018189
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 243
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 239
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium
;   OTHER INFORMATION: paratuberculosis
US-10-448-914A-239

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         71 CGCCTGGTCACCGTGACC 88
                ||| ||||| ||||| ||
Db          2 CGCATGGTCTCCGTGGCC 19


RESULT 3467
US-10-177-554-52/c
; Sequence 52, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Hong Zhang
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
;  FILE REFERENCE: RTS-0370
;  CURRENT APPLICATION NUMBER: US/10/177,554
;  CURRENT FILING DATE:  2002-06-20
;  NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 52
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-554-52

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2674 GTGTGTGTGGGTGAAATG 2691
                ||| ||||| ||||| ||
Db         20 GTGCGTGTGTGTGAAGTG 3


RESULT 3468
US-10-177-554-61/c
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-460-28

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1381 CTGTGCCGCGGTGTCTGC 1398
              |||||| |||| | ||||
Db         20 CTGTGCTGCGGAGGCTGC 3


RESULT 3460
US-10-174-460-88
; Sequence 88, Application US/10174460
; Publication No. US20030232441A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 4 EXPRESSION
;  FILE REFERENCE: PTS-0014
;  CURRENT APPLICATION NUMBER: US/10/174,460
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 88
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-174-460-88

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1381 CTGTGCCGCGGTGTCTGC 1398
              |||||| |||| | ||||
Db          1 CTGTGCTGCGGAGGCTGC 18


RESULT 3461
US-10-175-627-27/c
; Sequence 27, Application US/10175627
; Publication No. US20030232775A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Edward A. Dennis
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE
;  TITLE OF INVENTION:  BETA EXPRESSION
;  FILE REFERENCE: PTS-0005
;  CURRENT APPLICATION NUMBER: US/10/175,627
;  CURRENT FILING DATE:  2002-06-18
;  NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-175-627-27

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2686 GAAATGGAGATTTGGAAT 2703
              ||| ||| ||||||| ||
Db         20 GAACTGGGGATTTGGGAT 3


RESULT 3462
US-10-175-627-61
; Sequence 61, Application US/10175627
; Publication No. US20030232775A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Edward A. Dennis
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE,
;  TITLE OF INVENTION:  BETA EXPRESSION
;  FILE REFERENCE: PTS-0005
;  CURRENT APPLICATION NUMBER: US/10/175,627
;  CURRENT FILING DATE:  2002-06-18
;  NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 61
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-175-627-61

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2686 GAAATGGAGATTTGGAAT 2703
              ||| ||| ||||||| ||
Db          1 GAACTGGGGATTTGGGAT 18


RESULT 3463
US-10-348-073A-28/c
; Sequence 28, Application US/10348073A
; Publication No. US20030232777A1
; GENERAL INFORMATION:
;  APPLICANT: Marcusson, Eric G.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: Phosphatidylinositol-4 Phosphate 5-Kinase, Type 11 Beta
;  TITLE OF INVENTION:  Inhibitors For Inhibiting Angiogenesis
;  FILE REFERENCE: ISPH-0727
;  CURRENT APPLICATION NUMBER: US/10/348,073A
;  CURRENT FILING DATE:  2003-01-16
;  PRIOR APPLICATION NUMBER: 10/175,627
;  PRIOR FILING DATE: 2002-06-18
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-073A-28

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2686 GAAATGGAGATTTGGAAT 2703
              ||| ||| ||||||| ||
Db         20 GAACTGGGGATTTGGGAT 3


RESULT 3464
US-10-348-073A-62
; Sequence 62, Application US/10348073A
; Publication No. US20030232777A1
```

```
;  CURRENT FILING DATE:  2003-03-12
;  NUMBER OF SEQ ID NOS: 947
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 513
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-513

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2681 TGGGTGAAATGGAGATTT 2698
              ||| ||| |||||| |||
Db         19 TGGCTGAGATGGAGGTTT 2


RESULT 3455
US-10-173-208-25/c
; Sequence 25, Application US/10173208
; Publication No. US20030232435A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN PRECURSOR EXPRESSION
;  FILE REFERENCE: HTS-0023
;  CURRENT APPLICATION NUMBER: US/10/173,208
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-208-25

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1608 CCTGGGGGAAGAGTTTGT 1625
              ||  |||| |||||||||
Db         20 CCGAGGGGTAGAGTTTGT 3


RESULT 3456
US-10-173-208-61
; Sequence 61, Application US/10173208
; Publication No. US20030232435A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN PRECURSOR EXPRESSION
;  FILE REFERENCE: HTS-0023
;  CURRENT APPLICATION NUMBER: US/10/173,208
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 61
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-10-173-208-61

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1608 CCTGGGGGAAGAGTTTGT 1625
              ||  |||| |||||||||
Db          1 CCGAGGGGTAGAGTTTGT 18


RESULT 3457
US-10-173-817-75
; Sequence 75, Application US/10173817
; Publication No. US20030232438A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF KOX 1 EXPRESSION
;  FILE REFERENCE: RTS-0359
;  CURRENT APPLICATION NUMBER: US/10/173,817
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 75
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-817-75

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2704 TGAACTCTCTGCCTGTAA 2721
              |||  |||||| ||||||
Db          3 TGAGATCTCTGGCTGTAA 20


RESULT 3458
US-10-173-817-127/c
; Sequence 127, Application US/10173817
; Publication No. US20030232438A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF KOX 1 EXPRESSION
;  FILE REFERENCE: RTS-0359
;  CURRENT APPLICATION NUMBER: US/10/173,817
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 127
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-173-817-127

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2704 TGAACTCTCTGCCTGTAA 2721
              |||  |||||| ||||||
Db         18 TGAGATCTCTGGCTGTAA 1


RESULT 3459
US-10-174-460-28/c
; Sequence 28, Application US/10174460
; Publication No. US20030232441A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 4 EXPRESSION
;  FILE REFERENCE: PTS-0014
;  CURRENT APPLICATION NUMBER: US/10/174,460
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 28
```

```
  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2692 GAGATTTGGAATTGAACT 2709
                ||||  |||||||| | ||
Db         18 GAGAGTTGGAATTCATCT 1


RESULT 3451
US-10-360-510-102
; Sequence 102, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/10/360,510
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US/09/854,883
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 102
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-102

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1133 GCCGAATTTCCTAGTAAA 1150
                |  |||||  ||||  |||||
Db          2 GTCGAATATCCTGGTAAA 19


RESULT 3452
US-10-360-510-224/c
; Sequence 224, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/10/360,510
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US/09/854,883
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 224
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-224

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1287 GGACCAGCAGGCTCGCCC 1304
                ||  |  |||||||  |||||
Db         19 GGGCAAGCAGGCCCGCCC 2


RESULT 3453
US-10-360-522-25/c
; Sequence 25, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
;  APPLICANT: Allefs, Josephus J.H.M.
;  APPLICANT:  Vossen v.d., Edwin A.G.
;  TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
;  TITLE OF INVENTION:  FUNGAL RESISTANCE AND RELATED METHODS
;  FILE REFERENCE: U 014413-9
;  CURRENT APPLICATION NUMBER: US/10/360,522
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: EP 02075565.8
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: PCT/NL03/00091
;  PRIOR FILING DATE: 2003-02-07
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: reverse primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(20)
US-10-360-522-25

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2566 CTCTGTTCTTGGCTTGGA 2583
                |||  ||||  |||||||  |
Db         20 CTCGGTTCCTGGCTTGAA 3


RESULT 3454
US-10-388-263-513/c
; Sequence 513, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  McNeil, John
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Sasmor, Henri M.
;  APPLICANT:  Brooks, Douglas G.
;  APPLICANT:  Ohashi, Cara
;  APPLICANT:  Wyatt, Jacqueline R.
;  APPLICANT:  Borchers, Alexander
;  APPLICANT:  Vickers, Timothy A.
;  TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
;  TITLE OF INVENTION:  MODULATION BY OLIGONUCLEOTIDES AND
;  TITLE OF INVENTION:  GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
;  FILE REFERENCE: ISIS-4503
;  CURRENT APPLICATION NUMBER: US/10/388,263
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```
;  APPLICANT: SAITO et al.
;  TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
;  FILE REFERENCE: 2185-0648P
;  CURRENT APPLICATION NUMBER: US/10/148,835
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 213
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Designed
;   OTHER INFORMATION: oligonucleotide probe  for Southern hybridization
US-10-148-835-139

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        466 GCAGGCCTGGCCCGGCCG 483
              ||||||||| ||| || |
Db          3 GCAGGCCTGACCCTGCAG 20


RESULT 3447
US-10-148-355A-64/c
; Sequence 64, Application US/10148355A
; Publication No. US20030207831A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  ISIS PHARMACEUTICALS, INC.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTSP-0082
;  CURRENT APPLICATION NUMBER: US/10/148,355A
;  CURRENT FILING DATE:  2002-09-30
;  PRIOR APPLICATION NUMBER: 09/467,642
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-148-355A-64

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        898 GGCTGAAGTACAGAGGCG 915
              ||||| ||| ||| ||||
Db         20 GGCTGGAGTGCAGTGGCG 3


RESULT 3448
US-10-114-279-29
; Sequence 29, Application US/10114279
; Publication No. US20030219742A1
; GENERAL INFORMATION:
;  APPLICANT: Sanjay Bhanot
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HMGI-C EXPRESSION
;  FILE REFERENCE: RTS-0296
;  CURRENT APPLICATION NUMBER: US/10/114,279
;  CURRENT FILING DATE:  2002-03-29
;  NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-279-29

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        416 GCCGCCGCCATCAACCCC 433
              || ||| |||||||| ||
Db          1 GCTGCCACCATCAACACC 18


RESULT 3449
US-10-310-677-126
; Sequence 126, Application US/10310677
; Publication No. US20030219772A1
; GENERAL INFORMATION:
;  APPLICANT: Kuyl v.d., Antoinette C.
;  APPLICANT:  Cornelissen, Marion
;  TITLE OF INVENTION: Means and methods for treatment evaluation
;  FILE REFERENCE: P55190US10
;  CURRENT APPLICATION NUMBER: US/10/310,677
;  CURRENT FILING DATE:  2002-12-05
;  PRIOR APPLICATION NUMBER: EP 01200228.3
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: EP 01203703.2
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US 60/325,722
;  PRIOR FILING DATE: 2001-09-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: 3'TAG011GENE-2
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(20)
US-10-310-677-126

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2527 ATATATATACAGGGTATT 2544
              |||||| |||||| || |
Db          3 ATATATTTACAGGATAGT 20


RESULT 3450
US-10-146-860-88/c
; Sequence 88, Application US/10146860
; Publication No. US20030220273A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Mark P. Roach
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHODIESTERASE 4D EXPRESSION
;  FILE REFERENCE: RTS-0351
;  CURRENT APPLICATION NUMBER: US/10/146,860
;  CURRENT FILING DATE:  2002-05-15
;  NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 88
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-146-860-88
```

```
;  APPLICANT:  KIM, Cheol Min
;  APPLICANT:  PARK, Hee Kyung
;  TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
;  FILE REFERENCE: PP05020/PCT
;  CURRENT APPLICATION NUMBER: US/10/448,836
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019631
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019632
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019633
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019634
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019635
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-2000-0018189
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 243
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 162
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium smegmatis
US-10-448-836-162

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        104 CCGCTTGGGGGCTGGGGG 121
              ||  |||||||| |||||
Db          2 CCCGTTGGGGGCGGGGGG 19


RESULT 3443
US-10-448-836-239
; Sequence 239, Application US/10448836
; Publication No. US20030207313A1
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
;  APPLICANT:  KIM, Cheol Min
;  APPLICANT:  PARK, Hee Kyung
;  TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
;  FILE REFERENCE: PP05020/PCT
;  CURRENT APPLICATION NUMBER: US/10/448,836
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019631
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019632
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019633
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019634
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-1999-0019635
;  PRIOR FILING DATE: 1999-05-29
;  PRIOR APPLICATION NUMBER: KR 10-2000-0018189
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 243
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 239
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium
;   OTHER INFORMATION: paratuberculosis
US-10-448-836-239

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         71 CGCCTGGTCACCGTGACC 88
              ||| ||||| ||||| ||
Db          2 CGCATGGTCTCCGTGGCC 19


RESULT 3444
US-10-148-835-58/c
; Sequence 58, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
;  APPLICANT: SAITO et al.
;  TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
;  FILE REFERENCE: 2185-0648P
;  CURRENT APPLICATION NUMBER: US/10/148,835
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 213
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Designed
;   OTHER INFORMATION: oligonucleotide primer for PCR
US-10-148-835-58

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        601 CTCCGACCTGCTGCTGCC 618
              || |||| |||||||| |
Db         19 CTTCGACATGCTGCTGGC 2


RESULT 3445
US-10-148-835-60/c
; Sequence 60, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
;  APPLICANT: SAITO et al.
;  TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
;  FILE REFERENCE: 2185-0648P
;  CURRENT APPLICATION NUMBER: US/10/148,835
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 213
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Designed
;   OTHER INFORMATION: oligonucleotide primer for PCR
US-10-148-835-60

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1085 GAAGGTGAAGCTGTTCAT 1102
              ||||||| | ||| ||||
Db         20 GAAGGTGGACCTGATCAT 3


RESULT 3446
US-10-148-835-139
; Sequence 139, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
```

```
; SEQ ID NO 170
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-109-349A-170

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2723 TGTTCCCCAAATAATTGT 2740
              ||| |||||| ||||| |
Db          3 TGTGCCCCAAGTAATTTT 20


RESULT 3439
US-10-165-099-145
; Sequence 145, Application US/10165099
; Publication No. US20030188326A1
; GENERAL INFORMATION:
;  APPLICANT: D'Andrea, Alan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS OF CANCER SUSCEPTIBILI
;  TITLE OF INVENTION:  DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THEREOF
;  FILE REFERENCE: 7032/2055
;  CURRENT APPLICATION NUMBER: US/10/165,099
;  CURRENT FILING DATE:  2002-06-06
;  PRIOR APPLICATION NUMBER: US 09/998,027
;  PRIOR FILING DATE: 2001-11-02
;  PRIOR APPLICATION NUMBER: US 60/245,756
;  PRIOR FILING DATE: 2000-11-03
;  NUMBER OF SEQ ID NOS: 352
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-165-099-145

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1917 ATACCTTTTTTTTCAGTG 1934
              ||||||| |||| | |||
Db          2 ATACCTTCTTTTGCTGTG 19


RESULT 3440
US-10-321-856-320
; Sequence 320, Application US/10321856
; Publication No. US20030194393A1
; GENERAL INFORMATION:
;  APPLICANT: Milhausen, Michael James
;  TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
;  FILE REFERENCE: TX-1-C2-1
;  CURRENT APPLICATION NUMBER: US/10/321,856
;  CURRENT FILING DATE:  2002-12-17
;  PRIOR APPLICATION NUMBER: 09/216,393
;  PRIOR FILING DATE: 1998-12-18
;  PRIOR APPLICATION NUMBER: 08/994,825
;  PRIOR FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 366
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 320
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-10-321-856-320

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1485 AAACCCTGGAGAAAATGG 1502
              |||| |||| ||||| ||
Db          2 AAACTCTGGGGAAAACGG 19


RESULT 3441
US-10-430-196-75/c
; Sequence 75, Application US/10430196
; Publication No. US20030194738A1
;   GENERAL INFORMATION:
;        APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
;                   Miraglia; Brenda F. Baker
;        TITLE OF INVENTION: Antisense Oligonucleotide
;                            Compositions and Methods for the Modulation of
;                            Activating Protein 1
;        NUMBER OF SEQUENCES: 139
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Law Offices of Jane Massey Licata
;             STREET: 66 East Main Street
;             CITY: Marlton
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08053
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: WINDOWS 95
;             SOFTWARE: WORDPERFECT 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/430,196
;             FILING DATE: 05-May-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/923,517A
;             FILING DATE: 07-Aug-2001
;             APPLICATION NUMBER: 09/364,416
;             FILING DATE: 1999-07-30
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jane Massey Licata
;             REGISTRATION NUMBER: 32,257
;             REFERENCE/DOCKET NUMBER: ISPH-0209
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (609) 810-1515
;             TELEFAX: (609) 810-1454
;   INFORMATION FOR SEQ ID NO: 75:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20
;             TYPE: Nucleic Acid
;             STRANDEDNESS: Single
;             TOPOLOGY: Linear
;        ANTI-SENSE: Yes
;        SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-10-430-196-75

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         52 CGGCGGGGGCGGCGGCAG 69
              |||||| ||||||  |||
Db         20 CGGCGGCGGCGGCTACAG 3


RESULT 3442
US-10-448-836-162
; Sequence 162, Application US/10448836
; Publication No. US20030207313A1
; GENERAL INFORMATION:
;  APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
```

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;  APPLICANT:  Skrzypczynski, Zbigniew
;  APPLICANT:  Takova, Tsetska Y.
;  APPLICANT:  Thompson, Lisa C.
;  APPLICANT:  Vedvik, Kevin L.
;  TITLE OF INVENTION: RNA Detection Assays
;  FILE REFERENCE: FORS-06666
;  CURRENT APPLICATION NUMBER: US/10/084,839
;  CURRENT FILING DATE:  2002-02-26
;  NUMBER OF SEQ ID NOS: 4004
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 651
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-084-839-651

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        628 CGCCCTGGATGCCGCGGG 645
              |||| || ||||| ||||
Db         18 CGCCGTGCATGCCTCGGG 1


RESULT 3436
US-10-084-839-1861/c
; Sequence 1861, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
;  APPLICANT: Third Wave Technologies
;  APPLICANT:  Allawi, Hatim
;  APPLICANT:  Argue, Brad T.
;  APPLICANT:  Bartholomay, Christian T.
;  APPLICANT:  Chehak, LuAnne
;  APPLICANT:  Curtis, Michelle L.
;  APPLICANT:  Eis, Peggy S.
;  APPLICANT:  Hall, Jeff G.
;  APPLICANT:  Ip, Hon S.
;  APPLICANT:  Ji, Lin
;  APPLICANT:  Kaiser, Michael
;  APPLICANT:  Kwiatkowski, Jr., Robert W.
;  APPLICANT:  Lukowiak, Andrew A.
;  APPLICANT:  Lyamichev, Victor
;  APPLICANT:  Lymaicheva, Natalie E.
;  APPLICANT:  Ma, WuPo
;  APPLICANT:  Neri, Bruce P.
;  APPLICANT:  Olson, Sarah M.
;  APPLICANT:  Olson-Munoz, Marilyn C.
;  APPLICANT:  Schaefer, James J.
;  APPLICANT:  Skrzypczynski, Zbigniew
;  APPLICANT:  Takova, Tsetska Y.
;  APPLICANT:  Thompson, Lisa C.
;  APPLICANT:  Vedvik, Kevin L.
;  TITLE OF INVENTION: RNA Detection Assays
;  FILE REFERENCE: FORS-06666
;  CURRENT APPLICATION NUMBER: US/10/084,839
;  CURRENT FILING DATE:  2002-02-26
;  NUMBER OF SEQ ID NOS: 4004
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1861
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-084-839-1861

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        628 CGCCCTGGATGCCGCGGG 645
              |||| || ||||| ||||
Db         18 CGCCGTGCATGCCTCGGG 1


RESULT 3437
US-10-084-839-1866/c
; Sequence 1866, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
;  APPLICANT: Third Wave Technologies
;  APPLICANT:  Allawi, Hatim
;  APPLICANT:  Argue, Brad T.
;  APPLICANT:  Bartholomay, Christian T.
;  APPLICANT:  Chehak, LuAnne
;  APPLICANT:  Curtis, Michelle L.
;  APPLICANT:  Eis, Peggy S.
;  APPLICANT:  Hall, Jeff G.
;  APPLICANT:  Ip, Hon S.
;  APPLICANT:  Ji, Lin
;  APPLICANT:  Kaiser, Michael
;  APPLICANT:  Kwiatkowski, Jr., Robert W.
;  APPLICANT:  Lukowiak, Andrew A.
;  APPLICANT:  Lyamichev, Victor
;  APPLICANT:  Lymaicheva, Natalie E.
;  APPLICANT:  Ma, WuPo
;  APPLICANT:  Neri, Bruce P.
;  APPLICANT:  Olson, Sarah M.
;  APPLICANT:  Olson-Munoz, Marilyn C.
;  APPLICANT:  Schaefer, James J.
;  APPLICANT:  Skrzypczynski, Zbigniew
;  APPLICANT:  Takova, Tsetska Y.
;  APPLICANT:  Thompson, Lisa C.
;  APPLICANT:  Vedvik, Kevin L.
;  TITLE OF INVENTION: RNA Detection Assays
;  FILE REFERENCE: FORS-06666
;  CURRENT APPLICATION NUMBER: US/10/084,839
;  CURRENT FILING DATE:  2002-02-26
;  NUMBER OF SEQ ID NOS: 4004
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1866
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-084-839-1866

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        628 CGCCCTGGATGCCGCGGG 645
              |||| || ||||| ||||
Db         18 CGCCGTGCATGCCTCGGG 1


RESULT 3438
US-10-109-349A-170
; Sequence 170, Application US/10109349A
; Publication No. US20030186246A1
; GENERAL INFORMATION:
;  APPLICANT: Medical College of Ohio
;  APPLICANT:  Willey, James C.
;  APPLICANT:  Crawford, Erin L.
;  TITLE OF INVENTION: MULTIPLEX STANDARDIZED REVERSE TRANSCRIPTASE-POLYMERASE CHAIN REAC
;  TITLE OF INVENTION:  METHOD FOR ASSESSMENT OF GENE EXPRESSION IN SMALL BIOLOGICAL SAMI
;  FILE REFERENCE: 01154/2001-203
;  CURRENT APPLICATION NUMBER: US/10/109,349A
;  CURRENT FILING DATE:  2002-06-12
;  NUMBER OF SEQ ID NOS: 282
;  SOFTWARE: PatentIn version 3.1
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;  PRIOR FILING DATE: 2002-01-23
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:human herpes
;   OTHER INFORMATION: virus 1,2 Primer 1 (sense)
US-10-165-410A-15

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        499 AGCGGGGCTGCCCTCGCA 516
              ||||||||||  ||| |
Db         19 AGCGGGGCTGCGTTCGGA 2


RESULT 3432
US-10-364-360-1/c
; Sequence 1, Application US/10364360
; Publication No. US20030180324A1
; GENERAL INFORMATION:
;  APPLICANT: GUERTLER, Lutz Gerhard
;  APPLICANT:  HAUSER, Hans Peter
;  APPLICANT:  DONGMO DELOKO, Yvette Beatrice
;  APPLICANT:  ZEKENG, Leopold
;  APPLICANT:  KAPTUE, Lazare
;  TITLE OF INVENTION: LENTIVIRUS FROM THE GROUP OF IMMUNODEFICIENCY VIRUSES OF DRILL MO
;  TITLE OF INVENTION:  (MANDRILLUS LEUCOPHAEUS) AND THEIR USE
;  FILE REFERENCE: 067595/0106
;  CURRENT APPLICATION NUMBER: US/10/364,360
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: US/09/625,972
;  PRIOR FILING DATE: 2000-07-29
;  PRIOR APPLICATION NUMBER: DE 199 36 003.0
;  PRIOR FILING DATE: 1999-08-03
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: primer, non-genomic DNA
US-10-364-360-1

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2442 GACTTTTTTGAGACATGG 2459
              ||| |||| || ||||||
Db         19 GACATTTTGGACACATGG 2


RESULT 3433
US-10-032-585-5682/c
; Sequence 5682, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
;  APPLICANT: Terry, Roemer D.
;  APPLICANT:  Bo, Jiang
;  APPLICANT:  Charles, Boone
;  APPLICANT:  Howard, Bussey
;  TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;  FILE REFERENCE: 10182-005-999
;  CURRENT APPLICATION NUMBER: US/10/032,585
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 8000
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5682
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-10-032-585-5682

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1438 CAAATCCTACATGAACCC 1455
              ||||||| ||| ||| ||
Db         19 CAAATCCAACACGAAGCC 2


RESULT 3434
US-10-032-585-5723
; Sequence 5723, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
;  APPLICANT: Terry, Roemer D.
;  APPLICANT:  Bo, Jiang
;  APPLICANT:  Charles, Boone
;  APPLICANT:  Howard, Bussey
;  TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;  FILE REFERENCE: 10182-005-999
;  CURRENT APPLICATION NUMBER: US/10/032,585
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 8000
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5723
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-10-032-585-5723

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        244 TCCGCGGGTCCCCCACCT 261
              |||||  |||||||| ||
Db          1 TCCGCTTGTCCCCCATCT 18


RESULT 3435
US-10-084-839-651/c
; Sequence 651, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
;  APPLICANT: Third Wave Technologies
;  APPLICANT:  Allawi, Hatim
;  APPLICANT:  Argue, Brad T.
;  APPLICANT:  Bartholomay, Christian T.
;  APPLICANT:  Chehak, LuAnne
;  APPLICANT:  Curtis, Michelle L.
;  APPLICANT:  Eis, Peggy S.
;  APPLICANT:  Hall, Jeff G.
;  APPLICANT:  Ip, Hon S.
;  APPLICANT:  Ji, Lin
;  APPLICANT:  Kaiser, Michael
;  APPLICANT:  Kwiatkowski, Jr., Robert W.
;  APPLICANT:  Lukowiak, Andrew A.
;  APPLICANT:  Lyamichev, Victor
;  APPLICANT:  Lymaicheva, Natalie E.
;  APPLICANT:  Ma, WuPo
;  APPLICANT:  Neri, Bruce P.
;  APPLICANT:  Olson, Sarah M.
;  APPLICANT:  Olson-Munoz, Marilyn C.
;  APPLICANT:  Schaefer, James J.
```

```
  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        891 TGACAGTGGCTGAAGTAC 908
              ||||| ||||||| | ||
Db          3 TGACATTGGCTGATGGAC 20


RESULT 3428
US-10-056-790-67/c
; Sequence 67, Application US/10056790
; Publication No. US20030165497A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF
;  FILE REFERENCE: RRPCIP2002
;  CURRENT APPLICATION NUMBER: US/10/056,790
;  CURRENT FILING DATE:  2002-01-23
;  PRIOR APPLICATION NUMBER: US 09/908,419
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: US 60/219,289
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: US 60/277,487
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: US 60/277,471
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: US 60/304,863
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: US 60/296,076
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/305,017
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: US 60/328,605
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/328,491
;  PRIOR FILING DATE: 2001-10-10
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mouse origin
US-10-056-790-67

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        343 CTTTCCCCCTCCCTACCA 360
              |||||  ||||||| |||
Db         20 CTTTCAGCCTCCCTTCCA 3


RESULT 3429
US-10-055-728-126
; Sequence 126, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
;  APPLICANT: van der Kuyl, Antoinette C.
;  APPLICANT:  Cornelissen, Marion
;  TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
;  FILE REFERENCE: 5244US (REN/P55190US00)
;  CURRENT APPLICATION NUMBER: US/10/055,728
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/325,722
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 0120373.2
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 01200228.3
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 3'TAG011GENE-2
US-10-055-728-126

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2527 ATATATATACAGGGTATT 2544
              |||||| |||||| || |
Db          3 ATATATTTACAGGATAGT 20


RESULT 3430
US-10-113-901-11/c
; Sequence 11, Application US/10113901
; Publication No. US20030172065A1
; GENERAL INFORMATION:
;  APPLICANT: Sorenson, James L.
;  APPLICANT:  Woodward, Scott
;  APPLICANT:  Myres, Joel
;  TITLE OF INVENTION: System and Method for Molecular Genealogy Research
;  FILE REFERENCE: 4722.1US
;  CURRENT APPLICATION NUMBER: US/10/113,901
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/280,226
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: forward primer
US-10-113-901-11

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1775 TTTTTTTGAACCCCATTC 1792
              |||||||  |||||| ||
Db         20 TTTTTTTTTACCCCACTC 3


RESULT 3431
US-10-165-410A-15/c
; Sequence 15, Application US/10165410A
; Publication No. US20030175728A1
; GENERAL INFORMATION:
;  APPLICANT: Belousov, Yevgeniy S.
;  APPLICANT:  Afonina, Irina A.
;  APPLICANT:  Epoch Biosciences, Inc.
;  TITLE OF INVENTION: Real-Time Linear Detection Probes:  Sensitive 5'-Minor
;  TITLE OF INVENTION:  Groove Binder-Containing Probes for PCR Analysis
;  FILE REFERENCE: 17682A-007220US
;  CURRENT APPLICATION NUMBER: US/10/165,410A
;  CURRENT FILING DATE:  2003-03-17
;  PRIOR APPLICATION NUMBER: US 09/457,616
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: US 09/876,830
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/302,137
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/351,637
```

```
;  CURRENT FILING DATE:  2002-12-13
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-319-221-6

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1932 GTGTTAAGGTAATGGTTG 1949
              ||| | ||||| ||||||
Db          1 GTGCTCAGGTAGTGGTTG 18


RESULT 3424
US-10-172-094-56
; Sequence 56, Application US/10172094
; Publication No. US20030161830A1
; GENERAL INFORMATION:
;  APPLICANT: JACKSON, DONALD
;  APPLICANT:  LORENZI, MATTHEW
;  APPLICANT:  ATTAR, RICARDO
;  APPLICANT:  GOTTARDIS, MARCO
;  TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
;  FILE REFERENCE: 3053-4145US1
;  CURRENT APPLICATION NUMBER: US/10/172,094
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/298,296
;  PRIOR FILING DATE: 2001-06-14
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-094-56

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGG 2565
              |||  | ||||||||||
Db          3 AATGTACAGGATGCTGGG 20


RESULT 3425
US-10-172-094-58
; Sequence 58, Application US/10172094
; Publication No. US20030161830A1
; GENERAL INFORMATION:
;  APPLICANT: JACKSON, DONALD
;  APPLICANT:  LORENZI, MATTHEW
;  APPLICANT:  ATTAR, RICARDO
;  APPLICANT:  GOTTARDIS, MARCO
;  TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
;  FILE REFERENCE: 3053-4145US1
;  CURRENT APPLICATION NUMBER: US/10/172,094
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/298,296
;  PRIOR FILING DATE: 2001-06-14
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-094-58

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGG 2565
              |||  | ||||||||||
Db          3 AATGTACAGGATGCTGGG 20


RESULT 3426
US-10-172-094-59/c
; Sequence 59, Application US/10172094
; Publication No. US20030161830A1
; GENERAL INFORMATION:
;  APPLICANT: JACKSON, DONALD
;  APPLICANT:  LORENZI, MATTHEW
;  APPLICANT:  ATTAR, RICARDO
;  APPLICANT:  GOTTARDIS, MARCO
;  TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
;  FILE REFERENCE: 3053-4145US1
;  CURRENT APPLICATION NUMBER: US/10/172,094
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/298,296
;  PRIOR FILING DATE: 2001-06-14
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-094-59

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGG 2565
              |||  | ||||||||||
Db         18 AATGTACAGGATGCTGGG 1


RESULT 3427
US-10-172-094-79
; Sequence 79, Application US/10172094
; Publication No. US20030161830A1
; GENERAL INFORMATION:
;  APPLICANT: JACKSON, DONALD
;  APPLICANT:  LORENZI, MATTHEW
;  APPLICANT:  ATTAR, RICARDO
;  APPLICANT:  GOTTARDIS, MARCO
;  TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
;  FILE REFERENCE: 3053-4145US1
;  CURRENT APPLICATION NUMBER: US/10/172,094
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/298,296
;  PRIOR FILING DATE: 2001-06-14
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-094-79
```

```
;  APPLICANT: William Gaarde
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIO
;  FILE REFERENCE: RTS-0274
;  CURRENT APPLICATION NUMBER: US/10/006,191
;  CURRENT FILING DATE:  2001-12-10
;  NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 137
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-137

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
              ||| ||||| |||||| |
Db         18 TTTGTTTTTGTTTTAAGT 1


RESULT 3420
US-10-348-485-65
; Sequence 65, Application US/10348485
; Publication No. US20030148989A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett, C. Frank
;  APPLICANT:  Dean, Nicholas M.
;  APPLICANT:  Holmlund, Jon T.
;  APPLICANT:  Dorr, F. Andrew
;  TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
;  FILE REFERENCE: ISIS4954
;  CURRENT APPLICATION NUMBER: US/10/348,485
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/10/025,139
;  PRIOR FILING DATE: 2001-12-18
;  PRIOR APPLICATION NUMBER: US 08/829,637
;  PRIOR FILING DATE: 1997-03-31
;  PRIOR APPLICATION NUMBER: US 08/478,178
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: US 08/089,996
;  PRIOR FILING DATE: 1993-07-09
;  PRIOR APPLICATION NUMBER: US 07/852,852
;  PRIOR FILING DATE: 1992-03-16
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-485-65

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1660 TCTGCATCACCCGCCCCT 1677
              |||| || || |||||||
Db          2 TCTGGATGACGCGCCCCT 19


RESULT 3421
US-10-233-032A-22/c
; Sequence 22, Application US/10233032A
; Publication No. US20030157704A1
; GENERAL INFORMATION:
;  APPLICANT: Poole, Jason
;  APPLICANT:  Roninson, Igor
;  APPLICANT:  Chang, Bey-Dih
;  TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING
;  TITLE OF INVENTION:  EXPRESSION OF GENES REGULATED BY CDK INHIBITORS
;  FILE REFERENCE: 01-1156-A
;  CURRENT APPLICATION NUMBER: US/10/233,032A
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: US 09/861,925
;  PRIOR FILING DATE: 2002-05-21
;  PRIOR APPLICATION NUMBER: US 60/265,840
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Antisense PCR primer for CC3 promoter (spec Table IIIa)
US-10-233-032A-22

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        536 CTACTGCCCCACCTCTCC 553
              |||||  |||||||| ||
Db         20 CTACTAACCCACCTCCCC 3


RESULT 3422
US-10-376-566-65
; Sequence 65, Application US/10376566
; Publication No. US20030158144A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Mark P. Roach
;  APPLICANT:  Erich Koller
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR BETA EXPRESSION
;  FILE REFERENCE: RTS-0347
;  CURRENT APPLICATION NUMBER: US/10/376,566
;  CURRENT FILING DATE:  2003-02-27
;  PRIOR APPLICATION NUMBER: US/10/005,058
;  PRIOR FILING DATE: 2001-12-07
;  NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 65
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-376-566-65

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1173 GACCTCATCTTGGAGGAC 1190
              ||| ||||| |||||| |
Db          3 GACATCATCATGGAGGCC 20


RESULT 3423
US-10-319-221-6
; Sequence 6, Application US/10319221
; Publication No. US20030159169A1
; GENERAL INFORMATION:
;  APPLICANT: Collodi, Paul
;  APPLICANT:  Fan, Lianchun
;  APPLICANT:  Ma, Chunguang
;  TITLE OF INVENTION: CELL CULTURE SYSTEM AND METHODS OF USE
;  FILE REFERENCE: 290.00300101
;  CURRENT APPLICATION NUMBER: US/10/319,221
```

```
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
;  FILE REFERENCE: RTS-0256
;  CURRENT APPLICATION NUMBER: US/10/003,919
;  CURRENT FILING DATE:  2001-12-06
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-919-33

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1670 CCGCCCCTGGACTTCTTA 1687
              ||  || ||||||||||
Db          2 CCATCCTTGGACTTCTTA 19


RESULT 3415
US-10-003-919-54/c
; Sequence 54, Application US/10003919
; Publication No. US20030114401A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
;  FILE REFERENCE: RTS-0256
;  CURRENT APPLICATION NUMBER: US/10/003,919
;  CURRENT FILING DATE:  2001-12-06
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-919-54

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2013 GATCAAGTCCTCTGGTAG 2030
              || | |||||||||| ||
Db         20 GACCGAGTCCTCTGGAAG 3


RESULT 3416
US-10-008-140B-12/c
; Sequence 12, Application US/10008140B
; Publication No. US20030124512A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmasset, Ltd.
;  APPLICANT:  Stuyver , Lieven
;  TITLE OF INVENTION: Simultaneous  Quantification of Nucleic Acids in Diseased Cells
;  FILE REFERENCE: 08841. 105021
;  CURRENT APPLICATION NUMBER: US/10/008,140B
;  CURRENT FILING DATE:  2001-10-18
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: oligonulceotide (probe) used to detect HCV viral load
US-10-008-140B-12

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 GGCTGGGGGGATCCTGGA 130
              ||  |||||| |||||||
Db         20 GGGAGGGGGGGTCCTGGA 3


RESULT 3417
US-10-024-369-13
; Sequence 13, Application US/10024369
; Publication No. US20030134809A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander H. Borchers
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ABC TRANSPORTER MHC 1 EXPRESSION
;  FILE REFERENCE: RTS-0353
;  CURRENT APPLICATION NUMBER: US/10/024,369
;  CURRENT FILING DATE:  2001-12-17
;  NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-369-13

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        567 GCGCGGTGAGCGCCCGCA 584
              |||||||| || || |||
Db          3 GCGCGGTGGGCACCAGCA 20


RESULT 3418
US-10-017-621-85/c
; Sequence 85, Application US/10017621
; Publication No. US20030138952A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  Mark P. Roach
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 1 EXPRESSION
;  FILE REFERENCE: RTS-0350
;  CURRENT APPLICATION NUMBER: US/10/017,621
;  CURRENT FILING DATE:  2001-12-07
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 85
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-017-621-85

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        575 AGCGCCCGCAGGGATGCC 592
              |||| | | |||||||||
Db         20 AGCGGCTGGAGGGATGCC 3


RESULT 3419
US-10-006-191-137/c
; Sequence 137, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
```

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RESULT 3410
US-10-206-839-86/c
; Sequence 86, Application US/10206839
; Publication No. US20030099977A1
; GENERAL INFORMATION:
;  APPLICANT: Guida, Marco
;  APPLICANT:  Kurth, Janice
;  TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
;  TITLE OF INVENTION:  (STP2)
;  FILE REFERENCE: 4389-6 (formerly SEQ-16P)
;  CURRENT APPLICATION NUMBER: US/10/206,839
;  CURRENT FILING DATE:  2002-07-26
;  PRIOR APPLICATION NUMBER: 09/328,174
;  PRIOR FILING DATE: 1999-06-08
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 86
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
US-10-206-839-86

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2511 TCATAAGGTTTTATTCAT 2528
              ||||| ||| || |||||
Db         18 TCATAGGGTCTTCTTCAT 1


RESULT 3411
US-10-269-353-26
; Sequence 26, Application US/10269353
; Publication No. US20030104447A1
; GENERAL INFORMATION:
;  APPLICANT: Holtzman, Douglas A.
;  APPLICANT:  Goodearl, Andrew D.J.
;  APPLICANT:  McCarthy, Sean A.
;  TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
;  TITLE OF INVENTION:  PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
;  TITLE OF INVENTION:  USES
;  FILE REFERENCE: MPI2000-538OMNICN1M
;  CURRENT APPLICATION NUMBER: US/10/269,353
;  CURRENT FILING DATE:  2002-10-11
;  PRIOR APPLICATION NUMBER: US 09/790,264
;  PRIOR FILING DATE: 2001-02-21
;  PRIOR APPLICATION NUMBER: US 09/065,661
;  PRIOR FILING DATE: 1998-04-23
;  PRIOR APPLICATION NUMBER: US 09/298,531
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: US 09/065,363
;  PRIOR FILING DATE: 1998-04-23
;  PRIOR APPLICATION NUMBER: US 09/337,930
;  PRIOR FILING DATE: 1999-06-22
;  PRIOR APPLICATION NUMBER: US 09/102,705
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: US 09/363,630
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 09/124,538
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide for PCR
US-10-269-353-26

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1596 AACCCCTCCTGGCCTGGG 1613
              | |||||| ||||||| |
Db          1 AGCCCCTCATGGCCTGTG 18


RESULT 3412
US-10-035-485A-23/c
; Sequence 23, Application US/10035485A
; Publication No. US20030105044A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MATRIX METALLOPROTEINASE 1 EXPRESSION
;  FILE REFERENCE: RTS-0139
;  CURRENT APPLICATION NUMBER: US/10/035,485A
;  CURRENT FILING DATE:  2001-10-17
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-035-485A-23

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2237 CCCTTAAGGTACTGAAGC 2254
              |||| |||||  ||||||
Db         19 CCCTGAAGGTGATGAAGC 2


RESULT 3413
US-10-003-354-81
; Sequence 81, Application US/10003354
; Publication No. US20030114400A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE,
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0348
;  CURRENT APPLICATION NUMBER: US/10/003,354
;  CURRENT FILING DATE:  2001-12-06
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 81
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-354-81

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1556 AACAGGACTGCAAAAATC 1573
              ||||||| | ||| ||||
Db          1 AACAGGAATTCAACAATC 18


RESULT 3414
US-10-003-919-33
; Sequence 33, Application US/10003919
; Publication No. US20030114401A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
```

```
;  PRIOR APPLICATION NUMBER: US/09/659,845A
;  PRIOR FILING DATE: 2001-07-23
;  NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 146
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-271-887-146

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1674 CCCTGGACTTCTTAGTTG 1691
              ||||||||| ||| || |
Db         18 CCCTGGACTGCTTTGTGG 1


RESULT 3406
US-10-238-011-35/c
; Sequence 35, Application US/10238011
; Publication No. US20030091568A1
; GENERAL INFORMATION:
;  APPLICANT: Frey Jurgen
;  APPLICANT:  Frey, Jurgen
;  TITLE OF INVENTION: Inhibitors for the Formation of Soluble Human CD23
;  FILE REFERENCE: 516326-2002
;  CURRENT APPLICATION NUMBER: US/10/238,011
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: EP 00 107 515.9
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 09/827,406
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-238-011-35

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1743 ACAAGTACTGGCTCTTTA 1760
              ||| |||||||| ||| |
Db         20 ACAGGTACTGGCGCTTCA 3


RESULT 3407
US-10-001-076-43
; Sequence 43, Application US/10001076
; Publication No. US20030096775A1
; GENERAL INFORMATION:
;  APPLICANT: Mark J. Graham
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF COMPLEMENT COMPONENT C3 EXPRESSION
;  FILE REFERENCE: RTS-0329
;  CURRENT APPLICATION NUMBER: US/10/001,076
;  CURRENT FILING DATE:  2001-10-23
;  NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-076-43

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2676 GTGTGTGGGTGAAATGGA 2693
              |||| | |||||| ||||
Db          2 GTGTCTTGGTGAAGTGGA 19


RESULT 3408
US-10-145-493B-33/c
; Sequence 33, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
;  APPLICANT: Besterman, Jeffrey
;  APPLICANT:  MacLeod, Robert
;  APPLICANT:  Siders, William
;  TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
;  FILE REFERENCE: MET-015DV
;  CURRENT APPLICATION NUMBER: US/10/145,493B
;  CURRENT FILING DATE:  2002-05-14
;  PRIOR APPLICATION NUMBER: 09/420,692
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: US 60/104,804
;  PRIOR FILING DATE: 1998-10-19
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-145-493B-33

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2661 AGTGTGCAGTACAGTGTG 2678
              | ||||||||||  ||||
Db         19 ATTGTGCAGTACTTTGTG 2


RESULT 3409
US-10-206-839-85/c
; Sequence 85, Application US/10206839
; Publication No. US20030099977A1
; GENERAL INFORMATION:
;  APPLICANT: Guida, Marco
;  APPLICANT:  Kurth, Janice
;  TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
;  TITLE OF INVENTION:  (STP2)
;  FILE REFERENCE: 4389-6 (formerly SEQ-16P)
;  CURRENT APPLICATION NUMBER: US/10/206,839
;  CURRENT FILING DATE:  2002-07-26
;  PRIOR APPLICATION NUMBER: 09/328,174
;  PRIOR FILING DATE: 1999-06-08
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 85
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
US-10-206-839-85

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2511 TCATAAGGTTTTATTCAT 2528
              ||||| ||| || |||||
Db         18 TCATAGGGTCTTCTTCAT 1
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;  FILE REFERENCE: NIH-05043
;  CURRENT APPLICATION NUMBER: US/10/116,949
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-10-116-949-102

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1257 AACTTCTCAGCCAAGACC 1274
              ||||||||||||  |  ||
Db          1 AACTTCTCAGCCCAAGCC 18


RESULT 3402
US-10-067-125-56/c
; Sequence 56, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-56

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        683 CAGATGGACGAGGTGCAG 700
              |||  | ||||||||||||
Db         20 CAGGAGCACGAGGTGCAG 3


RESULT 3403
US-10-209-608-33/c
; Sequence 33, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-33

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2517 GGTTTTATTCATATATAT 2534
              ||||||  |  ||||||||
Db         18 GGTTTTTTATATATATAT 1


RESULT 3404
US-10-181-177-94/c
; Sequence 94, Application US/10181177
; Publication No. US20030083296A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
;  FILE REFERENCE: RTSP-0334
;  CURRENT APPLICATION NUMBER: US/10/181,177
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/00955
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: 09/487,445
;  PRIOR FILING DATE: 2000-01-19
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 94
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-177-94

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        898 GGCTGAAGTACAGAGGCG 915
              ||||| ||| ||| ||||
Db         19 GGCTGGAGTGCAGTGGCG 2


RESULT 3405
US-10-271-887-146/c
; Sequence 146, Application US/10271887
; Publication No. US20030087871A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION
;  FILE REFERENCE: RTS-0183
;  CURRENT APPLICATION NUMBER: US/10/271,887
;  CURRENT FILING DATE:  2002-10-15
```

```
; Publication No. US20030025538A1
; GENERAL INFORMATION:
;  APPLICANT: JACKSON, DONALD
;  APPLICANT:  LORENZI, MATTHEW
;  APPLICANT:  ATTAR, RICARDO
;  APPLICANT:  GOTTARDIS, MARCO
;  TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
;  FILE REFERENCE: 3053-4145US1
;  CURRENT APPLICATION NUMBER: US/10/072,094
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/298,296
;  PRIOR FILING DATE: 2001-06-14
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-072-094-58

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGG 2565
              |||  | ||||||||||||
Db          3 AATGTACAGGATGCTGGG 20


RESULT 3398
US-10-072-094-59/c
; Sequence 59, Application US/10072094
; Publication No. US20030025538A1
; GENERAL INFORMATION:
;  APPLICANT: JACKSON, DONALD
;  APPLICANT:  LORENZI, MATTHEW
;  APPLICANT:  ATTAR, RICARDO
;  APPLICANT:  GOTTARDIS, MARCO
;  TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
;  FILE REFERENCE: 3053-4145US1
;  CURRENT APPLICATION NUMBER: US/10/072,094
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/298,296
;  PRIOR FILING DATE: 2001-06-14
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-072-094-59

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGG 2565
              |||  | ||||||||||||
Db         18 AATGTACAGGATGCTGGG 1


RESULT 3399
US-10-072-094-79
; Sequence 79, Application US/10072094
; Publication No. US20030025538A1
; GENERAL INFORMATION:
;  APPLICANT: JACKSON, DONALD
;  APPLICANT:  LORENZI, MATTHEW
;  APPLICANT:  ATTAR, RICARDO
;  APPLICANT:  GOTTARDIS, MARCO
;  TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
;  FILE REFERENCE: 3053-4145US1
;  CURRENT APPLICATION NUMBER: US/10/072,094
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/298,296
;  PRIOR FILING DATE: 2001-06-14
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-072-094-79

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        891 TGACAGTGGCTGAAGTAC 908
              ||||| ||||||| | ||
Db          3 TGACATTGGCTGATGGAC 20


RESULT 3400
US-10-156-424A-17/c
; Sequence 17, Application US/10156424A
; Publication No. US20030039999A1
; GENERAL INFORMATION:
;  APPLICANT: Yoshinaga, Steve Kiyoshi
;  APPLICANT:  Suh, Woong-Kyung
;  APPLICANT:  Mak, Tak W.
;  TITLE OF INVENTION: B7 Related Protein-2 Molecules and Uses Thereof
;  FILE REFERENCE: 01-384-A
;  CURRENT APPLICATION NUMBER: US/10/156,424A
;  CURRENT FILING DATE:  2002-09-10
;  PRIOR APPLICATION NUMBER: 60/293,629
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: oligonucleotide; PCR primer 2245-71
US-10-156-424A-17

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1414 CAAAGAAGCCCTGATTGT 1431
              |||| |||||||| | ||
Db         20 CAAACAAGCCCTGCTCGT 3


RESULT 3401
US-10-116-949-102
; Sequence 102, Application US/10116949
; Publication No. US20030044911A1
; GENERAL INFORMATION:
;  APPLICANT: Lerman, Michael I.
;  APPLICANT:  Minna, John D.
;  APPLICANT:  Latif, Farida
;  APPLICANT:  Wei, Ming-Hui
;  APPLICANT:  Sekido, Yoshitaka
;  APPLICANT:  Gao, Boning
;  APPLICANT:  Duh, Fuh-Mei
;  TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
```

```
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME 2 EXPRESSIO
;  FILE REFERENCE: RTS-0378
;  CURRENT APPLICATION NUMBER: US/10/163,272
;  CURRENT FILING DATE:  2002-06-04
;  NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-163-272-54

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        974 AAATCGAAAAATGGAGGC 991
              |||| | ||| |||||||
Db         18 AAATTGGAAATTGGAGGC 1


RESULT 3393
US-10-163-272-128
; Sequence 128, Application US/10163272
; Publication No. US20030224517A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME 2 EXPRESSIO
;  FILE REFERENCE: RTS-0378
;  CURRENT APPLICATION NUMBER: US/10/163,272
;  CURRENT FILING DATE:  2002-06-04
;  NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 128
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-163-272-128

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        974 AAATCGAAAAATGGAGGC 991
              |||| | ||| |||||||
Db          3 AAATTGGAAATTGGAGGC 20


RESULT 3394
US-10-348-750-15
; Sequence 15, Application US/10348750
; Publication No. US20030225019A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Erich Koller
;  TITLE OF INVENTION: NOTCH1 INHIBITORS FOR INDUCING APOPTOSIS
;  FILE REFERENCE: ISPH-0729
;  CURRENT APPLICATION NUMBER: US/10/348,750
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 10/160,497
;  PRIOR FILING DATE: 2002-02-20
;  NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-750-15

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        464 CAGCAGGCCTGGCCCGGC 481
              |||||| ||||| | |||
Db          3 CAGCAGACCTGGGCAGGC 20


RESULT 3395
US-10-364-748-54
; Sequence 54, Application US/10364748
; Publication No. US20030224968A1
; GENERAL INFORMATION:
;  APPLICANT: Fink, John K.
;  APPLICANT:  Zhao, Xinping
;  TITLE OF INVENTION: Atlastin
;  FILE REFERENCE: UM-07745
;  CURRENT APPLICATION NUMBER: US/10/364,748
;  CURRENT FILING DATE:  2003-02-11
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-364-748-54

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2181
              ||||| || || ||||||
Db          1 CCTTTCTTATTATTTTTT 18


RESULT 3396
US-10-072-094-56
; Sequence 56, Application US/10072094
; Publication No. US20030025538A1
; GENERAL INFORMATION:
;  APPLICANT: JACKSON, DONALD
;  APPLICANT:  LORENZI, MATTHEW
;  APPLICANT:  ATTAR, RICARDO
;  APPLICANT:  GOTTARDIS, MARCO
;  TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
;  FILE REFERENCE: 3053-4145US1
;  CURRENT APPLICATION NUMBER: US/10/072,094
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/298,296
;  PRIOR FILING DATE: 2001-06-14
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-072-094-56

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGG 2565
              |||  | ||||||||||
Db          3 AATGTACAGGATGCTGGG 20


RESULT 3397
US-10-072-094-58
; Sequence 58, Application US/10072094
```

```
;  APPLICANT: Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 2 EXPRESSION
;  FILE REFERENCE: RTS-0204
;  CURRENT APPLICATION NUMBER: US/10/160,787
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 141
; SEQ ID NO 115
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: H. sapiens
;    FEATURE:
US-10-160-787-115

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2206 TCAAATGGGAGACTCTTT 2223
              ||||||||  |||| |||
Db         20 TCAAATGGTGGACTGTTT 3


RESULT 3388
US-10-161-983-29/c
; Sequence 29, Application US/10161983
; Publication No. US20030225015A1
; GENERAL INFORMATION:
;  APPLICANT: Donna T. Ward
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF RB2/P130 EXPRESSION
;  FILE REFERENCE: HTS-0020
;  CURRENT APPLICATION NUMBER: US/10/161,983
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 29
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-10-161-983-29

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1827 AATCTTTTAAATACATTC 1844
              ||| ||| ||||| ||||
Db         18 AATGTTTGAAATATATTC 1


RESULT 3389
US-10-161-983-61
; Sequence 61, Application US/10161983
; Publication No. US20030225015A1
; GENERAL INFORMATION:
;  APPLICANT: Donna T. Ward
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF RB2/P130 EXPRESSION
;  FILE REFERENCE: HTS-0020
;  CURRENT APPLICATION NUMBER: US/10/161,983
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 61
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: H. sapiens
;    FEATURE:
US-10-161-983-61

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1827 AATCTTTTAAATACATTC 1844
              ||| ||| ||||| ||||
Db          3 AATGTTTGAAATATATTC 20


RESULT 3390
US-10-161-996-64/c
; Sequence 64, Application US/10161996
; Publication No. US20030224515A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEROL REGULATORY ELEMENT-BINDING PROTEIN
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0395
;  CURRENT APPLICATION NUMBER: US/10/161,996
;  CURRENT FILING DATE:  2002-06-04
;  NUMBER OF SEQ ID NOS: 273
; SEQ ID NO 64
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-10-161-996-64

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        797 AAGGAGCTGGTGGGGGCC 814
              ||||| ||||||| || |
Db         19 AAGGATCTGGTGGTGGGC 2


RESULT 3391
US-10-161-996-198
; Sequence 198, Application US/10161996
; Publication No. US20030224515A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  Brenda F. Baker
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEROL REGULATORY ELEMENT-BINDING PROTEIN
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0395
;  CURRENT APPLICATION NUMBER: US/10/161,996
;  CURRENT FILING DATE:  2002-06-04
;  NUMBER OF SEQ ID NOS: 273
; SEQ ID NO 198
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: H. sapiens
;    FEATURE:
US-10-161-996-198

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        797 AAGGAGCTGGTGGGGGCC 814
              ||||| ||||||| || |
Db          2 AAGGATCTGGTGGTGGGC 19


RESULT 3392
US-10-163-272-54/c
; Sequence 54, Application US/10163272
; Publication No. US20030224517A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
```

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 546 ACCTCTCCGGGCTGGAGG 563
| | || ||||||||||
Db 18 AACACTGCGGGCTGGAGG 1

RESULT 3383
US-09-861-925-22/c
; Sequence 22, Application US/09861925
; Publication No. US20030064426A1
; GENERAL INFORMATION:
; APPLICANT: Roninson, Igor
; APPLICANT: Chang, Bey-Dih
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION OF
; TITLE OF INVENTION: REGULATED BY CDK INHIBITORS
; FILE REFERENCE: 99,216-F
; CURRENT APPLICATION NUMBER: US/09/861,925
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Antisense PCR primer for CC3 promoter (spec Table IIIa)
US-09-861-925-22

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 536 CTACTGCCCCACCTCTCC 553
||||| |||||||| ||
Db 20 CTACTAACCCACCTCCCC 3

RESULT 3384
US-09-949-428-222
; Sequence 222, Application US/09949428
; Publication No. US20030064372A1
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lusis, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder
; FILE REFERENCE: 02810.0014.NPUS01
; CURRENT APPLICATION NUMBER: US/09/949,428
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-428-222

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2251 AAGCTTTATTTGCATATT 2268
|||| | |||||||| ||
Db 1 AAGCCTCATTTGCATGTT 18

RESULT 3385
US-10-160-497-15
; Sequence 15, Application US/10160497
; Publication No. US20030224513A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH1 EXPRESSION
; FILE REFERENCE: RTS-0386
; CURRENT APPLICATION NUMBER: US/10/160,497
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-160-497-15

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 464 CAGCAGGCCTGGCCCGGC 481
|||||| ||||| | |||
Db 3 CAGCAGACCTGGGCAGGC 20

RESULT 3386
US-10-160-787-49
; Sequence 49, Application US/10160787
; Publication No. US20030225256A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 2 EXPRESSION
; FILE REFERENCE: RTS-0204
; CURRENT APPLICATION NUMBER: US/10/160,787
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 141
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-160-787-49

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2206 TCAAATGGGAGACTCTTT 2223
|||||||| |||| |||
Db 1 TCAAATGGTGGACTGTTT 18

RESULT 3387
US-10-160-787-115/c
; Sequence 115, Application US/10160787
; Publication No. US20030225256A1
; GENERAL INFORMATION:

```
;   GENERAL INFORMATION:
;        APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
;                   Miraglia; Brenda F. Baker
;        TITLE OF INVENTION: Antisense Oligonucleotide
;                            Compositions and Methods for the Modulation of
;                            Activating Protein 1
;        NUMBER OF SEQUENCES: 139
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Law Offices of Jane Massey Licata
;             STREET: 66 East Main Street
;             CITY: Marlton
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08053
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: WINDOWS 95
;             SOFTWARE: WORDPERFECT 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/923,517
;             FILING DATE: 07-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/364,416
;             FILING DATE: 1999-07-30
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jane Massey Licata
;             REGISTRATION NUMBER: 32,257
;             REFERENCE/DOCKET NUMBER: ISPH-0209
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (609) 810-1515
;             TELEFAX: (609) 810-1454
;   INFORMATION FOR SEQ ID NO: 75:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20
;             TYPE: Nucleic Acid
;             STRANDEDNESS: Single
;             TOPOLOGY: Linear
;        ANTI-SENSE: Yes
;        SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-923-517-75

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         52 CGGCGGGGGCGGCGGCAG 69
              |||||| ||||||  |||
Db         20 CGGCGGCGGCGGCTACAG 3


RESULT 3381
US-10-683-386-33/c
; Sequence 33, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-33

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2517 GGTTTTATTCATATATAT 2534
              |||||| |  ||||||||
Db         18 GGTTTTTTATATATATAT 1


RESULT 3382
US-09-991-681-16/c
; Sequence 16, Application US/09991681
; Publication No. US20020086316A1
;   GENERAL INFORMATION:
;        APPLICANT: BILLING-MEDEL, PATRICIA
;                   COHEN, MAURICE
;                   COLPITTS, TRACEY L.
;                   FRIEDMAN, PAULA N.
;                   GORDON, JULIAN
;                   GRANADOS, EDWARD N.
;                   HODGES, STEVEN C.
;                   KLASS, MICHAEL R.
;                   KRATOCHVIL, JON D.
;                   ROBERTS-RAPP, LISA
;        TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
;                            FOR DETECTING DISEASES OF THE PROSTATE
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Abbott Laboratories
;             STREET: 100 Abbott Park Road
;             CITY: Abbott Park
;             STATE: IL
;             COUNTRY: USA
;             ZIP: 60064-3500
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/991,681
;             FILING DATE: 26-Nov-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/065,383
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Becker, Cheryl L.
;             REGISTRATION NUMBER: 35,441
;             REFERENCE/DOCKET NUMBER: 6084.US.P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 847/935-1729
;             TELEFAX: 847/938-2623
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-991-681-16
```

```
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-10-264-958B-7

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        116 TGGGGGGATCCTGGATTT 133
              || || |||||||| |||
Db          3 TGTGGAGATCCTGGGTTT 20


RESULT 3376
US-10-642-802-43
; Sequence 43, Application US/10642802
; Publication No. US20040043956A1
; GENERAL INFORMATION:
;  APPLICANT: Mark J. Graham
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF COMPLEMENT COMPONENT C3 EXPRESSION
;  FILE REFERENCE: RTS-0329
;  CURRENT APPLICATION NUMBER: US/10/642,802
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/10/001,076
;  PRIOR FILING DATE: 2001-10-23
;  NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-642-802-43

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2676 GTGTGTGGGTGAAATGGA 2693
              |||| | |||||| ||||
Db          2 GTGTCTTGGTGAAGTGGA 19


RESULT 3377
US-10-665-216-154
; Sequence 154, Application US/10665216
; Publication No. US20040043957A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF UROKINASE PLASMINOGEN ACTIVATOR EXPRESSIC
;  FILE REFERENCE: RTS-0188
;  CURRENT APPLICATION NUMBER: US/10/665,216
;  CURRENT FILING DATE:  2003-09-19
;  PRIOR APPLICATION NUMBER: US/09/821,972
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 154
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-665-216-154

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        875 ACGTCTAAATACAAAGTG 892
              || |||| ||| ||||||
Db          3 ACATCTATATAAAAAGTG 20


RESULT 3378
US-10-672-981-37
; Sequence 37, Application US/10672981
; Publication No. US20040048825A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CREB EXPRESSION
;  FILE REFERENCE: RTS-0237
;  CURRENT APPLICATION NUMBER: US/10/672,981
;  CURRENT FILING DATE:  2003-09-26
;  PRIOR APPLICATION NUMBER: US/09/973,827
;  PRIOR FILING DATE: 2001-10-10
;  NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 37
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-672-981-37

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1510 CAGGAAATAAAATTGGAA 1527
              |||||| |||||||  ||
Db          1 CAGGAATTAAAATTATAA 18


RESULT 3379
US-09-736-271-9
; Sequence 9, Application US/09736271
; Publication No. US20010044937A1
; GENERAL INFORMATION:
;  APPLICANT: OREGON HEALTH SCIENCES UNIVERSITY
;  APPLICANT:  Schatten, Gerald
;  APPLICANT:  Chan, Anthony W.S.
;  TITLE OF INVENTION: METHODS FOR PRODUCING TRANSGENIC ANIMALS
;  FILE REFERENCE: 899-58374
;  CURRENT APPLICATION NUMBER: US/09/736,271
;  CURRENT FILING DATE:  2000-12-15
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide primer
US-09-736-271-9

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1932 GTGTTAAGGTAATGGTTG 1949
              ||| | ||||| ||||||
Db          3 GTGCTCAGGTAGTGGTTG 20


RESULT 3380
US-09-923-517-75/c
; Sequence 75, Application US/09923517
; Publication No. US20020039741A1
```

```
RESULT 3372
US-09-864-426A-1866/c
; Sequence 1866, Application US/09864426A
; Publication No. US20040018489A1
; GENERAL INFORMATION:
;  APPLICANT: Third Wave Technologies
;  APPLICANT:  Ma, Wu Po
;  APPLICANT:  Lyamichev, Victor
;  APPLICANT:  Saiser , Michael
;  TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
;  FILE REFERENCE: FORS-04946
;  CURRENT APPLICATION NUMBER: US/09/864,426A
;  CURRENT FILING DATE:  2001-05-24
;  NUMBER OF SEQ ID NOS: 2640
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1866
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-864-426A-1866

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        628 CGCCCTGGATGCCGCGGG 645
              |||| || ||||| ||||
Db         18 CGCCGTGCATGCCTCGGG 1


RESULT 3373
US-10-215-448-44
; Sequence 44, Application US/10215448
; Publication No. US20040029273A1
; GENERAL INFORMATION:
;  APPLICANT: Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF EDG1 EXPRESSION
;  FILE REFERENCE: RTS-0179
;  CURRENT APPLICATION NUMBER: US/10/215,448
;  CURRENT FILING DATE:  2002-08-09
;  NUMBER OF SEQ ID NOS: 105
; SEQ ID NO 44
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-215-448-44

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1012 GGACAAGATCGGGTTGAA 1029
              ||||| |||| || ||||
Db          2 GGACATGATCCGGATGAA 19


RESULT 3374
US-10-072-012-1009
; Sequence 1009, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE:  2002-01-31
;  PRIOR APPLICATION NUMBER: 60/265,102
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,395
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1391
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1009
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Ag2954 Forward
US-10-072-012-1009

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        328 TCAGCCGCCACCCTACTT 345
              |||||| | ||||| |||
Db          3 TCAGCCACTACCCTCCTT 20


RESULT 3375
US-10-264-958B-7
; Sequence 7, Application US/10264958B
; Publication No. US20040038224A1
; GENERAL INFORMATION:
;  APPLICANT: Hoffman, Hal
;  APPLICANT:  Kolodner, Richard
;  TITLE OF INVENTION: Isolated Cryopyrins, Nucleic Acid Molecules Encoding These, and U
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: LUD 5738.1 CIP (10209575)
;  CURRENT APPLICATION NUMBER: US/10/264,958B
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: US60/327,728
;  PRIOR FILING DATE: 2001-10-05
```

```
;  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-35

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1485 AAACCCTGGAGAAAATGG 1502
              ||||||||  ||  ||| ||
Db          2 AAACCCTGAAGCAAAAGG 19


RESULT 3368
US-09-793-807-17
; Sequence 17, Application US/09793807
; Publication No. US20030171310A1
; GENERAL INFORMATION:
;  APPLICANT: Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL EXPRESSION
;  FILE REFERENCE: RTS-0206
;  CURRENT APPLICATION NUMBER: US/09/793,807
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-793-807-17

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2677 TGTGTGGGTGAAATGGAG 2694
              ||||||||  ||||  |  ||
Db          2 TGTGTGGGCGAAAGGAAG 19


RESULT 3369
US-09-865-879-38/c
; Sequence 38, Application US/09865879
; Publication No. US20030180707A1
; GENERAL INFORMATION:
;  APPLICANT: Roninson, Igor
;  APPLICANT:  Dokmanovic, Milos
;  APPLICANT:  Chang, Bey-Dih
;  TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION OF
;  TITLE OF INVENTION:  REGULATED BY RETINOIDS
;  FILE REFERENCE: 99,216-H
;  CURRENT APPLICATION NUMBER: US/09/865,879
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/207,535
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Sense primer for ring finger protein RNF
US-09-865-879-38

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2635 TTCCTGTTGGGCTGAACC 2652
              |||||  ||||  |||  |||
Db         20 TTCCTTTTGGACTGCACC 3


RESULT 3370
US-09-864-426A-651/c
; Sequence 651, Application US/09864426A
; Publication No. US20040018489A1
; GENERAL INFORMATION:
;  APPLICANT: Third Wave Technologies
;  APPLICANT:  Ma, Wu Po
;  APPLICANT:  Lyamichev, Victor
;  APPLICANT:  Saiser , Michael
;  TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
;  FILE REFERENCE: FORS-04946
;  CURRENT APPLICATION NUMBER: US/09/864,426A
;  CURRENT FILING DATE:  2001-05-24
;  NUMBER OF SEQ ID NOS: 2640
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 651
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-864-426A-651

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        628 CGCCCTGGATGCCGCGGG 645
              ||||  ||  |||||  ||||
Db         18 CGCCGTGCATGCCTCGGG 1


RESULT 3371
US-09-864-426A-1861/c
; Sequence 1861, Application US/09864426A
; Publication No. US20040018489A1
; GENERAL INFORMATION:
;  APPLICANT: Third Wave Technologies
;  APPLICANT:  Ma, Wu Po
;  APPLICANT:  Lyamichev, Victor
;  APPLICANT:  Saiser , Michael
;  TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
;  FILE REFERENCE: FORS-04946
;  CURRENT APPLICATION NUMBER: US/09/864,426A
;  CURRENT FILING DATE:  2001-05-24
;  NUMBER OF SEQ ID NOS: 2640
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1861
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-864-426A-1861

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        628 CGCCCTGGATGCCGCGGG 645
              ||||  ||  |||||  ||||
Db         18 CGCCGTGCATGCCTCGGG 1
```

```
;  FILE REFERENCE: RTS-0191
;  CURRENT APPLICATION NUMBER: US/09/972,607
;  CURRENT FILING DATE:  2001-10-06
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 87
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-972-607-87

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1063 GACTCTCCTGACATCCTT 1080
              |||||| |||||| || |
Db         19 GACTCTGCTGACAGCCCT 2


RESULT 3363
US-09-973-827-37
; Sequence 37, Application US/09973827
; Publication No. US20030105038A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CREB EXPRESSION
;  FILE REFERENCE: RTS-0237
;  CURRENT APPLICATION NUMBER: US/09/973,827
;  CURRENT FILING DATE:  2001-10-10
;  NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 37
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-973-827-37

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1510 CAGGAAATAAAATTGGAA 1527
              |||||| |||||||  ||
Db          1 CAGGAATTAAAATTATAA 18


RESULT 3364
US-09-920-868A-12
; Sequence 12, Application US/09920868A
; Publication No. US20030113300A1
; GENERAL INFORMATION:
;  APPLICANT: Perfetti, Riccardo
;  TITLE OF INVENTION: HUMAN GLUCOSE-DEPENDENT INSULIN-SECRETING CELL LINE
;  FILE REFERENCE: 81476-0255389
;  CURRENT APPLICATION NUMBER: US/09/920,868A
;  CURRENT FILING DATE:  2001-08-02
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Human
US-09-920-868A-12

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        394 CTCGCATCTGGGGGAAGC 411
              ||| || |||| ||||||
Db          1 CTCACACCTGGTGGAAGC 18


RESULT 3365
US-09-998-716-27
; Sequence 27, Application US/09998716
; Publication No. US20030126628A1
; GENERAL INFORMATION:
;  APPLICANT: Avigenics, Inc
;  TITLE OF INVENTION: Chicken Ovomucoid
;  FILE REFERENCE: A181 8170
;  CURRENT APPLICATION NUMBER: US/09/998,716
;  CURRENT FILING DATE:  2001-11-30
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer OVMUa9
US-09-998-716-27

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2135 AAACGAAGCCTGCTGATT 2152
              ||| |||||| |||| ||
Db          1 AAATGAAGCCGGCTGTTT 18


RESULT 3366
US-09-908-147-34
; Sequence 34, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
;  FILE REFERENCE: RTS-0185
;  CURRENT APPLICATION NUMBER: US/09/908,147
;  CURRENT FILING DATE:  2001-07-17
;  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-34

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1485 AAACCCTGGAGAAAATGG 1502
              |||||||| || ||| ||
Db          1 AAACCCTGAAGCAAAAGG 18


RESULT 3367
US-09-908-147-35
; Sequence 35, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
;  FILE REFERENCE: RTS-0185
;  CURRENT APPLICATION NUMBER: US/09/908,147
;  CURRENT FILING DATE:  2001-07-17
```

US-09-915-814-95

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 547 CCTCTCCGGGCTGGAGGC 564
||| ||| |||||||||
Db 20 CCTGGCCGAGCTGGAGGC 3

RESULT 3358
US-09-920-394-58/c
; Sequence 58, Application US/09920394
; Publication No. US20030096773A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; APPLICANT: Kristina M. Lemonidis
; TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COENZYME A CHOLESTEROL ACYLTRANSFERA
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0589
; CURRENT APPLICATION NUMBER: US/09/920,394
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 62
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-394-58

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2204 CTTCAAATGGGAGACTCT 2221
|| ||||||||||||
Db 19 CTGTGAATGGGAGACTCT 2

RESULT 3359
US-09-864-636A-651/c
; Sequence 651, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwai, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 651
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-636A-651

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 628 CGCCCTGGATGCCGCGGG 645
|||| || ||||| ||||
Db 18 CGCCGTGCATGCCTCGGG 1

RESULT 3360
US-09-864-636A-1861/c
; Sequence 1861, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwai, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1861
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-636A-1861

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 628 CGCCCTGGATGCCGCGGG 645
|||| || ||||| ||||
Db 18 CGCCGTGCATGCCTCGGG 1

RESULT 3361
US-09-864-636A-1866/c
; Sequence 1866, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwai, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1866
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-636A-1866

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 628 CGCCCTGGATGCCGCGGG 645
|||| || ||||| ||||
Db 18 CGCCGTGCATGCCTCGGG 1

RESULT 3362
US-09-972-607-87/c
; Sequence 87, Application US/09972607
; Publication No. US20030105037A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION

```
  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        256 CCACCTCTCCTCCGCCGG 273
              || | |||||||||  |||
Db          3 CCCCATCTCCTCCGGCGG 20


RESULT 3353
US-09-816-460C-44/c
; Sequence 44, Application US/09816460C
; Publication No. US20030087235A1
; GENERAL INFORMATION:
;  APPLICANT: Dairkee, Shanaz H.
;  APPLICANT:  Li, Zheng
;  TITLE OF INVENTION: PROGNOSTIC METHODS FOR BREAST CANCER
;  FILE REFERENCE: CPMC-010/00US
;  CURRENT APPLICATION NUMBER: US/09/816,460C
;  CURRENT FILING DATE:  2001-03-23
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic primer
US-09-816-460C-44

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2027 GTAGGAGGCAAAGGTTCT 2044
              | ||||||  |||| ||||
Db         20 GCAGGAGGGAAAGTTTCT 3


RESULT 3354
US-09-967-669-13
; Sequence 13, Application US/09967669
; Publication No. US20030092650A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
;  FILE REFERENCE: RTS-0259
;  CURRENT APPLICATION NUMBER: US/09/967,669
;  CURRENT FILING DATE:  2001-09-28
;  NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-967-669-13

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        477 CCGGCCGCCAGAGCCAGG 494
              | ||||||  ||| |||||
Db          1 CAGGCCGCGAGACCCAGG 18


RESULT 3355
US-09-967-669-20
; Sequence 20, Application US/09967669
; Publication No. US20030092650A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
;  FILE REFERENCE: RTS-0259
;  CURRENT APPLICATION NUMBER: US/09/967,669
;  CURRENT FILING DATE:  2001-09-28
;  NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 20
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-967-669-20

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2704 TGAACTCTCTGCCTGTAA 2721
              | |||||||||  ||| ||
Db          1 TAAACTCTCTGGCTGGAA 18


RESULT 3356
US-09-998-027-145
; Sequence 145, Application US/09998027
; Publication No. US20030093819A1
; GENERAL INFORMATION:
;  APPLICANT: D'Andrea et al.
;  TITLE OF INVENTION: Methods and Compositions for the
;  TITLE OF INVENTION:  Diagnosis and Treatment of Cancers Associated with Defective
;  TITLE OF INVENTION:  DNA Repair Mechanisms
;  FILE REFERENCE: 2486/101
;  CURRENT APPLICATION NUMBER: US/09/998,027
;  CURRENT FILING DATE:  2001-11-02
;  NUMBER OF SEQ ID NOS: 191
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: MG779
US-09-998-027-145

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1917 ATACCTTTTTTTTCAGTG 1934
              |||||||  ||||  | |||
Db          2 ATACCTTCTTTTGCTGTG 19


RESULT 3357
US-09-915-814-95/c
; Sequence 95, Application US/09915814
; Publication No. US20030096771A1
; GENERAL INFORMATION:
;  APPLICANT: Madeline M. Butler
;  APPLICANT:  Andrew T. Watt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
;  FILE REFERENCE: ISPH-0587
;  CURRENT APPLICATION NUMBER: US/09/915,814
;  CURRENT FILING DATE:  2001-07-26
;  NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 95
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
```

```
; Publication No. US20030082152A1
; GENERAL INFORMATION:
;  APPLICANT: Katz, Adam J.
;  APPLICANT:  Llull, Ramon
;  APPLICANT:  Futrell, J. William
;  APPLICANT:  Hedrick, Marc H.
;  APPLICANT:  Benhaim, Prosper
;  APPLICANT:  Lorenz, Hermann Peter
;  APPLICANT:  Zhu, Min
;  TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
;  FILE REFERENCE: 30448.77USI1
;  CURRENT APPLICATION NUMBER: US/09/952,522B
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: PCT/US00/06232
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: 60/123,711
;  PRIOR FILING DATE: 1999-03-10
;  PRIOR APPLICATION NUMBER: 60/162,462
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: CHaT reverse
;   OTHER INFORMATION: primer
US-09-952-522B-50

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        825 CCACTGAGGTCTTCTGCT 842
              |||| ||| | |||||||
Db         18 CCACGGAGATGTTCTGCT 1


RESULT 3349
US-09-912-724-55
; Sequence 55, Application US/09912724
; Publication No. US20030083280A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF C-REACTIVE PROTEIN EXPRESSION
;  FILE REFERENCE: ISPH-0584
;  CURRENT APPLICATION NUMBER: US/09/912,724
;  CURRENT FILING DATE:  2001-07-25
;  NUMBER OF SEQ ID NOS: 63
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-912-724-55

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1239 TGTGTAAAGAATTCACAG 1256
              ||   ||||||||||||||
Db          1 TGAAGAAAGAATTCACAG 18


RESULT 3350
US-09-915-485-80
; Sequence 80, Application US/09915485
; Publication No. US20030083281A1
; GENERAL INFORMATION:
;  APPLICANT: Mark J. Graham
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
;  FILE REFERENCE: RTS-0251
;  CURRENT APPLICATION NUMBER: US/09/915,485
;  CURRENT FILING DATE:  2001-07-25
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 80
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-915-485-80

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1181 CTTGGAGGACGAAATGAG 1198
              | ||| |||| |||||||
Db          3 CCTGGTGGACTAAATGAG 20


RESULT 3351
US-09-922-146-43/c
; Sequence 43, Application US/09922146
; Publication No. US20030083285A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Brett P. Monia
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
;  FILE REFERENCE: RTS-0252
;  CURRENT APPLICATION NUMBER: US/09/922,146
;  CURRENT FILING DATE:  2001-08-01
;  NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-922-146-43

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        547 CCTCTCCGGGCTGGAGGC 564
              |||||| ||||||| | |
Db         19 CCTCTCGGGGCTGGGGCC 2


RESULT 3352
US-09-922-146-46
; Sequence 46, Application US/09922146
; Publication No. US20030083285A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Brett P. Monia
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
;  FILE REFERENCE: RTS-0252
;  CURRENT APPLICATION NUMBER: US/09/922,146
;  CURRENT FILING DATE:  2001-08-01
;  NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 46
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-922-146-46
```

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;  PRIOR APPLICATION NUMBER: 08/843,704
;  PRIOR FILING DATE: 1997-04-16
;  PRIOR APPLICATION NUMBER: 08/842,898
;  PRIOR FILING DATE: 1997-04-17
;  PRIOR APPLICATION NUMBER: 60/071,589
;  PRIOR FILING DATE: 1998-01-15
;  PRIOR APPLICATION NUMBER: 09/009,802
;  PRIOR FILING DATE: 1998-01-20
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-972-473-30

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1576 TCTCCACCGCACAGACTG 1593
              ||||||| ||||  ||||
Db         18 TCTCCACAGCACTCACTG 1


RESULT 3344
US-09-972-469-49
; Sequence 49, Application US/09972469
; Publication No. US20030073085A1
; GENERAL INFORMATION:
;  APPLICANT: Lai, Fang
;  APPLICANT:  Zhou, Daixing
;  TITLE OF INVENTION: AMPLIFYING EXPRESSED SEQUENCES FROM GENOMIC DNA OF HIGHER-ORDER
;  TITLE OF INVENTION:  EUKARYOTIC ORGANISMS FOR DNA ARRAYS
;  FILE REFERENCE: SP01-290
;  CURRENT APPLICATION NUMBER: US/09/972,469
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-972-469-49

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1571 ATCCTTCTCCACCGCACA 1588
              ||||||||||||  | |
Db          3 ATCCTTCTCCACCAAAGA 20


RESULT 3345
US-09-972-469-166
; Sequence 166, Application US/09972469
; Publication No. US20030073085A1
; GENERAL INFORMATION:
;  APPLICANT: Lai, Fang
;  APPLICANT:  Zhou, Daixing
;  TITLE OF INVENTION: AMPLIFYING EXPRESSED SEQUENCES FROM GENOMIC DNA OF HIGHER-ORDER
;  TITLE OF INVENTION:  EUKARYOTIC ORGANISMS FOR DNA ARRAYS
;  FILE REFERENCE: SP01-290
;  CURRENT APPLICATION NUMBER: US/09/972,469
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-972-469-166

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        881 AAATACAAAGTGACAGTG 898
              || | ||||| |||||||
Db          3 AACTCCAAAGCGACAGTG 20


RESULT 3346
US-09-972-469-186/c
; Sequence 186, Application US/09972469
; Publication No. US20030073085A1
; GENERAL INFORMATION:
;  APPLICANT: Lai, Fang
;  APPLICANT:  Zhou, Daixing
;  TITLE OF INVENTION: AMPLIFYING EXPRESSED SEQUENCES FROM GENOMIC DNA OF HIGHER-ORDER
;  TITLE OF INVENTION:  EUKARYOTIC ORGANISMS FOR DNA ARRAYS
;  FILE REFERENCE: SP01-290
;  CURRENT APPLICATION NUMBER: US/09/972,469
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 186
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-972-469-186

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1793 TTTCCTTCTCTGAAAGTG 1810
              | ||||||||||| || ||
Db         20 TGTCCTTCTCTGGAAATG 3


RESULT 3347
US-09-906-158-64/c
; Sequence 64, Application US/09906158
; Publication No. US20030078217A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3 EXPRESS
;  FILE REFERENCE: RTS-0257
;  CURRENT APPLICATION NUMBER: US/09/906,158
;  CURRENT FILING DATE:  2001-07-14
;  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-906-158-64

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2681 TGGGTGAAATGGAGATTT 2698
              ||| ||| |||||| |||
Db         19 TGGCTGAGATGGAGGTTT 2


RESULT 3348
US-09-952-522B-50/c
; Sequence 50, Application US/09952522B
```

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RESULT 3340
US-09-232-785-75/c
; Sequence 75, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
;  APPLICANT:  International Paper Co.
;  APPLICANT:  Echt, Craig. S
;  APPLICANT:  Nelson, C. Dana
;  TITLE OF INVENTION:  MICROSATELITE DNA MARKERS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE:  4481/1E188US1
;  CURRENT APPLICATION NUMBER: US/09/232,785
;  CURRENT FILING DATE:  1999-01-19
;  PRIOR APPLICATION NUMBER:  09/232,884
;  PRIOR FILING DATE:  1999-01-15
;  NUMBER OF SEQ ID NOS:  397
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 75
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Pinus taeda L.
US-09-232-785-75

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2446 TTTTTGAGACATGGGATC 2463
              ||| || |||| ||||||
Db         18 TTTCTGGGACAAGGGATC 1


RESULT 3341
US-09-784-674-560
; Sequence 560, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,674
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: No. US20030054346A1 available
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/021,701
;             FILING DATE: 10-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Choi, Wendy A.
;             REGISTRATION NUMBER: 36,697
;             REFERENCE/DOCKET NUMBER: 10971464-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-236-2386
;             TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 560:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 560:
US-09-784-674-560

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTAACTTTG 2193
              |||| |||||||||  ||
Db          1 TTTTCTTTTTAACCCTG 18


RESULT 3342
US-09-949-427-222
; Sequence 222, Application US/09949427
; Publication No. US20030054418A1
; GENERAL INFORMATION:
;  APPLICANT: Bodnar, Jackie S.
;  APPLICANT:  Castellani, Lawrence W.
;  APPLICANT:  Chatterjee, Aurobindo
;  APPLICANT:  de Jong, Pieter
;  APPLICANT:  Lusis, Aldons J.
;  APPLICANT:  Ohmen, Jeff
;  APPLICANT:  Ross, David
;  APPLICANT:  Tafuri, Sherrie
;  APPLICANT:  Wu, Chenyan
;  TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
;  FILE REFERENCE: 02810.0014.NPUS02
;  CURRENT APPLICATION NUMBER: US/09/949,427
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: 60/231,322
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-949-427-222

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2251 AAGCTTTATTTGCATATT 2268
              |||| | |||||||| ||
Db          1 AAGCCTCATTTGCATGTT 18


RESULT 3343
US-09-972-473-30/c
; Sequence 30, Application US/09972473
; Publication No. US20030068312A1
; GENERAL INFORMATION:
;  APPLICANT: McCarthy, Sean A.
;  TITLE OF INVENTION: NOVEL HUMAN DICKKOPF-RELATED PROTEIN AND NUCLEIC ACID
;  TITLE OF INVENTION:  MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-108CP2
;  CURRENT APPLICATION NUMBER: US/09/972,473
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: 09/263,022
;  PRIOR FILING DATE: 1999-03-05
```

```
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-824-322B-375

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2442 GACTTTTTTGAGACATGG 2459
              ||||| |||||||| ||
Db         18 GACTTCCTTGAGACACGG 1


RESULT 3336
US-09-470-526-4
; Sequence 4, Application US/09470526
; Publication No. US20030041342A1
; GENERAL INFORMATION:
;  APPLICANT: Yuejin Sun
;  APPLICANT: Dilkes, Brian R.
;  APPLICANT: Larkins, Brian A.
;  APPLICANT: Lowe, Keith S.
;  APPLICANT: Gordon-Kamm, William J.
;  APPLICANT: Dante, Ricardo
;  TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides,
;  TITLE OF INVENTION: and Uses Thereof
;  FILE REFERENCE: 1015
;  CURRENT APPLICATION NUMBER: US/09/470,526
;  CURRENT FILING DATE: 1999-12-22
;  EARLIER APPLICATION NUMBER: 60/109,414
;  EARLIER FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(20)
US-09-470-526-4

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        269 GCCGGGCAGCACCTCTAC 286
              ||  |||||||| |||||
Db          2 GCGCGGCAGCACTTCTAC 19


RESULT 3337
US-09-470-526-7
; Sequence 7, Application US/09470526
; Publication No. US20030041342A1
; GENERAL INFORMATION:
;  APPLICANT: Yuejin Sun
;  APPLICANT: Dilkes, Brian R.
;  APPLICANT: Larkins, Brian A.
;  APPLICANT: Lowe, Keith S.
;  APPLICANT: Gordon-Kamm, William J.
;  APPLICANT: Dante, Ricardo
;  TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides,
;  TITLE OF INVENTION: and Uses Thereof
;  FILE REFERENCE: 1015
;  CURRENT APPLICATION NUMBER: US/09/470,526
;  CURRENT FILING DATE: 1999-12-22
;  EARLIER APPLICATION NUMBER: 60/109,414
;  EARLIER FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(20)
US-09-470-526-7

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        269 GCCGGGCAGCACCTCTAC 286
              ||  |||||||| |||||
Db          2 GCGCGGCAGCACTTCTAC 19


RESULT 3338
US-09-880-313A-207
; Sequence 207, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
;  APPLICANT: Flemington, Erik K
;  TITLE OF INVENTION: Adaptors and Methods of Use
;  FILE REFERENCE: 9397/1000
;  CURRENT APPLICATION NUMBER: US/09/880,313A
;  CURRENT FILING DATE:  2001-06-13
;  NUMBER OF SEQ ID NOS: 276
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 207
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-880-313A-207

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        551 TCCGGGCTGGAGGCGGGC 568
              ||||||||| ||| || |
Db          3 TCCGGGCTGCAGGGGGCC 20


RESULT 3339
US-09-828-344-61/c
; Sequence 61, Application US/09828344
; Publication No. US20030044979A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
;  FILE REFERENCE: RTS-0147
;  CURRENT APPLICATION NUMBER: US/09/828,344
;  CURRENT FILING DATE:  2001-04-06
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 61
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-828-344-61

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1200 TGGCAGCTAGGAAGAACA 1217
              ||||||| ||||| || |
Db         20 TGGCAGCCAGGAACAAAA 3
```

```
;  PRIOR FILING DATE: 2000-10-06
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-972-714-11

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        888 AAGTGACAGTGGCTGAAG 905
              ||||||||  |||| | ||
Db          3 AAGTGACACTGGCAGCAG 20


RESULT 3332
US-09-969-373-3646
; Sequence 3646, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
;  APPLICANT: Effertz, Roger J.
;  APPLICANT:  Hauge, Brian M.
;  TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
;  FILE REFERENCE: 38-10(52679)A
;  CURRENT APPLICATION NUMBER: US/09/969,373
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 09/754,853
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 09/760,427
;  PRIOR FILING DATE: 2001-01-13
;  PRIOR APPLICATION NUMBER: US 09/855,768
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3646
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Glycine max
US-09-969-373-3646

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2697 TTGGAATTGAACTCTCTG 2714
              |||||  ||  ||||||  ||
Db          3 TTGGATTTCAACTCTTTG 20


RESULT 3333
US-09-824-322B-54
; Sequence 54, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Butler, Madeline M.
;  APPLICANT:  Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALP
;  TITLE OF INVENTION:  ALPHA) EXPRESSION
;  FILE REFERENCE: ISPH-0501
;  CURRENT APPLICATION NUMBER: US/09/824,322B
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 09/313,932
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: US 09/166,186
;  PRIOR FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 54
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic
US-09-824-322B-54

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTT 2174
              | |||||||  | ||||||
Db          3 TCTTTCTCCATGTTTTT 20


RESULT 3334
US-09-824-322B-358/c
; Sequence 358, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Butler, Madeline M.
;  APPLICANT:  Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPH
;  TITLE OF INVENTION:  ALPHA) EXPRESSION
;  FILE REFERENCE: ISPH-0501
;  CURRENT APPLICATION NUMBER: US/09/824,322B
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 09/313,932
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: US 09/166,186
;  PRIOR FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 358
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic
US-09-824-322B-358

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2099 TCAAACGGGGGCCTTCTG 2116
              ||||||  |||||||  | |
Db         20 TCAAACTGGGGCCTCCAG 3


RESULT 3335
US-09-824-322B-375/c
; Sequence 375, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Butler, Madeline M.
;  APPLICANT:  Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPH
;  TITLE OF INVENTION:  ALPHA) EXPRESSION
;  FILE REFERENCE: ISPH-0501
;  CURRENT APPLICATION NUMBER: US/09/824,322B
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 09/313,932
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: US 09/166,186
;  PRIOR FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 375
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
```

```
;  APPLICANT:  Muller-Schilling, Martina
;  APPLICANT:  Oren, Moshe
;  TITLE OF INVENTION: p53 Binding Areas
;  FILE REFERENCE: 4121-122
;  CURRENT APPLICATION NUMBER: US/09/834,291
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: PCT/DE99/03343
;  PRIOR FILING DATE: 1999-10-18
;  PRIOR APPLICATION NUMBER: DE 198 47 779.1
;  PRIOR FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-834-291-14

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1759 TATTCATTAAGCTTTTTT 1776
              | ||  ||||||||||||
Db          3 TGTTGCTTAAGCTTTTTT 20


RESULT 3328
US-09-733-294A-42/c
; Sequence 42, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  William Gaarde
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Edward V. Wancewicz
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
;  FILE REFERENCE: ISPH-0527
;  CURRENT APPLICATION NUMBER: US/09/733,294A
;  CURRENT FILING DATE:  2000-12-07
;  PRIOR APPLICATION NUMBER: 09/572,423
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-733-294A-42

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        626 CACGCCCTGGATGCCGCG 643
              ||| |||  |||||||||
Db         18 CACCCCCGCGATGCCGCG 1


RESULT 3329
US-09-854-883-102
; Sequence 102, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/09/854,883
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 102
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-102

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1133 GCCGAATTTCCTAGTAAA 1150
              | |||||  |||| |||||
Db          2 GTCGAATATCCTGGTAAA 19


RESULT 3330
US-09-854-883-224/c
; Sequence 224, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/09/854,883
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 224
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-224

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1287 GGACCAGCAGGCTCGCCC 1304
              || | ||||||| |||||
Db         19 GGGCAAGCAGGCCCGCCC 2


RESULT 3331
US-09-972-714-11
; Sequence 11, Application US/09972714
; Patent No. US20020106738A1
; GENERAL INFORMATION:
;  APPLICANT: Foussias, George
;  APPLICANT:  Diamandis, Eleftherios
;  TITLE OF INVENTION: NOVEL SIGLEC GENE
;  FILE REFERENCE: 11757.56USU1
;  CURRENT APPLICATION NUMBER: US/09/972,714
;  CURRENT FILING DATE:  2001-10-05
;  PRIOR APPLICATION NUMBER: US 60/239,007
```

```
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/471,968
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kerner, Ann-Louise
;      REGISTRATION NUMBER:  33,523
;      REFERENCE/DOCKET NUMBER:  HYZ-040CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 526-6000
;      TELEFAX:  (617) 526-5000
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-887-505-21

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 GGCTGGGGGGATCCTGGA 130
              ||  ||||||  |||||||
Db          3 GGGAGGGGGGGTCCTGGA 20


RESULT 3324
US-08-944-410-10/c
; Sequence 10, Application US/08944410
; Publication No. US20030050453A1
; GENERAL INFORMATION:
;  APPLICANT: Sorge, Joseph A.
;  TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
;  FILE REFERENCE: 04121.0018-00000
;  CURRENT APPLICATION NUMBER: US/08/944,410
;  CURRENT FILING DATE:  1997-10-06
;  NUMBER OF SEQ ID NOS: 113
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic primer
US-08-944-410-10

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        574 GAGCGCCCGCAGGGATGC 591
              ||  |||  ||||||  ||||
Db         19 GAACGCACGCAGGAATGC 2


RESULT 3325
US-09-216-393-320
; Sequence 320, Application US/09216393
; Patent No. US20010014447A1
; GENERAL INFORMATION:
;  APPLICANT: Milhausen, Michael James
;  TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: TX-1-C2
;  CURRENT APPLICATION NUMBER: US/09/216,393
;  CURRENT FILING DATE: 1998-12-18
;  EARLIER APPLICATION NUMBER: 08/994,825
;  EARLIER FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 364
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 320
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-216-393-320

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1485 AAACCCTGGAGAAAATGG 1502
              ||||  ||||  |||||  ||
Db          2 AAACTCTGGGGAAAACGG 19


RESULT 3326
US-09-790-264-26
; Sequence 26, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
;  APPLICANT: Holtzman, Douglas A.
;  APPLICANT:  Goodearl, Andrew D.J.
;  APPLICANT:  McCarthy, Sean A.
;  TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
;  TITLE OF INVENTION:  PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
;  TITLE OF INVENTION:  USES
;  FILE REFERENCE: 07334-322001
;  CURRENT APPLICATION NUMBER: US/09/790,264
;  CURRENT FILING DATE:  2001-02-21
;  PRIOR APPLICATION NUMBER: US 09/065,661
;  PRIOR FILING DATE: 1998-04-23
;  PRIOR APPLICATION NUMBER: US 09/298,531
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: US 09/065,363
;  PRIOR FILING DATE: 1998-04-23
;  PRIOR APPLICATION NUMBER: US 09/337,930
;  PRIOR FILING DATE: 1999-06-22
;  PRIOR APPLICATION NUMBER: US 09/102,705
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: US 09/363,630
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: US 09/124,538
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide for PCR
US-09-790-264-26

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1596 AACCCCTCCTGGCCTGGG 1613
              |  ||||||  |||||||  |
Db          1 AGCCCCTCATGGCCTGTG 18


RESULT 3327
US-09-834-291-14
; Sequence 14, Application US/09834291
; Patent No. US20020042064A1
; GENERAL INFORMATION:
;  APPLICANT: Krammer, Peter
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02022
US-09-823-634A-15

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1514 AAATAAAATTGGAACGAA 1531
              ||| ||||||||||  ||
Db          2 AAAAAAAATTGGAAAAAA 19


RESULT 3320
US-09-823-647B-15
; Sequence 15, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/09/823,647B
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02022
US-09-823-647B-15

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1514 AAATAAAATTGGAACGAA 1531
              ||| ||||||||||  ||
Db          2 AAAAAAAATTGGAAAAAA 19


RESULT 3321
US-10-367-470-15
; Sequence 15, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02022
US-10-367-470-15

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1514 AAATAAAATTGGAACGAA 1531
              ||| ||||||||||  ||
Db          2 AAAAAAAATTGGAAAAAA 19


RESULT 3322
US-08-983-605-16/c
; Sequence 16, Application US/08983605A
; Publication No. US20020066118A1
; GENERAL INFORMATION:
;  APPLICANT: Roder, Marion
;  TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
;  TITLE OF INVENTION: Triticum Aestivum and Tribe Triticase and the Use of
;  TITLE OF INVENTION: Said Markers
;  FILE REFERENCE: 2936.10400
;  CURRENT APPLICATION NUMBER: US/08/983,605A
;  CURRENT FILING DATE: 1998-05-01
;  EARLIER APPLICATION NUMBER: DE 195 25 284.5
;  EARLIER FILING DATE: 1995-06-28
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-08-983-605-16

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        389 CCCTACTCGCATCTGGGG 406
              |||| ||| ||||| |||
Db         20 CCCTTCTCCCATCTAGGG 3


RESULT 3323
US-08-887-505-21
; Sequence 21, Application US/08887505
; Publication No. US20020081577A1
;  GENERAL INFORMATION:
;    APPLICANT:  Kilkuskie, Robert E.
;    APPLICANT:  Frank, Bruce L.
;    APPLICANT:  Goodchild, John
;    APPLICANT:  Wolfe, Jia L.
;    APPLICANT:  Roberts, Peter C.
;    APPLICANT:  Hamlin, Jr., Henry A.
;    APPLICANT:  Roberts, No. US20020081577A11 A.
;    APPLICANT:  Walther, Debra M.
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES SPECIFIC FOR
;    TITLE OF INVENTION:  HEPATITIS C VIRUS
;    NUMBER OF SEQUENCES:  172
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hale and Dorr LLP
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/887,505
;      FILING DATE:
```

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              ||:|| | ||| :||:||
Db          2 ACUGGAAGCCCUUCCUGG 19


RESULT 3315
US-10-206-705-147/c
; Sequence 147, Application US/10206705
; Publication No. US20040019001A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine Phosphat
;  TITLE OF INVENTION:  (PTP-1B) Gene Expression using Short Interfering RNA
;  FILE REFERENCE: 900/035 (MBHB02-738)
;  CURRENT APPLICATION NUMBER: US/10/206,705
;  CURRENT FILING DATE:  2002-07-26
;  NUMBER OF SEQ ID NOS: 388
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-206-705-147

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2645 GCTGAACCCTAAGGTGAG 2662
              ||||| ||| ||||||  |
Db         19 GCTGATCCCAAAGGTGGG 2


RESULT 3316
US-10-206-705-263/c
; Sequence 263, Application US/10206705
; Publication No. US20040019001A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine Phosphat
;  TITLE OF INVENTION:  (PTP-1B) Gene Expression using Short Interfering RNA
;  FILE REFERENCE: 900/035 (MBHB02-738)
;  CURRENT APPLICATION NUMBER: US/10/206,705
;  CURRENT FILING DATE:  2002-07-26
;  NUMBER OF SEQ ID NOS: 388
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 263
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-206-705-263

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1590 ACTGGGAACCCCTCCTGG 1607
              ||||| | ||| ||||||
Db         18 ACTGGAAGCCCTTCCTGG 1


RESULT 3317
US-10-206-705-332
; Sequence 332, Application US/10206705
; Publication No. US20040019001A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine Phosphate
;  TITLE OF INVENTION:  (PTP-1B) Gene Expression using Short Interfering RNA
;  FILE REFERENCE: 900/035 (MBHB02-738)
;  CURRENT APPLICATION NUMBER: US/10/206,705
;  CURRENT FILING DATE:  2002-07-26
;  NUMBER OF SEQ ID NOS: 388
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-206-705-332

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   72.2%;  Pred. No. 3.3e+03;
  Matches   13;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2645 GCTGAACCCTAAGGTGAG 2662
              ||:|| ||| ||||:| |
Db          1 GCUGAUCCCAAAGGUGGG 18


RESULT 3318
US-10-257-294-12/c
; Sequence 12, Application US/10257294
; Publication No. US20040023231A1
; GENERAL INFORMATION:
;  APPLICANT: Abu-Khabar, Khalid
;  APPLICANT:  Williams, Bryan
;  APPLICANT:  Frevel, Mathias
;  APPLICANT:  Silverman, Robert
;  TITLE OF INVENTION: System for Identifying and Analyzing Expression of ARE-Containing
;  FILE REFERENCE: 26473/04185
;  CURRENT APPLICATION NUMBER: US/10/257,294
;  CURRENT FILING DATE:  2001-04-12
;  PRIOR APPLICATION NUMBER: PCT/US01/11993
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: US 60/198,870
;  PRIOR FILING DATE: 2000-04-12
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-257-294-12

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2255 TTTATTTGCATATTTATT 2272
              |||||||   ||||||||
Db         18 TTTATTTATTTATTTATT 1


RESULT 3319
US-09-823-634A-15
; Sequence 15, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
;  TITLE OF INVENTION:  MISMATCHES USING RNASE H
;  FILE REFERENCE: 47541-20006.00
;  CURRENT APPLICATION NUMBER: US/09/823,634A
;  CURRENT FILING DATE:  2002-02-28
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
```

```
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: downstream amplification primer 99-950 for SEQ 2237, in complemen
US-10-349-143-10102

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2377 TTGAGTGTACAGATTTTA 2394
              | |||||| |||| ||||
Db          1 TGGAGTGTTCAGAATTTA 18


RESULT 3311
US-10-349-143-10254/c
; Sequence 10254, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10254
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: downstream amplification primer 99-10735 for SEQ 2389, in complem
US-10-349-143-10254

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2735 AATTGTTGTGTGTATGAT 2752
              ||||| ||||||||   ||
Db         18 AATTGGTGTGTGTAGAAT 1


RESULT 3312
US-10-444-925-320
; Sequence 320, Application US/10444925
; Publication No. US20040009946A1
; GENERAL INFORMATION:
;  APPLICANT: Lewis, Stephen Patrick
;  APPLICANT:  Klinghoffer, Richard
;  APPLICANT:  Wilson, Linda K.
;  TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
;  TITLE OF INVENTION:  BY RNA INTERFERENCE
;  FILE REFERENCE: 200125.441
;  CURRENT APPLICATION NUMBER: US/10/444,925
;  CURRENT FILING DATE:  2003-05-23
;  NUMBER OF SEQ ID NOS: 599
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 320
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Small interfering RNA
US-10-444-925-320

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1274 CGGACACCCCATGGGACC 1291
              |||||| ||||: | |||
Db          2 CGGACAACCCAUAGUACC 19


RESULT 3313
US-10-444-925-321
; Sequence 321, Application US/10444925
; Publication No. US20040009946A1
; GENERAL INFORMATION:
;  APPLICANT: Lewis, Stephen Patrick
;  APPLICANT:  Klinghoffer, Richard
;  APPLICANT:  Wilson, Linda K.
;  TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
;  TITLE OF INVENTION:  BY RNA INTERFERENCE
;  FILE REFERENCE: 200125.441
;  CURRENT APPLICATION NUMBER: US/10/444,925
;  CURRENT FILING DATE:  2003-05-23
;  NUMBER OF SEQ ID NOS: 599
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 321
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Small interfering RNA
US-10-444-925-321

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1274 CGGACACCCCATGGGACC 1291
              |||||| ||||: | |||
Db          1 CGGACAACCCAUAGUACC 18


RESULT 3314
US-10-206-705-78
; Sequence 78, Application US/10206705
; Publication No. US20040019001A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine Phosphat
;  TITLE OF INVENTION:  (PTP-1B) Gene Expression using Short Interfering RNA
;  FILE REFERENCE: 900/035 (MBHB02-738)
;  CURRENT APPLICATION NUMBER: US/10/206,705
;  CURRENT FILING DATE:  2002-07-26
;  NUMBER OF SEQ ID NOS: 388
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 78
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-206-705-78

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 3.3e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1590 ACTGGGAACCCCTCCTGG 1607
```

```
;  TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
;  TITLE OF INVENTION:  Using the Same
;  FILE REFERENCE: 21402-211
;  CURRENT APPLICATION NUMBER: US/10/015,115
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: 60/248,153
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: 60/249,598
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/264,240
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: 60/266,127
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/269,562
;  PRIOR FILING DATE: 2001-02-16
;  PRIOR APPLICATION NUMBER: 60/304,348
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: 60/309,261
;  PRIOR FILING DATE: 2001-07-31
;  PRIOR APPLICATION NUMBER: 60/313,283
;  PRIOR FILING DATE: 2001-08-17
;  NUMBER OF SEQ ID NOS: 205
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 170
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
;   OTHER INFORMATION: Sequence
US-10-015-115-170

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        269 GCCGGGCAGCACCTCTAC 286
              | ||||||| |||| |||
Db          1 GTCGGGCAGGACCTTTAC 18


RESULT 3308
US-10-349-143-4542
; Sequence 4542, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4542
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-15728 for SEQ 608,
US-10-349-143-4542

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1967 ATATTTACCTTGAAAAAA 1984
              |||||||||| || | ||
Db          1 ATATTTACCTGGAGAGAA 18


RESULT 3309
US-10-349-143-6906
; Sequence 6906, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6906
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-21312 for SEQ 2972,
US-10-349-143-6906

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2661 AGTGTGCAGTACAGTGTG 2678
              || ||||||||||   |||
Db          1 AGAGTGCAGTACATGGTG 18


RESULT 3310
US-10-349-143-10102
; Sequence 10102, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10102
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
```

```
;   OTHER INFORMATION: potential microsequencing oligo for 5-140-120.mis2
US-10-126-704-130

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTTTGAA 2195
              |||||| ||||| | |||
Db         19 TTTTTTCTTAACCTAGAA 2


RESULT 3304
US-10-251-117-844
; Sequence 844, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering RNA
;  FILE REFERENCE: 900/042 (MBHB02-468-A)
;  CURRENT APPLICATION NUMBER: US/10/251,117
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/163,552
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 09/916,466
;  PRIOR FILING DATE: 2001-07-25
;  PRIOR APPLICATION NUMBER: US 60/296,249
;  PRIOR FILING DATE: 2001-06-06
;  NUMBER OF SEQ ID NOS: 1213
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 844
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-251-117-844

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   38.9%;  Pred. No. 3.3e+03;
  Matches    7;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1786 CCCATTCTTTCCTTCTCT 1803
              ||||:: :::||:  :|:
Db          2 CCCAUUUUUUCCUAAUCU 19


RESULT 3305
US-10-251-117-1151/c
; Sequence 1151, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering RNA
;  FILE REFERENCE: 900/042 (MBHB02-468-A)
;  CURRENT APPLICATION NUMBER: US/10/251,117
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 10/163,552
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 09/916,466
;  PRIOR FILING DATE: 2001-07-25
;  PRIOR APPLICATION NUMBER: US 60/296,249
;  PRIOR FILING DATE: 2001-06-06
;  NUMBER OF SEQ ID NOS: 1213
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1151
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-251-117-1151

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1786 CCCATTCTTTCCTTCTCT 1803
              |||||| ||||||  |||
Db         18 CCCATTTTTTCCTAATCT 1


RESULT 3306
US-10-400-382-296/c
; Sequence 296, Application US/10400382
; Publication No. US20030190659A1
; GENERAL INFORMATION:
;  APPLICANT: LaCasse, Eric
;  APPLICANT:  McManus, Daniel
;  APPLICANT:  Durkin, Jonathan P.
;  TITLE OF INVENTION: Antisense IAP Nucleobase Oligomers and
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 07891/025004
;  CURRENT APPLICATION NUMBER: US/10/400,382
;  CURRENT FILING DATE:  2003-03-27
;  PRIOR APPLICATION NUMBER: US 60/367,853
;  PRIOR FILING DATE: 2002-03-27
;  NUMBER OF SEQ ID NOS: 460
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 296
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: based on Homo sapiens.
;   OTHER INFORMATION: DNA/RNA hybrid.
US-10-400-382-296

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1318 GAACATACAGAACTGCTT 1335
              ||||| | ||||| ||||
Db         19 GAACACATAGAACAGCTT 2


RESULT 3307
US-10-015-115-170
; Sequence 170, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
;  APPLICANT: Malyankar, Uriel M
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Kekuda, Ramesha
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Taupier, Raymond J
;  APPLICANT:  Li, Li
;  APPLICANT:  Padigaru, Muralidhara
```

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;  CURRENT FILING DATE:  2002-08-20
;  PRIOR APPLICATION NUMBER: US 60/315,315
;  PRIOR FILING DATE: 2001-08-28
;  NUMBER OF SEQ ID NOS: 347
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense r
US-10-224-005-95

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 3.3e+03;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        112 GGGCTGGGGGGATCCTGG 129
              ||||:|||  | :||:||
Db          1 GGGCUGGGCAGGUCCUGG 18


RESULT 3300
US-10-224-005-256/c
; Sequence 256, Application US/10224005
; Publication No. US20030143732A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Fosnaugh, Kathy
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (AD
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering RNA
;  FILE REFERENCE: 900/041 (MBHB01-1110-A)
;  CURRENT APPLICATION NUMBER: US/10/224,005
;  CURRENT FILING DATE:  2002-08-20
;  PRIOR APPLICATION NUMBER: US 60/315,315
;  PRIOR FILING DATE: 2001-08-28
;  NUMBER OF SEQ ID NOS: 347
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 256
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-224-005-256

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        112 GGGCTGGGGGGATCCTGG 129
              ||||||||  | ||||||
Db         19 GGGCTGGGCAGGTCCTGG 2


RESULT 3301
US-10-391-413-19
; Sequence 19, Application US/10391413
; Publication No. US20030167482A1
; GENERAL INFORMATION:
;  APPLICANT: KIMURA, Toru et al.
;  TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
;  FILE REFERENCE: 0020-5120P
;  CURRENT APPLICATION NUMBER: US/10/391,413
;  CURRENT FILING DATE:  2003-03-19
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Adapter DNA used to ligate the various parts of the rSZexII
;   OTHER INFORMATION: plasmid
US-10-391-413-19

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1724 GACCTATTATCAGAAGGT 1741
              || ||||||||||  | ||
Db          2 GAACTATTATCAGGACGT 19


RESULT 3302
US-10-126-704-105
; Sequence 105, Application US/10126704
; Publication No. US20030170647A1
; GENERAL INFORMATION:
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
;  TITLE OF INVENTION:  AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
;  FILE REFERENCE: 44.US5.DIV
;  CURRENT APPLICATION NUMBER: US/10/126,704
;  CURRENT FILING DATE:  2002-04-20
;  PRIOR APPLICATION NUMBER: US 60/091,315
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/111,909
;  PRIOR FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: Patent.pm
; SEQ ID NO 105
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: potential microsequencing oligo for 5-129-144.mis1
US-10-126-704-105

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAA 2792
              | ||| |||| |||||||
Db          2 TCTTATAATTAAAAAAAA 19


RESULT 3303
US-10-126-704-130/c
; Sequence 130, Application US/10126704
; Publication No. US20030170647A1
; GENERAL INFORMATION:
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
;  TITLE OF INVENTION:  AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
;  FILE REFERENCE: 44.US5.DIV
;  CURRENT APPLICATION NUMBER: US/10/126,704
;  CURRENT FILING DATE:  2002-04-20
;  PRIOR APPLICATION NUMBER: US 60/091,315
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/111,909
;  PRIOR FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: Patent.pm
; SEQ ID NO 130
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
```

```
;  PRIOR FILING DATE: 1995-02-07
;  PRIOR APPLICATION NUMBER: 07/961,813
;  PRIOR FILING DATE: 1992-10-16
;  PRIOR APPLICATION NUMBER: 08/359,945
;  PRIOR FILING DATE: 1994-12-20
;  PRIOR APPLICATION NUMBER: 08/221,655
;  PRIOR FILING DATE: 1994-04-01
;  PRIOR APPLICATION NUMBER: 07/967,622
;  PRIOR FILING DATE: 1992-10-28
;  PRIOR APPLICATION NUMBER: 08/376,062
;  PRIOR FILING DATE: 1995-01-20
;  PRIOR APPLICATION NUMBER: 08/010,829
;  PRIOR FILING DATE: 1993-01-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: EGF anti-sense
;   OTHER INFORMATION: strand
US-10-199-830-4

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db         19 TAAATAAAAGATGCCCTG 2


RESULT 3296
US-10-005-956-65/c
; Sequence 65, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: D0053NP
;  CURRENT APPLICATION NUMBER: US/10/005,956
;  CURRENT FILING DATE:  2001-12-03
;  PRIOR APPLICATION NUMBER: 60/251,015
;  PRIOR FILING DATE: 2000-12-04
;  PRIOR APPLICATION NUMBER: 60/263,678
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/273,037
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1579
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-005-956-65

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         47 GCGCGCGGCGGGGGCGGC 64
              | ||||||||||||  ||
Db         19 GGGCGCGGCGGGGGGAGC 2


RESULT 3297
US-10-005-956-129/c
; Sequence 129, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;  FILE REFERENCE: D0053NP
;  CURRENT APPLICATION NUMBER: US/10/005,956
;  CURRENT FILING DATE:  2001-12-03
;  PRIOR APPLICATION NUMBER: 60/251,015
;  PRIOR FILING DATE: 2000-12-04
;  PRIOR APPLICATION NUMBER: 60/263,678
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/273,037
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1579
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 129
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-005-956-129

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         47 GCGCGCGGCGGGGGCGGC 64
              | ||||||||||||  ||
Db         18 GGGCGCGGCGGGGGGCGC 1


RESULT 3298
US-10-239-316-26
; Sequence 26, Application US/10239316
; Publication No. US20030125253A1
; GENERAL INFORMATION:
;  APPLICANT: TANIYAMA, Yoshio
;  APPLICANT:  KITA, Shunbun
;  APPLICANT:  SATOMI, Tomoko Komiyama
;  TITLE OF INVENTION: No. US20030125253A1el Protein, Process for Producing The Same And
;  FILE REFERENCE: 2703US0P
;  CURRENT APPLICATION NUMBER: US/10/239,316
;  CURRENT FILING DATE:  2002-09-19
;  PRIOR APPLICATION NUMBER: PCT/JP01/02279
;  PRIOR FILING DATE: 2001-03-22
;  PRIOR APPLICATION NUMBER: JP2000-088595
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 59
; SEQ ID NO 26
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-239-316-26

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAGCA 468
              ||| | |||||||||| ||
Db          2 CACGGCCAGCCAGCAACA 19


RESULT 3299
US-10-224-005-95
; Sequence 95, Application US/10224005
; Publication No. US20030143732A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Fosnaugh, Kathy
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (AD
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering RNA
;  FILE REFERENCE: 900/041 (MBHB01-1110-A)
;  CURRENT APPLICATION NUMBER: US/10/224,005
```

```
; GENERAL INFORMATION:
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
;  TITLE OF INVENTION:  AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
;  FILE REFERENCE: GENSET.031A
;  CURRENT APPLICATION NUMBER: US/10/071,179
;  CURRENT FILING DATE:  2002-02-07
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/345,882
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/091,315
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/111,909
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: Patent.pm
; SEQ ID NO 105
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: potential microsequencing oligo for 5-129-144.mis1
US-10-071-179-105

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAA 2792
              | ||| |||| |||||||
Db          2 TCTTATAATTAAAAAAAA 19


RESULT 3293
US-10-071-179-130/c
; Sequence 130, Application US/10071179
; Publication No. US20030108882A1
; GENERAL INFORMATION:
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
;  TITLE OF INVENTION:  AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
;  FILE REFERENCE: GENSET.031A
;  CURRENT APPLICATION NUMBER: US/10/071,179
;  CURRENT FILING DATE:  2002-02-07
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/345,882
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/091,315
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/111,909
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: Patent.pm
; SEQ ID NO 130
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: potential microsequencing oligo for 5-140-120.mis2
US-10-071-179-130

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTTTGAA 2195
              |||||| ||||| | |||
Db         19 TTTTTTCTTAACCTAGAA 2


RESULT 3294
US-10-199-830-3
; Sequence 3, Application US/10199830
; Publication No. US20030109008A1
; GENERAL INFORMATION:
;  APPLICANT: Weiss, Samuel
;  APPLICANT:  Reynolds, Brent
;  APPLICANT:  Hammang, Joseph P
;  APPLICANT:  Baetge, E. E
;  TITLE OF INVENTION: Methods of Making cDNA Libraries
;  FILE REFERENCE: 17810-705 DIV12CON2
;  CURRENT APPLICATION NUMBER: US/10/199,830
;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: 08/486,313
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/270,412
;  PRIOR FILING DATE: 1994-07-05
;  PRIOR APPLICATION NUMBER: 07/726,812
;  PRIOR FILING DATE: 1991-07-08
;  PRIOR APPLICATION NUMBER: 08/385,404
;  PRIOR FILING DATE: 1995-02-07
;  PRIOR APPLICATION NUMBER: 07/961,813
;  PRIOR FILING DATE: 1992-10-16
;  PRIOR APPLICATION NUMBER: 08/359,945
;  PRIOR FILING DATE: 1994-12-20
;  PRIOR APPLICATION NUMBER: 08/221,655
;  PRIOR FILING DATE: 1994-04-01
;  PRIOR APPLICATION NUMBER: 07/967,622
;  PRIOR FILING DATE: 1992-10-28
;  PRIOR APPLICATION NUMBER: 08/376,062
;  PRIOR FILING DATE: 1995-01-20
;  PRIOR APPLICATION NUMBER: 08/010,829
;  PRIOR FILING DATE: 1993-01-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: EGF sense
;   OTHER INFORMATION: strand
US-10-199-830-3

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db          1 TAAATAAAAGATGCCCTG 18


RESULT 3295
US-10-199-830-4/c
; Sequence 4, Application US/10199830
; Publication No. US20030109008A1
; GENERAL INFORMATION:
;  APPLICANT: Weiss, Samuel
;  APPLICANT:  Reynolds, Brent
;  APPLICANT:  Hammang, Joseph P
;  APPLICANT:  Baetge, E. E
;  TITLE OF INVENTION: Methods of Making cDNA Libraries
;  FILE REFERENCE: 17810-705 DIV12CON2
;  CURRENT APPLICATION NUMBER: US/10/199,830
;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: 08/486,313
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/270,412
;  PRIOR FILING DATE: 1994-07-05
;  PRIOR APPLICATION NUMBER: 07/726,812
;  PRIOR FILING DATE: 1991-07-08
;  PRIOR APPLICATION NUMBER: 08/385,404
```

```
; GENERAL INFORMATION:
;  APPLICANT: LEGRAIN, Pierre
;  APPLICANT:  BENAROUS, Richard
;  APPLICANT:  BLOT, Guillaume
;  APPLICANT:  LASSOT, Irina
;  TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TrCP
;  FILE REFERENCE: B4717A
;  CURRENT APPLICATION NUMBER: US/10/023,530
;  CURRENT FILING DATE:  2002-04-22
;  PRIOR APPLICATION NUMBER: 60/256,276
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: RasSF1dsRNA185
;   LOCATION: (1)..(19)
;   OTHER INFORMATION: Sense strand sequence
;   OTHER INFORMATION: Antisense strand SEQ ID NO.21
;   FEATURE:
;   NAME/KEY: RasSF1dsRNA185
;   LOCATION: (1)..(19)
;   OTHER INFORMATION: Sense strand sequence (dTdT in 3')
US-10-023-530-20

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        834 TCTTCTGCTCAGTCCCTG 851
              ||||||||||| || | |
Db         19 TCTTCTGCTCAATCTCAG 2


RESULT 3289
US-10-079-429-77
; Sequence 77, Application US/10079429
; Publication No. US20030027177A1
; GENERAL INFORMATION:
;  APPLICANT: Haseltine et al.
;  TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
;  FILE REFERENCE: PF106P3D1
;  CURRENT APPLICATION NUMBER: US/10/079,429
;  CURRENT FILING DATE:  2002-02-22
;  PRIOR APPLICATION NUMBER: PCT/US95/01035
;  PRIOR FILING DATE: 1995-01-25
;  PRIOR APPLICATION NUMBER: 08/468,024
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: 08/465,769
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: 08/294,312
;  PRIOR FILING DATE: 1994-08-23
;  PRIOR APPLICATION NUMBER: 08/210,143
;  PRIOR FILING DATE: 1994-03-16
;  PRIOR APPLICATION NUMBER: 08/187,757
;  PRIOR FILING DATE: 1994-01-27
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 77
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer useful for amplifying codons 439 to 472 of hMLH3
US-10-079-429-77

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        484 CCAGAGCCAGGAGGGAGC 501
              ||||| ||| || |||||
Db          2 CCAGAACCAAGAAGGAGC 19


RESULT 3290
US-10-220-310-5
; Sequence 5, Application US/10220310
; Publication No. US20030073660A1
; GENERAL INFORMATION:
;  APPLICANT: Universit degli Studi di Ferrara
;  APPLICANT:  Associazione veneta per la lotta alla Talassemia
;  APPLICANT:  Associazione per la lotta alla Talassemia di Ferrara
;  APPLICANT:  Chiesi Farmaceutici S.p.A.
;  TITLE OF INVENTION: Synthetic oligonucleotides as inducers of erythroid differentiat
;  FILE REFERENCE: Erythroid differentiation
;  CURRENT APPLICATION NUMBER: US/10/220,310
;  CURRENT FILING DATE:  2000-03-13
;  PRIOR APPLICATION NUMBER: TO2000A000234
;  PRIOR FILING DATE: 2000-03-13
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-220-310-5

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||| ||| ||| ||||||
Db          2 TTTCTTTCTTTCTTTTTT 19


RESULT 3291
US-10-220-310-5/c
; Sequence 5, Application US/10220310
; Publication No. US20030073660A1
; GENERAL INFORMATION:
;  APPLICANT: Universit degli Studi di Ferrara
;  APPLICANT:  Associazione veneta per la lotta alla Talassemia
;  APPLICANT:  Associazione per la lotta alla Talassemia di Ferrara
;  APPLICANT:  Chiesi Farmaceutici S.p.A.
;  TITLE OF INVENTION: Synthetic oligonucleotides as inducers of erythroid differentiati
;  FILE REFERENCE: Erythroid differentiation
;  CURRENT APPLICATION NUMBER: US/10/220,310
;  CURRENT FILING DATE:  2000-03-13
;  PRIOR APPLICATION NUMBER: TO2000A000234
;  PRIOR FILING DATE: 2000-03-13
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-220-310-5

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||| ||| ||| |||
Db         19 AAAAAAGAAAGAAAGAAA 2


RESULT 3292
US-10-071-179-105
; Sequence 105, Application US/10071179
; Publication No. US20030108882A1
```

```
US-10-398-519-32
; Sequence 32, Application US/10398519
; Publication No. US20040072258A1
; GENERAL INFORMATION:
;  APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &
;  APPLICANT:  INDUSTRIAL DEVELOPMENT LTD.
;  TITLE OF INVENTION: ISOPRENOID-DEPENDENT RAS ANCHORAGE (IDRA) PROTEINS
;  FILE REFERENCE: THYREOS 3.4-007
;  CURRENT APPLICATION NUMBER: US/10/398,519
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: 60/237,858
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: antisense oligonucleotide
US-10-398-519-32

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        999 TGCGGGAGAAGTTGGACA 1016
              || ||| || ||||||||
Db          1 TGTGGGGGACGTTGGACA 18


RESULT 3286
US-10-092-900A-381
; Sequence 381, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Taupier Jr., Raymond J.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Li, Li
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Guo, Xiaojia Sasha
;  APPLICANT:  Tchernev,, Velizar T.
;  APPLICANT:  Fernandes, Elma R.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Liu, Yi
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Leite, Mario W.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Alsobrook, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-290C
;  CURRENT APPLICATION NUMBER: US/10/092,900A
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: USSN 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/283,675
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: USSN 60/338,092
;  PRIOR FILING DATE: 2001-12-03
;  PRIOR APPLICATION NUMBER: USSN 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/274,191
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/325,681
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: USSN 60/304,354
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: USSN 60/279,995
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: USSN 60/294,899
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: USSN 60/287,424
;  PRIOR FILING DATE: 2001-04-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 381
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-092-900A-381

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        269 GCCGGGCAGCACCTCTAC 286
              | ||||||| |||| |||
Db          1 GTCGGGCAGGACCTTTAC 18


RESULT 3287
US-10-415-657-18
; Sequence 18, Application US/10415657
; Publication No. US20040048277A1
; GENERAL INFORMATION:
;  APPLICANT: Cenix BioScience GmbH
;  TITLE OF INVENTION: Eukaryotic cell division genes and their use in diagnosis and trea
;  TITLE OF INVENTION:  of proliferative diseases
;  FILE REFERENCE: CE61773US
;  CURRENT APPLICATION NUMBER: US/10/415,657
;  CURRENT FILING DATE:  2003-09-08
;  PRIOR APPLICATION NUMBER: US 60/246,750
;  PRIOR FILING DATE: 2000-11-09
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide for PCR amplification (example 3)
US-10-415-657-18

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1492 GGAGAAAATGGAGAAACA 1509
              | ||||| ||| ||||||
Db          2 GAAGAAATTGGGGAAACA 19


RESULT 3288
US-10-023-530-20/c
; Sequence 20, Application US/10023530
; Publication No. US20030007956A1
```

```
;  PRIOR APPLICATION NUMBER: 08/338,730
;  PRIOR FILING DATE: 1994-11-14
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:chemically
;   OTHER INFORMATION: synthesized
US-09-925-911-3

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db          1 TAAATAAAAGATGCCCTG 18


RESULT 3282
US-09-925-911-4/c
; Sequence 4, Application US/09925911
; Publication No. US20030049837A1
; GENERAL INFORMATION:
;  APPLICANT: Weiss et al.
;  TITLE OF INVENTION: In Vitro and In Vivo Proliferation and Use of
;  TITLE OF INVENTION:  Multipotent Neural Stem Cells and Their Progeny
;  FILE REFERENCE: 17810-705 (CTI-N5 DIV11CON)
;  CURRENT APPLICATION NUMBER: US/09/925,911
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 08/484,203
;  PRIOR FILING DATE: 2001-06-07
;  PRIOR APPLICATION NUMBER: 08/270,412
;  PRIOR FILING DATE: 1994-07-05
;  PRIOR APPLICATION NUMBER: 07/726,812
;  PRIOR FILING DATE: 1991-07-08
;  PRIOR APPLICATION NUMBER: 08/385,404
;  PRIOR FILING DATE: 1995-02-07
;  PRIOR APPLICATION NUMBER: 07/961,813
;  PRIOR FILING DATE: 1992-10-16
;  PRIOR APPLICATION NUMBER: 08/359,945
;  PRIOR FILING DATE: 1994-12-20
;  PRIOR APPLICATION NUMBER: 08/221,655
;  PRIOR FILING DATE: 1994-04-01
;  PRIOR APPLICATION NUMBER: 07/967,622
;  PRIOR FILING DATE: 1992-10-28
;  PRIOR APPLICATION NUMBER: 08/376,062
;  PRIOR FILING DATE: 1995-01-20
;  PRIOR APPLICATION NUMBER: 08/010,829
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: 08/149,508
;  PRIOR FILING DATE: 1993-11-09
;  PRIOR APPLICATION NUMBER: 08/311,099
;  PRIOR FILING DATE: 1994-09-23
;  PRIOR APPLICATION NUMBER: 08/338,730
;  PRIOR FILING DATE: 1994-11-14
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:chemically
;   OTHER INFORMATION: synthesized
US-09-925-911-4

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db         19 TAAATAAAAGATGCCCTG 2


RESULT 3283
US-09-902-176A-47/c
; Sequence 47, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
;  APPLICANT: Schreiber, Stefan
;  APPLICANT:  Hampe, Jochen
;  APPLICANT:  Mascheretti, Silvia
;  TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
;  TITLE OF INVENTION:  the TNF Receptor II and Method for Detecting
;  TITLE OF INVENTION:  No. US20030099943A1-Responders to Anti-TNF-Therapy
;  FILE REFERENCE: 25481-P001US
;  CURRENT APPLICATION NUMBER: US/09/902,176A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: EP 00114786.7
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-09-902-176A-47

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2566 CTCTGTTCTTGGCTTGGA 2583
              ||||| ||||||| || |
Db         19 CTCTGCTCTTGGCCTGCA 2


RESULT 3284
US-10-343-114-43
; Sequence 43, Application US/10343114
; Publication No. US20040072998A1
; GENERAL INFORMATION:
;  APPLICANT: Wissenbach, Ulrich
;  TITLE OF INVENTION: Trp8, Trp9 and Trp10, Novel Markers for Cancer
;  FILE REFERENCE: 012627-034
;  CURRENT APPLICATION NUMBER: US/10/343,114
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: PCT/EP01/08309
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-343-114-43

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        359 CAGCAGCTGGCCTACTCC 376
              |||| ||||| ||| |||
Db          2 CAGCTGCTGGTCTATTCC 19


RESULT 3285
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  754:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-754

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2256 TTATTTGCATATTTATTT 2273
              ||||||   |||||||||
Db         19 TTATTTATTTATTTATTT 2


RESULT 3279
US-09-785-548-16/c
; Sequence 16, Application US/09785548
; Patent No. US20020155577A1
; GENERAL INFORMATION:
;  APPLICANT: AVENTIS PHARMACEUTICALS, INC.
;  TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARK
;  FILE REFERENCE: ST00005
;  CURRENT APPLICATION NUMBER: US/09/785,548
;  CURRENT FILING DATE:  2001-02-20
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of the artificial sequence:oligonucleotide
US-09-785-548-16

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1315 GACGAACATACAGAACTG 1332
              || |||||  ||||||||
Db         19 GATGAACAGGCAGAACTG 2


RESULT 3280
US-09-853-526-565
; Sequence 565, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Ilya, Chumakov
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: PROSTATE CANCER GENE
;  FILE REFERENCE: GENSET.18CP1CP
;  CURRENT APPLICATION NUMBER: US/09/853,526
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: 09/338,907
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: 08/996,306
;  PRIOR FILING DATE: 1997-12-22
;  PRIOR APPLICATION NUMBER: 60/099,658
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 09/218,207
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: Patent.pm
; SEQ ID NO 565
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1..19
;   OTHER INFORMATION: potential microsequencing oligo for 99-148-366.mis2
US-09-853-526-565

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        560 GAGGCGGGCGCGGTGAGC 577
              |||||||  || ||||||
Db          1 GAGGCGGCAGCCGTGAGC 18


RESULT 3281
US-09-925-911-3
; Sequence 3, Application US/09925911
; Publication No. US20030049837A1
; GENERAL INFORMATION:
;  APPLICANT: Weiss et al.
;  TITLE OF INVENTION: In Vitro and In Vivo Proliferation and Use of
;  TITLE OF INVENTION:  Multipotent Neural Stem Cells and Their Progeny
;  FILE REFERENCE: 17810-705 (CTI-N5 DIV11CON)
;  CURRENT APPLICATION NUMBER: US/09/925,911
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 08/484,203
;  PRIOR FILING DATE: 2001-06-07
;  PRIOR APPLICATION NUMBER: 08/270,412
;  PRIOR FILING DATE: 1994-07-05
;  PRIOR APPLICATION NUMBER: 07/726,812
;  PRIOR FILING DATE: 1991-07-08
;  PRIOR APPLICATION NUMBER: 08/385,404
;  PRIOR FILING DATE: 1995-02-07
;  PRIOR APPLICATION NUMBER: 07/961,813
;  PRIOR FILING DATE: 1992-10-16
;  PRIOR APPLICATION NUMBER: 08/359,945
;  PRIOR FILING DATE: 1994-12-20
;  PRIOR APPLICATION NUMBER: 08/221,655
;  PRIOR FILING DATE: 1994-04-01
;  PRIOR APPLICATION NUMBER: 07/967,622
;  PRIOR FILING DATE: 1992-10-28
;  PRIOR APPLICATION NUMBER: 08/376,062
;  PRIOR FILING DATE: 1995-01-20
;  PRIOR APPLICATION NUMBER: 08/010,829
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: 08/149,508
;  PRIOR FILING DATE: 1993-11-09
;  PRIOR APPLICATION NUMBER: 08/311,099
;  PRIOR FILING DATE: 1994-09-23
```

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;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..18
;   OTHER INFORMATION: upstream amplification primer 99-7792 for SEQ 1988,
US-10-349-143-5922

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        343 CTTTCCCCCTCCCTACCA 360
              ||||  |||||||| |||
Db         18 CTTTATCCCTCCCTTCCA 1


RESULT 3275
US-10-349-143-7191
; Sequence 7191, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7191
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..18
;   OTHER INFORMATION: upstream amplification primer 99-2765 for SEQ 3257,
US-10-349-143-7191

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        773 AACCCTCTGAACCTCCCC 790
              ||| |||| ||||||| |
Db          1 AACACTCTCAACCTCCTC 18


RESULT 3276
US-10-416-041-19
; Sequence 19, Application US/10416041
; Publication No. US20040093635A1
; GENERAL INFORMATION:
;  APPLICANT: Van Enckevort, Lenora Johanna Gertruda
;  APPLICANT:  Jacobsen, Evert
;  APPLICANT:  Stiekema, Willem Johannes
;  APPLICANT:  Pereira, Andy
;  TITLE OF INVENTION: DNA SEQUENCES ENCODING PROTEINS CONFERRING PHYTOPHTHORA
;  TITLE OF INVENTION:  INFESTANS RESISTANCE ON PLANTS
;  FILE REFERENCE: U 014591-5
;  CURRENT APPLICATION NUMBER: US/10/416,041
;  CURRENT FILING DATE:  2003-10-24
;  PRIOR APPLICATION NUMBER: EP 00203911.3
;  PRIOR FILING DATE: 2000-11-09
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-416-041-19

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1913 AACAATACCTTTTTTTTC 1930
              |||||| ||||| || ||
Db          1 AACAATGCCTTTCTTCTC 18


RESULT 3277
US-09-901-484A-565
; Sequence 565, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  TITLE OF INVENTION: Prostate Cancer Gene
;  FILE REFERENCE: GEN-T111XC3D2
;  CURRENT APPLICATION NUMBER: US/09/901,484A
;  CURRENT FILING DATE:  2001-07-09
;  PRIOR APPLICATION NUMBER: US 08/996,306
;  PRIOR FILING DATE: 1997-12-22
;  PRIOR APPLICATION NUMBER: US 60/099,658
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: US 09/218,207
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: US 09/338,907
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: US 09/853,526
;  PRIOR FILING DATE: 2001-05-11
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 565
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(19)
;   OTHER INFORMATION: potential microsequencing oligo for 99-148-366.mis2
US-09-901-484A-565

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        560 GAGGCGGGCGCGGTGAGC 577
              |||||||  || ||||||
Db          1 GAGGCGGCAGCCGTGAGC 18


RESULT 3278
US-09-263-959-754/c
; Sequence 754, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
```

```
RESULT 3271
US-10-388-263-192/c
; Sequence 192, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  McNeil, John
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Sasmor, Henri M.
;  APPLICANT:  Brooks, Douglas G.
;  APPLICANT:  Ohashi, Cara
;  APPLICANT:  Wyatt, Jacqueline R.
;  APPLICANT:  Borchers, Alexander
;  APPLICANT:  Vickers, Timothy A.
;  TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
;  TITLE OF INVENTION:  MODULATION BY OLIGONUCLEOTIDES AND
;  TITLE OF INVENTION:  GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
;  FILE REFERENCE: ISIS-4503
;  CURRENT APPLICATION NUMBER: US/10/388,263
;  CURRENT FILING DATE:  2003-03-12
;  NUMBER OF SEQ ID NOS: 947
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 192
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-192

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1150 ACCAGTGGCAGAATATTT 1167
              ||||||| |||| | ||
Db         18 ACCAGTGGAAGAACAATT 1

RESULT 3272
US-10-388-263-867
; Sequence 867, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  McNeil, John
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Sasmor, Henri M.
;  APPLICANT:  Brooks, Douglas G.
;  APPLICANT:  Ohashi, Cara
;  APPLICANT:  Wyatt, Jacqueline R.
;  APPLICANT:  Borchers, Alexander
;  APPLICANT:  Vickers, Timothy A.
;  TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
;  TITLE OF INVENTION:  MODULATION BY OLIGONUCLEOTIDES AND
;  TITLE OF INVENTION:  GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
;  FILE REFERENCE: ISIS-4503
;  CURRENT APPLICATION NUMBER: US/10/388,263
;  CURRENT FILING DATE:  2003-03-12
;  NUMBER OF SEQ ID NOS: 947
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 867
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-867

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1777 TTTTTGAACCCCATTCTT 1794
              | ||| || |||||||||
Db          1 TGTTTCAAGCCCATTCTT 18

RESULT 3273
US-10-336-213B-47
; Sequence 47, Application US/10336213B
; Publication No. US20040002153A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  Robert McKay
;  APPLICANT:  Tim Vickers
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
;  FILE REFERENCE: ISIS0004-100
;  CURRENT APPLICATION NUMBER: US/10/336,213B
;  CURRENT FILING DATE:  2003-01-03
;  PRIOR APPLICATION NUMBER: US 60/411,780
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: US 09/878,582
;  PRIOR FILING DATE: 2001-06-11
;  PRIOR APPLICATION NUMBER: US 09/577,902
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: PCT/US99/29594
;  PRIOR FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: US 09/358,381
;  PRIOR FILING DATE: 1999-07-21
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 47
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-336-213B-47

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1777 TTTTTGAACCCCATTCTT 1794
              | ||| || |||||||||
Db          1 TGTTTCAAGCCCATTCTT 18

RESULT 3274
US-10-349-143-5922/c
; Sequence 5922, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5922
;   LENGTH: 18
```

; OTHER INFORMATION: A novel FISSR-PCR primer for genotyping eukaryotes
US-10-357-488-36

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         47 GCGCGCGGCGGGGGCGGC 64
              | | ||||||| ||||||
Db         18 GAGTGCGGCGGCGGCGGC 1
```

RESULT 3267
US-10-239-956-26/c
; Sequence 26, Application US/10239956
; Publication No. US20030208041A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Yingcong
; APPLICANT: Cully, Doris F.
; APPLICANT: Ludmerer, Steven W.
; TITLE OF INVENTION: DERMACENTOR VARIABILIS GABA-GATED
; TITLE OF INVENTION: CHLORIDE CHANNELS
; FILE REFERENCE: 20437P
; CURRENT APPLICATION NUMBER: US/10/239,956
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: PCT/US01/09955
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/193,791
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Segment from dermacentor variabilis
US-10-239-956-26

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1437 ACAAATCCTACATGAACC 1454
              ||||| || ||| |||||
Db         18 ACAAACCCGACAGGAACC 1
```

RESULT 3268
US-10-404-300A-40
; Sequence 40, Application US/10404300A
; Publication No. US20030215856A1
; GENERAL INFORMATION:
; APPLICANT: Church, George
; APPLICANT: Bulyk, Martha
; TITLE OF INVENTION: SURFACE-BOUND, DOUBLE-STRANDED DNA PROTEIN ARRAYS
; FILE REFERENCE: 10498-00050
; CURRENT APPLICATION NUMBER: US/10/404,300A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 09/132,368
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/061,604
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-404-300A-40

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2774 TTGTTAGAATTGAAAAAA 2791
              ||||||||||  || ||
Db          1 TTGTTAGAATTCTAACAA 18
```

RESULT 3269
US-10-404-300A-40/c
; Sequence 40, Application US/10404300A
; Publication No. US20030215856A1
; GENERAL INFORMATION:
; APPLICANT: Church, George
; APPLICANT: Bulyk, Martha
; TITLE OF INVENTION: SURFACE-BOUND, DOUBLE-STRANDED DNA PROTEIN ARRAYS
; FILE REFERENCE: 10498-00050
; CURRENT APPLICATION NUMBER: US/10/404,300A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 09/132,368
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/061,604
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-404-300A-40

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2774 TTGTTAGAATTGAAAAAA 2791
              ||||||||||  || ||
Db         18 TTGTTAGAATTCTAACAA 1
```

RESULT 3270
US-10-297-068-1065
; Sequence 1065, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 1314OP1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1065
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1065

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        633 TGGATGCCGCGGGCCTGG 650
              |||||||| || || |||
Db          1 TGGATGCCACGTGCGTGG 18
```

```
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Human immunodeficiency virus
US-10-043-875-875

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        679 TCACCAGATGGACGAGGT 696
              ||| | ||||||||||
Db          1 TCAATACATGGACGAGGT 18


RESULT 3263
US-10-067-125-180
; Sequence 180, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 180
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-180

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1565 GCAAAAATCCTTCTCCAC 1582
              |||||| ||| |||| ||
Db          1 GCAAAACTCCGTCTCTAC 18


RESULT 3264
US-10-209-608-48
; Sequence 48, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: Patentln version 3.1
; SEQ ID NO 48
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-48

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              ||||||||||   ||||
Db          1 TTTTTTTTTTTCCCCCC 18


RESULT 3265
US-10-197-290-39/c
; Sequence 39, Application US/10197290
; Publication No. US20030083300A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Elizabeth J. Ackermann
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTSP-0421
;  CURRENT APPLICATION NUMBER: US/10/197,290
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 09/857,299
;  PRIOR FILING DATE: 2001-20-04
;  PRIOR APPLICATION NUMBER: PCT/US99/22083
;  PRIOR FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 39
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-197-290-39

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1150 ACCAGTGGCAGAATATTT 1167
              |||||||| |||| | ||
Db         18 ACCAGTGGAAGAACAATT 1


RESULT 3266
US-10-357-488-36/c
; Sequence 36, Application US/10357488
; Publication No. US20030194730A1
; GENERAL INFORMATION:
;  APPLICANT: Centre For DNA Fingerprinting and Diagnostics
;  TITLE OF INVENTION: No. US20030194730A1el FISSR-PCR primers and markers and a method c
;  TITLE OF INVENTION:  primers and markers for identifying genetic constitution and bree
;  TITLE OF INVENTION:  varities.
;  FILE REFERENCE: 782-indian
;  CURRENT APPLICATION NUMBER: US/10/357,488
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 260/MAS/2002
;  PRIOR FILING DATE: 2002-04-08
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 28
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-462-261-28

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        253 CCCCCACCTCTCCTCCGC 270
              | |||||||| ||||| |
Db          1 CGCCCACCTCCCCTCCTC 18


RESULT 3259
US-10-683-386-48
; Sequence 48, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-48

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              |||||||||||   ||||
Db          1 TTTTTTTTTTTTCCCCCC 18


RESULT 3260
US-10-252-155-90/c
; Sequence 90, Application US/10252155
; Publication No. US20040068096A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS IN ORGANIC ANION TRANSPORT
;  TITLE OF INVENTION:  MULTI-DRUG RESISTANT PROTEINS
;  FILE REFERENCE: D0152 NP
;  CURRENT APPLICATION NUMBER: US/10/252,155
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US 60/324,172
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: US 60/333,700
;  PRIOR FILING DATE: 2001-11-27
;  NUMBER OF SEQ ID NOS: 783
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-252-155-90

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        658 CCTGGGGCTCCACGACAT 675
              | | ||||||||||||| |
Db         18 CATTGGGCTCCACGACCT 1


RESULT 3261
US-10-028-056-17
; Sequence 17, Application US/10028056
; Publication No. US20020152483A1
; GENERAL INFORMATION:
;  APPLICANT: REUE, KAREN
;  APPLICANT:  PTERFY, MIKLOS
;  TITLE OF INVENTION: A NOVEL GENE ASSOCIATED WITH REGULATION OF ADIPOSITY AND INSULIN
;  FILE REFERENCE: 407T-898010US
;  CURRENT APPLICATION NUMBER: US/10/028,056
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: US 60/257,772
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR primer
US-10-028-056-17

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 GGCTGGGGGGATCCTGGA 130
              || || ||||| ||||||
Db          1 GGTTGTGGGGACCCTGGA 18


RESULT 3262
US-10-043-875-875
; Sequence 875, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
;  APPLICANT: De Smet, Koenraad
;  APPLICANT:  Stuyver, Lieven
;  TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
;  TITLE OF INVENTION:  Transcriptase Gene
;  FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
;  CURRENT APPLICATION NUMBER: US/10/043,875
;  CURRENT FILING DATE:  2002-04-03
;  PRIOR APPLICATION NUMBER: 60/286,102
;  PRIOR FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: EP 01870085.6
;  PRIOR FILING DATE: 2001-04-20
;  PRIOR APPLICATION NUMBER: EP 01870005.4
;  PRIOR FILING DATE: 2001-01-11
;  NUMBER OF SEQ ID NOS: 884
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 875
```

```
RESULT 3255
US-09-961-077-1159/c
; Sequence 1159, Application US/09961077
; Publication No. US20030014775A1
;   GENERAL INFORMATION:
;        APPLICANT: Zwick, Michael G.
;                   Edington, Brent E.
;                   McSwiggen, James A.
;                   Merlo, Patricia Ann Owens
;                   Guo, Lining
;                   Skokut, Thomas A.
;                   Young, Scott A.
;                   Folkerts, Otto
;                   Merlo, Donald J.
;        TITLE OF INVENTION: COMPOSITION AND METHODS FOR
;                            MODULATION OF GENE EXPRESSION
;                            IN PLANTS
;        NUMBER OF SEQUENCES: 1263
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: Word Perfect 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/961,077
;             FILING DATE: 21-Sep-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/679,645
;             FILING DATE: July 12, 1996
;             APPLICATION NUMBER: 60/001,135
;             FILING DATE: July 13, 1995
;             APPLICATION NUMBER: 08/300,726
;             FILING DATE: September 2, 1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 219/247
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 1159:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1159:
US-09-961-077-1159

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         42 GGCCCGCGCGCGGCGGGG 59
              || | ||| |||||||||
Db         18 GGGCGGCGAGCGGCGGGG 1


RESULT 3256
US-09-950-935-9/c
; Sequence 9, Application US/09950935
; Publication No. US20030032022A1
; GENERAL INFORMATION:
;  APPLICANT: Hill, Joseph A.
;  APPLICANT:  Wang, Zhigang C.
;  TITLE OF INVENTION: Variants of IL-1 Beta Gene CD46 Gene for Diagnosing Unexplained Re
;  TITLE OF INVENTION:  Pregnancy Loss
;  FILE REFERENCE: B0801/7227 (ERP)
;  CURRENT APPLICATION NUMBER: US/09/950,935
;  CURRENT FILING DATE:  2001-09-12
;  PRIOR APPLICATION NUMBER: US60/231,785
;  PRIOR FILING DATE: 2000-09-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-950-935-9

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1751 TGGCTCTTTATTCATTAA 1768
              |||| || | ||||||||
Db         18 TGGCCCTGTCTTCATTAA 1


RESULT 3257
US-10-462-261-19
; Sequence 19, Application US/10462261
; Publication No. US20040029248A1
; GENERAL INFORMATION:
;  APPLICANT: Garrett M. Brodeur
;  APPLICANT:  Peter S. White
;  TITLE OF INVENTION: CHD5 ENCODING NUCLEIC ACIDS,
;  TITLE OF INVENTION:  POLYPEPTIDES, ANTIBODIES AND METHODS OF USE THEREOF
;  FILE REFERENCE: CHOP0162
;  CURRENT APPLICATION NUMBER: US/10/462,261
;  CURRENT FILING DATE:  2003-06-16
;  PRIOR APPLICATION NUMBER: 60/388,848
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-462-261-19

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        253 CCCCCACCTCTCCTCCGC 270
              | |||||||| ||||| |
Db          1 CGCCCACCTCCCCTCCTC 18


RESULT 3258
US-10-462-261-28
; Sequence 28, Application US/10462261
; Publication No. US20040029248A1
; GENERAL INFORMATION:
;  APPLICANT: Garrett M. Brodeur
;  APPLICANT:  Peter S. White
;  TITLE OF INVENTION: CHD5 ENCODING NUCLEIC ACIDS,
;  TITLE OF INVENTION:  POLYPEPTIDES, ANTIBODIES AND METHODS OF USE THEREOF
;  FILE REFERENCE: CHOP0162
;  CURRENT APPLICATION NUMBER: US/10/462,261
;  CURRENT FILING DATE:  2003-06-16
;  PRIOR APPLICATION NUMBER: 60/388,848
```

```
;  APPLICANT:  Hauge, Brian M.
;  TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
;  FILE REFERENCE: 38-10(52679)A
;  CURRENT APPLICATION NUMBER: US/09/969,373
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 09/754,853
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 09/760,427
;  PRIOR FILING DATE: 2001-01-13
;  PRIOR APPLICATION NUMBER: US 09/855,768
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2933
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-969-373-2933

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGTCACC 2334
              |||||| |||||||  ||
Db         18 TTGTTGTTGCTTGTTCCC 1


RESULT 3253
US-09-263-959-759/c
; Sequence 759, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  759:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-759

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2255 TTTATTTGCATATTTATT 2272
              |||||||  ||||||||
Db         18 TTTATTTATTTATTTATT 1


RESULT 3254
US-09-961-077-607/c
; Sequence 607, Application US/09961077
; Publication No. US20030014775A1
;   GENERAL INFORMATION:
;        APPLICANT: Zwick, Michael G.
;                   Edington, Brent E.
;                   McSwiggen, James A.
;                   Merlo, Patricia Ann Owens
;                   Guo, Lining
;                   Skokut, Thomas A.
;                   Young, Scott A.
;                   Folkerts, Otto
;                   Merlo, Donald J.
;        TITLE OF INVENTION: COMPOSITION AND METHODS FOR
;                            MODULATION OF GENE EXPRESSION
;                            IN PLANTS
;        NUMBER OF SEQUENCES: 1263
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: Word Perfect 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/961,077
;             FILING DATE: 21-Sep-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/679,645
;             FILING DATE: July 12, 1996
;             APPLICATION NUMBER: 60/001,135
;             FILING DATE: July 13, 1995
;             APPLICATION NUMBER: 08/300,726
;             FILING DATE: September 2, 1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 219/247
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 607:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 607:
US-09-961-077-607

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        152 GGGACGCCGGACGCCATG 169
              |||| | ||| |||||||
Db         18 GGGATGGCGGCCGCCATG 1
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;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 199953US0XDIV
;  CURRENT APPLICATION NUMBER: US/10/209,608
;  CURRENT FILING DATE:  2002-08-01
;  PRIOR APPLICATION NUMBER: US/09/725,265
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-44

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              ||||||||||||   ||||
Db         18 TTTTTTTTTTTTTCCCCC 1


RESULT 3249
US-10-057-783A-46
; Sequence 46, Application US/10057783A
; Publication No. US20040091955A1
; GENERAL INFORMATION:
;  APPLICANT: Forster, Anthony C.
;  TITLE OF INVENTION: Process and compositions for peptide, protein and
;  TITLE OF INVENTION:  peptidomimetic synthesis
;  FILE REFERENCE: 1
;  CURRENT APPLICATION NUMBER: US/10/057,783A
;  CURRENT FILING DATE:  2002-01-25
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:FROM SYNTHETIC
;   OTHER INFORMATION: DNA
US-10-057-783A-46

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAAC 2189
              ||||||||||  || |||
Db          1 TTTTTTTTTAATTCAAC 18


RESULT 3250
US-09-878-582-47
; Sequence 47, Application US/09878582
; Patent No. US20020058638A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
;  FILE REFERENCE: ISPH-0463
;  CURRENT APPLICATION NUMBER: US/09/878,582
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: 09/577,902
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: US 09/358,381
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: PCT/US99/29594,
;  PRIOR FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 47
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-878-582-47

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1777 TTTTTGAACCCCATTCTT 1794
              | ||| || ||||||||||
Db          1 TGTTTCAAGCCCATTCTT 18


RESULT 3251
US-09-891-517-44/c
; Sequence 44, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  TORIMURA, MASAKI
;  APPLICANT:  KURATA, SHINYA
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS O
;  TITLE OF INVENTION:  NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA O
;  TITLE OF INVENTION:  METHOD
;  FILE REFERENCE: 210352US-1994-163-0-X
;  CURRENT APPLICATION NUMBER: US/09/891,517
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: JP2000-193133
;  PRIOR FILING DATE: 2000-06-27
;  PRIOR APPLICATION NUMBER: JP2000-236115
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP2000-292483
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-09-891-517-44

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              ||||||||||||   ||||
Db         18 TTTTTTTTTTTTTCCCCC 1


RESULT 3252
US-09-969-373-2933/c
; Sequence 2933, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
;  APPLICANT: Effertz, Roger J.
```

```
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 576-0200
;              TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 7:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 15 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: DNA (genomic)
;         HYPOTHETICAL: YES
;                       (ix)  Features:
;         SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-880-727-7

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              :||||||||||||||
Db          2 VAAAAAAAAAAAAA 15


RESULT 3246
US-09-880-727-7/c
; Sequence 7, Application US/09880727
; Publication No. US20030064364A1
;   GENERAL INFORMATION:
;         APPLICANT: Lockhart, David J.
;                    Chee, Mark
;                    Gunderson, Kevin
;                    Chaoqiang, Lai
;                    Wodicka, Lisa
;                    Cronin, Maureen T.
;                    Lee, Danny
;                    Tran, Huu M.
;                    Matsuzaki, Hajime
;                    McGall, Glenn H.
;         TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
;         NUMBER OF SEQUENCES: 32
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Joe Liebeschuetz
;              STREET: Two Embarcadero Center, Eighth Floor
;              CITY: San Francisco
;              STATE: CA
;              COUNTRY: USA
;              ZIP: 94111-3834
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/880,727
;              FILING DATE: 13-Jun-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/882,649
;              FILING DATE: <Unknown>
;              APPLICATION NUMBER: US 60/035,170
;              FILING DATE: 09-JAN-1997
;              APPLICATION NUMBER: PCT/US97/01603
;              FILING DATE: 22-JAN-1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Liebeschuetz, Joe
;              REGISTRATION NUMBER: 37,505
;              REFERENCE/DOCKET NUMBER: 018547-019410US
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 576-0200
;              TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 7:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 15 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: DNA (genomic)
;         HYPOTHETICAL: YES
;                       (ix)  Features:
;         SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-880-727-7

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.3e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2179
              |||||||||||||:
Db         15 TTTTTTTTTTTTB 2


RESULT 3247
US-10-683-386-44/c
; Sequence 44, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
;  TITLE OF INVENTION:  NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
;  TITLE OF INVENTION:  THE METHOD
;  FILE REFERENCE: 0163-0758-0X
;  CURRENT APPLICATION NUMBER: US/10/683,386
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: US/09/556,127
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: JP 1999-111601
;  PRIOR FILING DATE: 1999-04-20
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-44

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTGAACCCC 1788
              ||||||||||   ||||
Db         18 TTTTTTTTTTTTCCCCC 1


RESULT 3248
US-10-209-608-44/c
; Sequence 44, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
;  APPLICANT: KURANE, RYUICHIRO
;  APPLICANT:  KANAGAWA, TAKAHIRO
;  APPLICANT:  KAMAGATA, YOICHI
;  APPLICANT:  YAMADA, KAZUTAKA
;  APPLICANT:  YOKOMAKU, TOYOKAZU
;  APPLICANT:  KOYAMA, OSAMU
;  APPLICANT:  FURUSHO, KENTA
;  TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
```

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;  CURRENT FILING DATE:  2003-09-30
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1296
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-675-685-1296

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 25;
  Best Local Similarity   73.9%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
                ||||  |  |||||||| |||
Db          2 AGAAGGGGGGAAAAAAAAAGAAA 24


RESULT 3243
US-10-291-808-65
; Sequence 65, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
;  APPLICANT: McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE: P-PH 3457
;  CURRENT APPLICATION NUMBER: US/10/291,808
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: US/09/300,958
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/083,331
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: 60/098,070
;  PRIOR FILING DATE: 1998-08-27
;  PRIOR APPLICATION NUMBER: 60/118,624
;  PRIOR FILING DATE: 1999-02-04
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-65

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.1e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTA 2187
                ||||||||||||:
Db          1 TTTTTTTTTTTTV 14


RESULT 3244
US-10-291-808-65/c
; Sequence 65, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
;  APPLICANT: McClelland, Michael
;  APPLICANT:  Welsh, John
;  APPLICANT:  Trenkle, Thomas
;  TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
;  TITLE OF INVENTION:  Using Same
;  FILE REFERENCE: P-PH 3457
;  CURRENT APPLICATION NUMBER: US/10/291,808
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: US/09/300,958
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/083,331
;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: 60/098,070
;  PRIOR FILING DATE: 1998-08-27
;  PRIOR APPLICATION NUMBER: 60/118,624
;  PRIOR FILING DATE: 1999-02-04
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
;   LENGTH: 14
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-65

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.1e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
                :||||||||||||
Db         14 BAAAAAAAAAAAAA 1


RESULT 3245
US-09-880-727-7
; Sequence 7, Application US/09880727
; Publication No. US20030064364A1
;   GENERAL INFORMATION:
;        APPLICANT: Lockhart, David J.
;                   Chee, Mark
;                   Gunderson, Kevin
;                   Chaoqiang, Lai
;                   Wodicka, Lisa
;                   Cronin, Maureen T.
;                   Lee, Danny
;                   Tran, Huu M.
;                   Matsuzaki, Hajime
;                   McGall, Glenn H.
;        TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Joe Liebeschuetz
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/880,727
;             FILING DATE: 13-Jun-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/882,649
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 60/035,170
;             FILING DATE: 09-JAN-1997
;             APPLICATION NUMBER: PCT/US97/01603
;             FILING DATE: 22-JAN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Liebeschuetz, Joe
;             REGISTRATION NUMBER: 37,505
;             REFERENCE/DOCKET NUMBER: 018547-019410US
```

```
; Sequence 2602, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2602
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2602

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1925 TTTTTCAGTGTTAAG 1939
              ||||||||| |||||
Db          5 TTTTTCAGTTTTAAG 19


RESULT 3239
US-09-782-837-34
; Sequence 34, Application US/09782837
; Patent No. US20020127714A1
; GENERAL INFORMATION:
;  APPLICANT: HOUSMAN, DAVID E.
;  APPLICANT:  LEDLEY, FRED D.
;  APPLICANT:  STANTON, VINCENT P., JR.
;  TITLE OF INVENTION: INHIBITORS OF ALTERNATIVE ALLELES OF GENES ENCODING
;  TITLE OF INVENTION:  PRODUCTS THAT MEDIATE CELL RESPONSE TO ENVIRONMENTAL
;  TITLE OF INVENTION:  CHANGES
;  FILE REFERENCE: 233/055
;  CURRENT APPLICATION NUMBER: US/09/782,837
;  CURRENT FILING DATE:  2001-02-14
;  PRIOR APPLICATION NUMBER: 09/045,054
;  PRIOR FILING DATE: 1998-03-19
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Glutamate-ammonia ligase (glutamine synthase)
;   OTHER INFORMATION: The letter "r" stands for a or g.
US-09-782-837-34

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              || | ||:||||||||||
Db          5 AACATAARAAAAAAAAA 21


RESULT 3240
US-10-374-686-4/c
; Sequence 4, Application US/10374686
; Publication No. US20040002089A1
; GENERAL INFORMATION:
;  APPLICANT: Dubertret, Benoit
;  APPLICANT:  Calame, Michel
;  APPLICANT:  Libchaber, Albert
;  TITLE OF INVENTION: Methods Employing Fluorescent Quenching
;  TITLE OF INVENTION:  by Metal Surfaces
;  FILE REFERENCE: 600-1-260PCTUS
;  CURRENT APPLICATION NUMBER: US/10/374,686
;  CURRENT FILING DATE:  2003-02-26
;  PRIOR APPLICATION NUMBER: PCT/US01/41941
;  PRIOR FILING DATE: 2001-08-29
;  PRIOR APPLICATION NUMBER: 60/228728
;  PRIOR FILING DATE: 2000-08-29
;  PRIOR APPLICATION NUMBER: 60/280350
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-374-686-4

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 21;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||| |||||||
Db         16 TTTTTTTGTTTTTTT 2


RESULT 3241
US-09-827-998-1296
; Sequence 1296, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1296
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1296

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 25;
  Best Local Similarity   73.9%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
              ||||  |   ||||||||| |||
Db          2 AGAAGGGGGGAAAAAAAAAGAAA 24


RESULT 3242
US-10-675-685-1296
; Sequence 1296, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: PB0114
;  CURRENT APPLICATION NUMBER: US/10/675,685
```

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;  FILE REFERENCE: HTS-0055
;  CURRENT APPLICATION NUMBER: US/10/303,541
;  CURRENT FILING DATE:  2002-11-21
;  NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-541-28

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2712 CTGCCTGTAAATGTT 2726
              ||| ||||||||||
Db          6 CTGTCTGTAAATGTT 20


RESULT 3234
US-10-303-541-64/c
; Sequence 64, Application US/10303541
; Publication No. US20040102399A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF HYPOTHETICAL PROTEIN 669 EXPRESSION
;  FILE REFERENCE: HTS-0055
;  CURRENT APPLICATION NUMBER: US/10/303,541
;  CURRENT FILING DATE:  2002-11-21
;  NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-303-541-64

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2712 CTGCCTGTAAATGTT 2726
              ||| ||||||||||
Db         15 CTGTCTGTAAATGTT 1


RESULT 3235
US-10-688-706-144
; Sequence 144, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 144
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-144

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2504 TAACACATCATAAGG 2518
              | ||||||||||||||
Db          1 TCACACATCATAAGG 15


RESULT 3236
US-10-688-706-227
; Sequence 227, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 227
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-227

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2503 ATAACACATCATAAG 2517
              || ||||||||||||
Db          6 ATCACACATCATAAG 20


RESULT 3237
US-10-688-706-2305
; Sequence 2305, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2305
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2305

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1925 TTTTTCAGTGTTAAG 1939
              ||||||||| |||||
Db          6 TTTTTCAGTTTTAAG 20


RESULT 3238
US-10-688-706-2602
```

```
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-231A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||.||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3229
US-10-298-994-50
; Sequence 50, Application US/10298994
; Publication No. US20040097446A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: MODULATION OF CHECKPOINT KINASE 1 EXPRESSION
;  FILE REFERENCE: HTS-0006
;  CURRENT APPLICATION NUMBER: US/10/298,994
;  CURRENT FILING DATE:  2002-11-16
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 50
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-298-994-50

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1654 ACTGGTTCTGCATCA 1668
              ||||||||||||| |
Db          4 ACTGGTTCTGCATGA 18


RESULT 3230
US-10-298-994-91
; Sequence 91, Application US/10298994
; Publication No. US20040097446A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: MODULATION OF CHECKPOINT KINASE 1 EXPRESSION
;  FILE REFERENCE: HTS-0006
;  CURRENT APPLICATION NUMBER: US/10/298,994
;  CURRENT FILING DATE:  2002-11-16
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 91
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-298-994-91

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1654 ACTGGTTCTGCATCA 1668
              ||||||||||||| |
Db          2 ACTGGTTCTGCATGA 16


RESULT 3231
US-10-298-994-165/c
; Sequence 165, Application US/10298994
; Publication No. US20040097446A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: MODULATION OF CHECKPOINT KINASE 1 EXPRESSION
;  FILE REFERENCE: HTS-0006
;  CURRENT APPLICATION NUMBER: US/10/298,994
;  CURRENT FILING DATE:  2002-11-16
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 165
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-298-994-165

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1654 ACTGGTTCTGCATCA 1668
              ||||||||||||| |
Db         17 ACTGGTTCTGCATGA 3


RESULT 3232
US-10-298-994-198/c
; Sequence 198, Application US/10298994
; Publication No. US20040097446A1
; GENERAL INFORMATION:
;  APPLICANT: William Gaarde
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: MODULATION OF CHECKPOINT KINASE 1 EXPRESSION
;  FILE REFERENCE: HTS-0006
;  CURRENT APPLICATION NUMBER: US/10/298,994
;  CURRENT FILING DATE:  2002-11-16
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 198
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: M. musculus
;   FEATURE:
US-10-298-994-198

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1654 ACTGGTTCTGCATCA 1668
              ||||||||||||| |
Db         19 ACTGGTTCTGCATGA 5


RESULT 3233
US-10-303-541-28
; Sequence 28, Application US/10303541
; Publication No. US20040102399A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF HYPOTHETICAL PROTEIN 669 EXPRESSION
```

```
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2626 TTTGTCTCGTTCCTG 2640
              |||| ||||||||||
Db          1 TTTGGCTCGTTCCTG 15


RESULT 3224
US-10-289-762-5708/c
; Sequence 5708, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5708
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-5708

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        275 CAGCACCTCTACAGC 289
              ||||| |||||||||
Db         15 CAGCAGCTCTACAGC 1


RESULT 3225
US-10-289-762-6474/c
; Sequence 6474, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6474
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-6474

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        744 TTCGCAAAGGTCCCA 758
              ||||||||| |||||
Db         20 TTCGCAAAGATCCCA 6


RESULT 3226
US-10-188-777-36/c
; Sequence 36, Application US/10188777
; Publication No. US20040006220A1
; GENERAL INFORMATION:
;  APPLICANT: Sanjay Bhanot
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR 2 EXPRESSION
;  FILE REFERENCE: RTS-0358
;  CURRENT APPLICATION NUMBER: US/10/188,777
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 36
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-777-36

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCC 246
              || ||||||||||||
Db         17 CACCAATGGGAATCC 3


RESULT 3227
US-10-188-777-98
; Sequence 98, Application US/10188777
; Publication No. US20040006220A1
; GENERAL INFORMATION:
;  APPLICANT: Sanjay Bhanot
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR 2 EXPRESSION
;  FILE REFERENCE: RTS-0358
;  CURRENT APPLICATION NUMBER: US/10/188,777
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 98
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-188-777-98

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCC 246
              || ||||||||||||
Db          4 CACCAATGGGAATCC 18


RESULT 3228
US-10-012-231A-469/c
; Sequence 469, Application US/10012231A
; Publication No. US20040014130A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C23
;  CURRENT APPLICATION NUMBER: US/10/012,231A
;  CURRENT FILING DATE:  2002-06-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
```

```
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-2377

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2361 TTTAAGAAACAGTGC 2375
              ||||||||||| ||||
Db          6 TTTAAGAAACGGTGC 20


RESULT 3219
US-10-289-762-2867/c
; Sequence 2867, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2867
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-2867

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2626 TTTGTCTCGTTCCTG 2640
              |||| ||||||||||
Db         15 TTTGGCTCGTTCCTG 1


RESULT 3220
US-10-289-762-3480
; Sequence 3480, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3480
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-3480

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1548 AGGGAAGGAACAGGA 1562
              ||||||||||||| |
Db          6 AGGGAAGGAACAGAA 20


RESULT 3221
US-10-289-762-3520
; Sequence 3520, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prev
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3520
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-3520

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        794 CAGAAGGAGCTGGTG 808
              |||||||| ||||||
Db          5 CAGAAGGACCTGGTG 19


RESULT 3222
US-10-289-762-4153/c
; Sequence 4153, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4153
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-4153

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1706 AGCTATCTCCTAACT 1720
              |||||||||||| |||
Db         18 AGCTATCTCCTTACT 4


RESULT 3223
US-10-289-762-5364
; Sequence 5364, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5364
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-5364

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
```

```
RESULT 3214
US-10-165-216-11/c
; Sequence 11, Application US/10165216
; Publication No. US20030228675A1
; GENERAL INFORMATION:
;  APPLICANT: Otterness, Diane M.
;  APPLICANT:  Abraham, Robert T.
;  TITLE OF INVENTION: ATM Related Kinase ATX, Nucleic Acids
;  TITLE OF INVENTION:  Encoding Same and Methods of Use
;  FILE REFERENCE: P-LJ 5222
;  CURRENT APPLICATION NUMBER: US/10/165,216
;  CURRENT FILING DATE:  2002-06-06
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
US-10-165-216-11

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGC 501
              ||| ||||||||||||
Db         20 GAGACAGGAGGGAGC 6


RESULT 3215
US-10-174-020-67/c
; Sequence 67, Application US/10174020
; Publication No. US20030232770A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EXP
;  FILE REFERENCE: RTS-0369
;  CURRENT APPLICATION NUMBER: US/10/174,020
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-020-67

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2133 AGAAACGAAGCCTGC 2147
              ||||||| |||||||
Db         17 AGAAACGCAGCCTGC 3


RESULT 3216
US-10-174-020-134
; Sequence 134, Application US/10174020
; Publication No. US20030232770A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EXP
;  FILE REFERENCE: RTS-0369
;  CURRENT APPLICATION NUMBER: US/10/174,020
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 134
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-174-020-134

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2133 AGAAACGAAGCCTGC 2147
              ||||||| |||||||
Db          4 AGAAACGCAGCCTGC 18


RESULT 3217
US-10-011-795A-469/c
; Sequence 469, Application US/10011795A
; Publication No. US20040005626A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C25
;  CURRENT APPLICATION NUMBER: US/10/011,795A
;  CURRENT FILING DATE:  2001-12-07
;  Prior application removed - See file Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-795A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||| |||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3218
US-10-289-762-2377
; Sequence 2377, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prever
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2377
;   LENGTH: 20
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;  PRIOR APPLICATION NUMBER: 60/101472
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101474
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101476
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101477
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101479
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101741
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101743
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101915
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101916
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/102207
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102240
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102307
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102330
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102331
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102484
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102487
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102570
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102571
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102684
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102687
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102965
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: 60/103258
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103314
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103315
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103328
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103395
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103396
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103401
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||.||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3213
US-10-388-263-506/c
; Sequence 506, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  McNeil, John
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Sasmor, Henri M.
;  APPLICANT:  Brooks, Douglas G.
;  APPLICANT:  Ohashi, Cara
;  APPLICANT:  Wyatt, Jacqueline R.
;  APPLICANT:  Borchers, Alexander
;  APPLICANT:  Vickers, Timothy A.
;  TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
;  TITLE OF INVENTION:  MODULATION BY OLIGONUCLEOTIDES AND
;  TITLE OF INVENTION:  GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
;  FILE REFERENCE: ISIS-4503
;  CURRENT APPLICATION NUMBER: US/10/388,263
;  CURRENT FILING DATE:  2003-03-12
;  NUMBER OF SEQ ID NOS: 947
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 506
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-506

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        835 CTTCTGCTCAGTCCC 849
              ||||||||||| |||
Db         15 CTTCTGCTCAGGCCC 1
```

```
RESULT 3211
US-10-360-510-210/c
; Sequence 210, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/10/360,510
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US/09/854,883
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 210
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-210

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        479 GGCCGCCAGAGCCAG 493
              ||||||||||||| ||
Db         18 GGCCGCCAGAGCGAG 4


RESULT 3212
US-10-006-746A-469/c
; Sequence 469, Application US/10006746A
; Publication No. US20030220471A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C5
;  CURRENT APPLICATION NUMBER: US/10/006,746A
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100711
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100848
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100849
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100919
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101014
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101068
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101071
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101471
;  PRIOR FILING DATE: 1998-09-23
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;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-394A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3208
US-10-015-390A-469/c
; Sequence 469, Application US/10015390A
; Publication No. US20030216562A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C53
;  CURRENT APPLICATION NUMBER: US/10/015,390A
;  CURRENT FILING DATE:  2002-07-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-390A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3209
US-10-156-603-18/c
; Sequence 18, Application US/10156603
; Publication No. US20030220275A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Erich Koller
;  TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION
;  FILE REFERENCE: HTS-0016
;  CURRENT APPLICATION NUMBER: US/10/156,603
;  CURRENT FILING DATE:  2002-05-23
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-156-603-18

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2187 AACTTTGAAAGTTAA 2201
              |||||||  |||||||
Db         17 AACTTTGCAAGTTAA 3


RESULT 3210
US-10-360-510-130
; Sequence 130, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/10/360,510
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US/09/854,883
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 130
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-130

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2003 CTTCTTCAGAGATCA 2017
              | ||||||||||||||
Db          6 CATCTTCAGAGATCA 20
```

```
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C49
;  CURRENT APPLICATION NUMBER: US/10/015,519A
;  CURRENT FILING DATE:  2002-06-25
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-519A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3205
US-10-005-344-214/c
; Sequence 214, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
;  APPLICANT: Loren J. Miraglia
;  APPLICANT:  Pamela Nero
;  APPLICANT:  Mark J. Graham
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Erich Koller
;  APPLICANT:  MingYi Chiang
;  APPLICANT:  Mano Manoharan
;  TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
;  FILE REFERENCE: ISPH-0622
;  CURRENT APPLICATION NUMBER: US/10/005,344
;  CURRENT FILING DATE:  2001-12-04
;  PRIOR APPLICATION NUMBER: US 09/048,810
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/280,805
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 379
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 214
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-005-344-214

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2520 TTTATTCATATATAT 2534
              |||||||| ||||||
Db         15 TTTATTCACATATAT 1


RESULT 3206
US-10-013-915A-469/c
; Sequence 469, Application US/10013915A
; Publication No. US20030204053A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C37
;  CURRENT APPLICATION NUMBER: US/10/013,915A
;  CURRENT FILING DATE:  2002-06-25
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-915A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3207
US-10-015-394A-469/c
; Sequence 469, Application US/10015394A
; Publication No. US20030204054A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C41
;  CURRENT APPLICATION NUMBER: US/10/015,394A
;  CURRENT FILING DATE:  2001-12-11
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
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US-10-012-753A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
||||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3201
US-10-015-385A-469/c
; Sequence 469, Application US/10015385A
; Publication No. US20030195347A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C51
; CURRENT APPLICATION NUMBER: US/10/015,385A
; CURRENT FILING DATE: 2002-07-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-385A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
||||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3202
US-10-007-236A-469/c
; Sequence 469, Application US/10007236A
; Publication No. US20030198993A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C12
; CURRENT APPLICATION NUMBER: US/10/007,236A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-007-236A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
||||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3203
US-10-015-389A-469/c
; Sequence 469, Application US/10015389A
; Publication No. US20030199675A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C48
; CURRENT APPLICATION NUMBER: US/10/015,389A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-389A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
||||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3204
US-10-015-519A-469/c
; Sequence 469, Application US/10015519A
; Publication No. US20030203401A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

 Query Match 0.5%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
 |||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3198
US-10-015-388A-469/c
; Sequence 469, Application US/10015388A
; Publication No. US20030191299A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C44
; CURRENT APPLICATION NUMBER: US/10/015,388A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-388A-469

 Query Match 0.5%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
 |||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3199
US-10-302-262-16/c
; Sequence 16, Application US/10302262
; Publication No. US20030191300A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/10/302,262
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/734,846
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-302-262-16

 Query Match 0.5%; Score 13.4; DB 1; Length 20;
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2104 CGGGGGCCTTCTGGT 2118
 ||||| ||||||||||
Db 20 CGGGGTCCTTCTGGT 6

RESULT 3200
US-10-012-753A-469/c
; Sequence 469, Application US/10012753A
; Publication No. US20030195334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C17
; CURRENT APPLICATION NUMBER: US/10/012,753A
; CURRENT FILING DATE: 2001-12-07
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
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; PRIOR APPLICATION NUMBER: 60/099812
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; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
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; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
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; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20

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;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C50
;  CURRENT APPLICATION NUMBER: US/10/015,480A
;  CURRENT FILING DATE:  2002-06-25
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-480A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3195
US-10-015-715A-469/c
; Sequence 469, Application US/10015715A
; Publication No. US20030190668A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C56
;  CURRENT APPLICATION NUMBER: US/10/015,715A
;  CURRENT FILING DATE:  2002-06-25
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-715A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3196
US-10-012-237A-469/c
; Sequence 469, Application US/10012237A
; Publication No. US20030191281A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C21
;  CURRENT APPLICATION NUMBER: US/10/012,237A
;  CURRENT FILING DATE:  2002-06-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-237A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3197
US-10-013-906A-469/c
; Sequence 469, Application US/10013906A
; Publication No. US20030191282A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C36
;  CURRENT APPLICATION NUMBER: US/10/013,906A
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
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;  CURRENT APPLICATION NUMBER: US/10/013,912A
;  CURRENT FILING DATE:  2001-12-10
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-912A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3192
US-10-015-653A-469/c
; Sequence 469, Application US/10015653A
; Publication No. US20030187195A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C43
;  CURRENT APPLICATION NUMBER: US/10/015,653A
;  CURRENT FILING DATE:  2002-06-25
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-653A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3193
US-10-012-101B-469/c
; Sequence 469, Application US/10012101B
; Publication No. US20030187239A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C6
;  CURRENT APPLICATION NUMBER: US/10/012,101B
;  CURRENT FILING DATE:  2001-12-06
;  Prior application removed - See file Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-101B-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3194
US-10-015-480A-469/c
; Sequence 469, Application US/10015480A
; Publication No. US20030190667A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
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; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
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; PRIOR APPLICATION NUMBER: 60/101479
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        203 GAGGACTGCGAGGAT 217
              ||||||.||||||||
Db         19 GAGGACGGCGAGGAT 5
```

RESULT 3191
US-10-013-912A-469/c
; Sequence 469, Application US/10013912A
; Publication No. US20030187194A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C32

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;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-754A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3189
US-10-013-910A-469/c
; Sequence 469, Application US/10013910A
; Publication No. US20030187192A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C33
;  CURRENT APPLICATION NUMBER: US/10/013,910A
;  CURRENT FILING DATE:  2002-06-25
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-910A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3190
US-10-013-911A-469/c
; Sequence 469, Application US/10013911A
; Publication No. US20030187193A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C39
;  CURRENT APPLICATION NUMBER: US/10/013,911A
;  CURRENT FILING DATE:  2001-12-10
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100711
;  PRIOR FILING DATE: 1998-09-17
```

```
US-10-093-311-27
; Sequence 27, Application US/10093311
; Publication No. US20030186439A1
; GENERAL INFORMATION:
;  APPLICANT: Nakauchi, Hiromitsu
;  APPLICANT:  Suzuki, Atsushi
;  APPLICANT:  Taniguchi, Hideki
;  APPLICANT:  Fukao, Katashi
;  TITLE OF INVENTION: Self-Renewing Pluripotent Hepatic Stem
;  TITLE OF INVENTION:  Cells
;  FILE REFERENCE: 59150-8016
;  CURRENT APPLICATION NUMBER: US/10/093,311
;  CURRENT FILING DATE:  2002-03-06
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-093-311-27

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2427 TGGTGCACTTCTTAC 2441
                ||||||||||| |||
Db          5 TGGTGCACTTCCTAC 19


RESULT 3186
US-10-012-137A-469/c
; Sequence 469, Application US/10012137A
; Publication No. US20030187189A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C29
;  CURRENT APPLICATION NUMBER: US/10/012,137A
;  CURRENT FILING DATE:  2002-06-25
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-137A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
                ||||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3187
US-10-012-752A-469/c
; Sequence 469, Application US/10012752A
; Publication No. US20030187190A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C24
;  CURRENT APPLICATION NUMBER: US/10/012,752A
;  CURRENT FILING DATE:  2002-06-25
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-752A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
                ||||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3188
US-10-012-754A-469/c
; Sequence 469, Application US/10012754A
; Publication No. US20030187191A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C18
;  CURRENT APPLICATION NUMBER: US/10/012,754A
;  CURRENT FILING DATE:  2002-06-25
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
```

```
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C35
;  CURRENT APPLICATION NUMBER: US/10/013,909A
;  CURRENT FILING DATE:  2002-06-25
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-909A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3183
US-10-015-671A-469/c
; Sequence 469, Application US/10015671A
; Publication No. US20030186319A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C47
;  CURRENT APPLICATION NUMBER: US/10/015,671A
;  CURRENT FILING DATE:  2001-12-11
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-671A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3184
US-10-015-610A-469/c
; Sequence 469, Application US/10015610A
; Publication No. US20030186361A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C52
;  CURRENT APPLICATION NUMBER: US/10/015,610A
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-610A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3185
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;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3180
US-10-012-064A-469/c
; Sequence 469, Application US/10012064A
; Publication No. US20030180836A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C19
;  CURRENT APPLICATION NUMBER: US/10/012,064A
;  CURRENT FILING DATE:  2002-07-15
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-064A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3181
US-10-331-907-164/c
; Sequence 164, Application US/10331907
; Publication No. US20030181660A1
;   GENERAL INFORMATION:
;        APPLICANT: Todd, John A
;                   Hess, John W
;                   Caskey, Charles T
;                   Cox, Roger D
;                   Gerhold, David
;                   Hammond, Holly
;                   Hey, Patricia
;                   Kawaguchi, Yoshihiko
;                   Merriman, Tony R
;                   Metzker, Michael L
;        TITLE OF INVENTION: No. US20030181660A1el LDL-Receptor
;        NUMBER OF SEQUENCES: 455
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Nixon and Vanderhye
;             STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
;             CITY: Arlington
;             STATE: Virginia
;             COUNTRY: US
;             ZIP: VA 22201-4714
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/331,907
;             FILING DATE: 31-Dec-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/402,923A
;             FILING DATE: 14-Feb-2001
;             APPLICATION NUMBER: PCT/GB98/01102
;             FILING DATE: 15-APR-1998
;             APPLICATION NUMBER: US 60/043,553
;             FILING DATE: 15-APR-1997
;             APPLICATION NUMBER: US 60/048,740
;             FILING DATE: 05-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: B.J.Sadoff
;             REGISTRATION NUMBER: 36,663
;             REFERENCE/DOCKET NUMBER: 620-81
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703)816-4091
;             TELEFAX: (703)816-4100
;   INFORMATION FOR SEQ ID NO: 164:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-10-331-907-164

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        914 CGACTGTCCCCACCT 928
              | ||||||||||||||
Db         20 CAACTGTCCCCACCT 6


RESULT 3182
US-10-013-909A-469/c
; Sequence 469, Application US/10013909A
; Publication No. US20030186318A1
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
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; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882

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;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C66
;  CURRENT APPLICATION NUMBER: US/10/017,306A
;  CURRENT FILING DATE:  2002-06-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-306A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3178
US-10-211-884-164/c
; Sequence 164, Application US/10211884
; Publication No. US20030175900A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Hillan,Kenneth J.
;  APPLICANT:  Marsters,Scot A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Pitti,Robert M.
;  APPLICANT:  Roy,Margaret Ann
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stone,Donna M.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
;  FILE REFERENCE: P2931R1C1
;  CURRENT APPLICATION NUMBER: US/10/211,884
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: 60/014699
;  PRIOR FILING DATE: 1996-04-01
;  PRIOR APPLICATION NUMBER: 60/026943
;  PRIOR FILING DATE: 1996-09-23
;  PRIOR APPLICATION NUMBER: 60/059121
;  PRIOR FILING DATE: 1997-07-17
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/062037
;  PRIOR FILING DATE: 1997-10-10
;  PRIOR APPLICATION NUMBER: 60/063755
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063045
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063046
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/066511
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/066772
;  PRIOR FILING DATE: 1997-11-24
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 164
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide Probe.
US-10-211-884-164

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3179
US-10-017-867A-469/c
; Sequence 469, Application US/10017867A
; Publication No. US20030180792A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C60
;  CURRENT APPLICATION NUMBER: US/10/017,867A
;  CURRENT FILING DATE:  2001-12-13
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
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;  APPLICANT:  Pirrung, Michael C.
;  TITLE OF INVENTION: METHOD OF ANALYZING mRNA SPLICE VARIANTS USING ARRAYED PRIMER EXT
;  TITLE OF INVENTION:  (APEX)
;  FILE REFERENCE: 5405-274
;  CURRENT APPLICATION NUMBER: US/10/092,208
;  CURRENT FILING DATE:  2002-03-06
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide 5-V4.
US-10-092-208-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2678 GTGTGGGTGAAATGG 2692
              |||||| ||||||||
Db          6 GTGTGGTTGAAATGG 20


RESULT 3175
US-10-294-203-14
; Sequence 14, Application US/10294203
; Publication No. US20030170680A1
; GENERAL INFORMATION:
;  APPLICANT: Froehler, Brian
;  APPLICANT:  Wagner, Rick
;  APPLICANT:  Mateucci, Mark
;  APPLICANT:  Jones, Robert J.
;  APPLICANT:  Gutierrez, Arnold J.
;  APPLICANT:  Pudlo, Jeff
;  TITLE OF INVENTION: Enhanced Triple-Helix And Double-Helix Formation With Oligomers
;  TITLE OF INVENTION:  Containing Modified Pyrimidines
;  FILE REFERENCE: GLIS0155
;  CURRENT APPLICATION NUMBER: US/10/294,203
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: 08/599,738
;  PRIOR FILING DATE: 1996-02-12
;  PRIOR APPLICATION NUMBER: 10/024,818
;  PRIOR FILING DATE: 2001-12-18
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (9)..(9)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (17)..(17)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
US-10-294-203-14

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||| ||  |||||| ||
Db          2 TTTTNTTNATTTTTTNTT 19


RESULT 3176
US-10-294-203-14/c
; Sequence 14, Application US/10294203
; Publication No. US20030170680A1
; GENERAL INFORMATION:
;  APPLICANT: Froehler, Brian
;  APPLICANT:  Wagner, Rick
;  APPLICANT:  Mateucci, Mark
;  APPLICANT:  Jones, Robert J.
;  APPLICANT:  Gutierrez, Arnold J.
;  APPLICANT:  Pudlo, Jeff
;  TITLE OF INVENTION: Enhanced Triple-Helix And Double-Helix Formation With Oligomers
;  TITLE OF INVENTION:  Containing Modified Pyrimidines
;  FILE REFERENCE: GLIS0155
;  CURRENT APPLICATION NUMBER: US/10/294,203
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: 08/599,738
;  PRIOR FILING DATE: 1996-02-12
;  PRIOR APPLICATION NUMBER: 10/024,818
;  PRIOR FILING DATE: 2001-12-18
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (9)..(9)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (17)..(17)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
US-10-294-203-14

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              || ||||||  || ||||
Db         19 AANAAAAAATNAANAAAA 2

RESULT 3177
US-10-017-306A-469/c
; Sequence 469, Application US/10017306A
; Publication No. US20030170718A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
```

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;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-253A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3172
US-10-015-392A-469/c
; Sequence 469, Application US/10015392A
; Publication No. US20030166901A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C58
;  CURRENT APPLICATION NUMBER: US/10/015,392A
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-392A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3173
US-10-210-951-164/c
; Sequence 164, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Hillan,Kenneth J.
;  APPLICANT:  Marsters,Scot A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Pitti,Robert M.
;  APPLICANT:  Roy,Margaret Ann
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stone,Donna M.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
;  FILE REFERENCE: P2931R1C1
;  CURRENT APPLICATION NUMBER: US/10/210,951
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: 60/014699
;  PRIOR FILING DATE: 1996-04-01
;  PRIOR APPLICATION NUMBER: 60/026943
;  PRIOR FILING DATE: 1996-09-23
;  PRIOR APPLICATION NUMBER: 60/059121
;  PRIOR FILING DATE: 1997-07-17
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/062037
;  PRIOR FILING DATE: 1997-10-10
;  PRIOR APPLICATION NUMBER: 60/063755
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063045
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063046
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/066511
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/066772
;  PRIOR FILING DATE: 1997-11-24
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 164
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide Probe.
US-10-210-951-164

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3174
US-10-092-208-12
; Sequence 12, Application US/10092208
; Publication No. US20030170637A1
; GENERAL INFORMATION:
;  APPLICANT: Kim, Hyunsoo
```

; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5
```

RESULT 3171
US-10-017-253A-469/c
; Sequence 469, Application US/10017253A
; Publication No. US20030166055A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C62
; CURRENT APPLICATION NUMBER: US/10/017,253A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-130A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
||||||.|||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3170
US-10-006-172A-469/c
; Sequence 469, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476

```
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3166
US-10-006-041A-469/c
; Sequence 469, Application US/10006041A
; Publication No. US20030130490A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C8
;  CURRENT APPLICATION NUMBER: US/10/006,041A
;  CURRENT FILING DATE:  2001-12-06
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-041A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3167
US-10-015-822A-469/c
; Sequence 469, Application US/10015822A
; Publication No. US20030130491A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C38
;  CURRENT APPLICATION NUMBER: US/10/015,822A
;  CURRENT FILING DATE:  2002-06-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-822A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3168
US-10-015-387A-469/c
; Sequence 469, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C54
;  CURRENT APPLICATION NUMBER: US/10/015,387A
;  CURRENT FILING DATE:  2001-12-12
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-387A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3169
US-10-006-130A-469/c
; Sequence 469, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
```

```
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C59
;  CURRENT APPLICATION NUMBER: US/10/015,391A
;  CURRENT FILING DATE:  2001-12-12
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-391A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3163
US-10-000-213-81/c
; Sequence 81, Application US/10000213
; Publication No. US20030125271A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Mark P. Roach
;  APPLICANT:  Kenneth Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF VITAMIN D NUCLEAR RECEPTOR EXPRESSION
;  FILE REFERENCE: RTS-0327
;  CURRENT APPLICATION NUMBER: US/10/000,213
;  CURRENT FILING DATE:  2001-11-14
;  NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 81
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-000-213-81

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2143 CCTGCTGATTGATTT 2157
              ||||||| ||||||
Db         20 CCTGCTGAATGATTT 6


RESULT 3164
US-10-017-407A-469/c
; Sequence 469, Application US/10017407A
; Publication No. US20030125535A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C61
;  CURRENT APPLICATION NUMBER: US/10/017,407A
;  CURRENT FILING DATE:  2002-06-25
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-407A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3165
US-10-011-833A-469/c
; Sequence 469, Application US/10011833A
; Publication No. US20030129650A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C22
;  CURRENT APPLICATION NUMBER: US/10/011,833A
;  CURRENT FILING DATE:  2002-06-25
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-833A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
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;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3160
US-10-006-063A-469/c
; Sequence 469, Application US/10006063A
; Publication No. US20030114652A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C3
;  CURRENT APPLICATION NUMBER: US/10/006,063A
;  CURRENT FILING DATE:  2002-03-15
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-063A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3161
US-10-020-063A-469/c
; Sequence 469, Application US/10020063A
; Publication No. US20030119097A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C65
;  CURRENT APPLICATION NUMBER: US/10/020,063A
;  CURRENT FILING DATE:  2002-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-020-063A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3162
US-10-015-391A-469/c
; Sequence 469, Application US/10015391A
; Publication No. US20030120053A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
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; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
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; PRIOR APPLICATION NUMBER: 60/100662
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; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
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; PRIOR FILING DATE: 1998-09-30
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; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14

US-10-002-491-84
; Sequence 84, Application US/10002491
; Publication No. US20030109467A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF FXR EXPRESSION
; FILE REFERENCE: RTS-0239
; CURRENT APPLICATION NUMBER: US/10/002,491
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 84
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-002-491-84

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1897 CCTAGATCAACAGAT 1911
||||| |||||||||
Db 1 CCTAGTTCAACAGAT 15

RESULT 3157
US-10-011-692A-469/c
; Sequence 469, Application US/10011692A
; Publication No. US20030109672A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C30
; CURRENT APPLICATION NUMBER: US/10/011,692A
; CURRENT FILING DATE: 2001-12-07
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-692A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
|||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3158
US-10-006-768A-469/c
; Sequence 469, Application US/10006768A
; Publication No. US20030113793A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C10
; CURRENT APPLICATION NUMBER: US/10/006,768A
; CURRENT FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-768A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
|||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3159
US-10-017-610A-469/c
; Sequence 469, Application US/10017610A
; Publication No. US20030113795A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C64
; CURRENT APPLICATION NUMBER: US/10/017,610A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01

```
; GENERAL INFORMATION:
;  APPLICANT: Froehler, Brian
;  APPLICANT:  Wagner, Rick
;  APPLICANT:  Mateucci, Mark
;  APPLICANT:  Jones, Robert J.
;  APPLICANT:  Gutierrez, Arnold J.
;  APPLICANT:  Pudlo, Jeff
;  TITLE OF INVENTION: Enhanced Triple-Helix And Double-Helix Formation With Oligomers
;  TITLE OF INVENTION:  Containing Modified Pyrimidines
;  FILE REFERENCE: GLIS0143
;  CURRENT APPLICATION NUMBER: US/10/024,818
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: 08/599,738
;  PRIOR FILING DATE: 1996-02-12
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (9)..(9)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (17)..(17)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
US-10-024-818-14

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              |||| ||  |||||| ||
Db          2 TTTTNTTNATTTTTTNTT 19


RESULT 3154
US-10-024-818-14/c
; Sequence 14, Application US/10024818
; Publication No. US20030096980A1
; GENERAL INFORMATION:
;  APPLICANT: Froehler, Brian
;  APPLICANT:  Wagner, Rick
;  APPLICANT:  Mateucci, Mark
;  APPLICANT:  Jones, Robert J.
;  APPLICANT:  Gutierrez, Arnold J.
;  APPLICANT:  Pudlo, Jeff
;  TITLE OF INVENTION: Enhanced Triple-Helix And Double-Helix Formation With Oligomers
;  TITLE OF INVENTION:  Containing Modified Pyrimidines
;  FILE REFERENCE: GLIS0143
;  CURRENT APPLICATION NUMBER: US/10/024,818
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: 08/599,738
;  PRIOR FILING DATE: 1996-02-12
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (9)..(9)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (17)..(17)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
US-10-024-818-14

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              || ||||||  || ||||
Db         19 AANAAAAAATNAANAAAA 2


RESULT 3155
US-10-015-386A-469/c
; Sequence 469, Application US/10015386A
; Publication No. US20030099625A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C55
;  CURRENT APPLICATION NUMBER: US/10/015,386A
;  CURRENT FILING DATE:  2001-12-12
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-386A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3156
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;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101477
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101479
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101741
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101743
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101915
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101916
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/102207
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102240
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102307
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102330
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102331
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102484
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102487
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102570
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102571
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102684
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102687
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102965
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: 60/103258
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103314
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103315
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103328
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103395
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;  PRIOR APPLICATION NUMBER: 60/103396
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103401
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3152
US-10-012-755A-469/c
; Sequence 469, Application US/10012755A
; Publication No. US20030096955A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C28
;  CURRENT APPLICATION NUMBER: US/10/012,755A
;  CURRENT FILING DATE:  2002-06-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-755A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3153
US-10-024-818-14
; Sequence 14, Application US/10024818
; Publication No. US20030096980A1
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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C31
; CURRENT APPLICATION NUMBER: US/10/013,430A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-430A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
||||||.||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3151
US-10-011-671A-469/c
; Sequence 469, Application US/10011671A
; Publication No. US20030096954A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C27
; CURRENT APPLICATION NUMBER: US/10/011,671A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476

; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-10-02
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; PRIOR FILING DATE: 1998-10-07
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; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        203 GAGGACTGCGAGGAT 217
              |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5
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RESULT 3150
US-10-013-430A-469/c
; Sequence 469, Application US/10013430A
; Publication No. US20030092883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone

; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
||||||.|||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3148
US-10-013-913A-469/c
; Sequence 469, Application US/10013913A
; Publication No. US20030083462A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C40
; CURRENT APPLICATION NUMBER: US/10/013,913A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-913A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
||||||.|||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3149
US-10-007-194A-469/c
; Sequence 469, Application US/10007194A
; Publication No. US20030092061A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C6
; CURRENT APPLICATION NUMBER: US/10/007,194A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
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; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
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; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
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; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104

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;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102965
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: 60/103258
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103314
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103315
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103328
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103395
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103396
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103401
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105881
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/105882
;  PRIOR FILING DATE: 1998-10-27
;  PRIOR APPLICATION NUMBER: 60/106023
;  PRIOR FILING DATE: 1998-10-28

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  |||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3146
US-10-006-117A-469/c
; Sequence 469, Application US/10006117A
; Publication No. US20030082627A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C13
;  CURRENT APPLICATION NUMBER: US/10/006,117A
;  CURRENT FILING DATE:  2002-03-19
;  Prior Application removed - See File Wrapper or Palm
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-117A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  |||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3147
US-10-017-527A-469/c
; Sequence 469, Application US/10017527A
; Publication No. US20030082628A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C63
;  CURRENT APPLICATION NUMBER: US/10/017,527A
;  CURRENT FILING DATE:  2001-12-13
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
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; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C15
; CURRENT APPLICATION NUMBER: US/10/006,116A
; CURRENT FILING DATE: 2001-12-16
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
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; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
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; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
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; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687

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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3142
US-10-015-393A-469/c
; Sequence 469, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C46
;  CURRENT APPLICATION NUMBER: US/10/015,393A
;  CURRENT FILING DATE:  2002-06-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-393A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3143
US-10-015-869A-469/c
; Sequence 469, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C45
;  CURRENT APPLICATION NUMBER: US/10/015,869A
;  CURRENT FILING DATE:  2002-06-25
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-869A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3144
US-10-012-121A-469/c
; Sequence 469, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C20
;  CURRENT APPLICATION NUMBER: US/10/012,121A
;  CURRENT FILING DATE:  2001-12-07
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-121A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3145
US-10-006-116A-469/c
; Sequence 469, Application US/10006116A
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;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C68
;  CURRENT APPLICATION NUMBER: US/10/226,254A
;  CURRENT FILING DATE:  2002-08-21
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-226-254A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  |||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3139
US-10-144-140-62
; Sequence 62, Application US/10144140
; Publication No. US20030211606A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DYRK4 EXPRESSION
;  FILE REFERENCE: RTS-0362
;  CURRENT APPLICATION NUMBER: US/10/144,140
;  CURRENT FILING DATE:  2002-05-10
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 62
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-144-140-62

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        924 CACCTGAATGCTTAA 938
              ||||||||||| ||
Db          1 CACCTGAATGCTGAA 15


RESULT 3140
US-10-006-856A-469/c
; Sequence 469, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C14
;  CURRENT APPLICATION NUMBER: US/10/006,856A
;  CURRENT FILING DATE:  2002-05-10
;  NUMBER OF SEQ ID NOS: 477
;  Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  |||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3141
US-10-006-818A-469/c
; Sequence 469, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C4
;  CURRENT APPLICATION NUMBER: US/10/006,818A
;  CURRENT FILING DATE:  2001-12-06
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-907A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
|||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3136
US-10-015-499A-469/c
; Sequence 469, Application US/10015499A
; Publication No. US20030065142A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-499A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
|||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3137
US-10-211-858-164/c
; Sequence 164, Application US/10211858
; Publication No. US20030211096A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Hillan,Kenneth J.
; APPLICANT: Marsters,Scot A.
; APPLICANT: Pan,James
; APPLICANT: Pitti,Robert M.
; APPLICANT: Roy,Margaret Ann
; APPLICANT: Smith,Victoria
; APPLICANT: Stone,Donna M.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/211,858
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 164
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe.
US-10-211-858-164

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217
|||||| ||||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3138
US-10-226-254A-469/c
; Sequence 469, Application US/10226254A
; Publication No. US20030224478A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James

; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        203 GAGGACTGCGAGGAT 217
              |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5
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RESULT 3135
US-10-013-907A-469/c
; Sequence 469, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

```
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US 09/290,640
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-619-220-78

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2441 CGACTTTTTTGAGAC 2455
              || |||||||||||
Db          1 CGGCTTTTTTGAGAC 15


RESULT 3133
US-09-949-428-228
; Sequence 228, Application US/09949428
; Publication No. US20030064372A1
; GENERAL INFORMATION:
;  APPLICANT: Bodnar, Jackie S.
;  APPLICANT:  Castellani, Lawrence W.
;  APPLICANT:  Chatterjee, Aurobindo
;  APPLICANT:  de Jong, Pieter
;  APPLICANT:  Lusis, Aldons J.
;  APPLICANT:  Ohmen, Jeff
;  APPLICANT:  Ross, David
;  APPLICANT:  Tafuri, Sherrie
;  APPLICANT:  Wu, Chenyan
;  TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder
;  FILE REFERENCE: 02810.0014.NPUS01
;  CURRENT APPLICATION NUMBER: US/09/949,428
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: 60/231,322
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-949-428-228

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2427 TGGTGCACTTCTTAC 2441
              ||||||||||||| |
Db          1 TGGTGCACTTCTTCC 15


RESULT 3134
US-10-006-485A-469/c
; Sequence 469, Application US/10006485A
; Publication No. US20030064062A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C9
;  CURRENT APPLICATION NUMBER: US/10/006,485A
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
```

```
;       NUMBER OF SEQUENCES: 250
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, 8th Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/510,378
;            FILING DATE: 22-Feb-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/544,381
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: US 08/510,521
;            FILING DATE: 02-AUG-1995
;            APPLICATION NUMBER: PCT/US94/12305
;            FILING DATE: 26-OCT-1994
;            APPLICATION NUMBER: US 08/284,064
;            FILING DATE: 02-AUG-1994
;            APPLICATION NUMBER: US 08/143,312
;            FILING DATE: 26-OCT-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Liebeschuetz, Joe
;            REGISTRATION NUMBER: 37,505
;            REFERENCE/DOCKET NUMBER: 018547-004130US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-576-0200
;            TELEFAX: 415-576-0300
;   INFORMATION FOR SEQ ID NO: 224:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 20 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (probe)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-510-378-224

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2205 TTCAAATGGGAGACT 2219
                || ||||||||||||
Db         18 TTAAAATGGGAGACT 4


RESULT 3130
US-09-838-028-12/c
; Sequence 12, Application US/09838028
; Publication No. US20030175857A1
; GENERAL INFORMATION:
;  APPLICANT: Lind, Peter
;  APPLICANT:  Berthold, Malin
;  TITLE OF INVENTION: No. US20030175857A1el G Protein-Coupled Receptor
;  FILE REFERENCE: 00125US2
;  CURRENT APPLICATION NUMBER: US/09/838,028
;  CURRENT FILING DATE:  2001-04-19
;  PRIOR APPLICATION NUMBER: 60/198,600
;  PRIOR FILING DATE: 2000-04-19
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Primer
US-09-838-028-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2674 GTGTGTGTGGGTGAA 2688
                | ||||||||||||||
Db         15 GGGTGTGTGGGTGAA 1


RESULT 3131
US-10-015-395A-469/c
; Sequence 469, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C57
;  CURRENT APPLICATION NUMBER: US/10/015,395A
;  CURRENT FILING DATE:  2001-12-12
;  Prior application removed - See file Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-395A-469

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
                |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3132
US-10-619-220-78
; Sequence 78, Application US/10619220
; Publication No. US20040033979A1
; GENERAL INFORMATION:
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Wyatt, Jacqueline
;  APPLICANT:  Zhang, Hong
;  TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
;  FILE REFERENCE: ISPH-545
;  CURRENT APPLICATION NUMBER: US/10/619,220
;  CURRENT FILING DATE:  2003-07-14
;  PRIOR APPLICATION NUMBER: 09/802,669
;  PRIOR FILING DATE: 2001-03-01
;  PRIOR APPLICATION NUMBER: US 09/665,615
```

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;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102331
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102484
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102487
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102570
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102571
;  PRIOR FILING DATE: 1998-09-30
;  PRIOR APPLICATION NUMBER: 60/102684
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102687
;  PRIOR FILING DATE: 1998-10-01
;  PRIOR APPLICATION NUMBER: 60/102965
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: 60/103258
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103314
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103315
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103328
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103395
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103396
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103401
;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
;  PRIOR FILING DATE: 1998-10-06
;  PRIOR APPLICATION NUMBER: 60/103633
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103678
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103679
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/103711
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/104257
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: 60/104987
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105000
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105002
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: 60/105104
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/105169
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105266
;  PRIOR FILING DATE: 1998-10-22
;  PRIOR APPLICATION NUMBER: 60/105693
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105694
;  PRIOR FILING DATE: 1998-10-26
;  PRIOR APPLICATION NUMBER: 60/105807

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||  ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3127
US-09-906-158-57/c
; Sequence 57, Application US/09906158
; Publication No. US20030078217A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3 EXPRESSI
;  FILE REFERENCE: RTS-0257
;  CURRENT APPLICATION NUMBER: US/09/906,158
;  CURRENT FILING DATE:  2001-07-14
;  NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 57
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-906-158-57

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        835 CTTCTGCTCAGTCCC 849
              ||||||||||| |||
Db         15 CTTCTGCTCAGGCCC 1


RESULT 3128
US-09-816-460C-20/c
; Sequence 20, Application US/09816460C
; Publication No. US20030087235A1
; GENERAL INFORMATION:
;  APPLICANT: Dairkee, Shanaz H.
;  APPLICANT:  Li, Zheng
;  TITLE OF INVENTION: PROGNOSTIC METHODS FOR BREAST CANCER
;  FILE REFERENCE: CPMC-010/00US
;  CURRENT APPLICATION NUMBER: US/09/816,460C
;  CURRENT FILING DATE:  2001-03-23
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic primer
US-09-816-460C-20

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1543 AGAGTAGGGAAGGAA 1557
              |||||  |||||||||
Db         19 AGAGTGGGGAAGGAA 5


RESULT 3129
US-09-510-378-224/c
; Sequence 224, Application US/09510378
; Publication No. US20030165823A1
;   GENERAL INFORMATION:
;        APPLICANT: Cronin, Maureen T.
;                   Miyada, Charles Garrett
;                   Hubbell, Earl A.
;                   Chee, Mark
;                   Fodor, Stephen P.A.
;                   Huang, Xiaohua C.
;                   Lipshutz, Robert J.
;                   Lobban, Peter E.
;                   Morris, Macdonald S.
;                   Sheldon, Edward L.
;        TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
;                            Detecting Cystic Fibrosis
```

```
                  |||||||||||||| |
Db          1 TGGTGCACTTCTTCC 15


RESULT 3126
US-09-946-374-469/c
; Sequence 469, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C1
;  CURRENT APPLICATION NUMBER: US/09/946,374
;  CURRENT FILING DATE:  2001-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/099536
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099602
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099642
;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099741
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099754
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099763
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099792
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099808
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099812
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099815
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/099816
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 60/100385
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100661
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100662
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100664
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100683
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100684
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100710
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100711
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100848
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100849
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/100919
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/100930
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/101014
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101068
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101071
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/101279
;  PRIOR FILING DATE: 1998-09-22
;  PRIOR APPLICATION NUMBER: 60/101471
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101472
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101474
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101475
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101476
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101477
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101479
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: 60/101738
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101741
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101743
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101915
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/101916
;  PRIOR FILING DATE: 1998-09-24
;  PRIOR APPLICATION NUMBER: 60/102207
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102240
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102307
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 60/102330
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;  NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 467
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-824-322B-467

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2098 TTCAAACGGGGGCCT 2112
              ||||||| |||||||
Db         16 TTCAAACTGGGGCCT 2


RESULT 3123
US-09-232-785-218/c
; Sequence 218, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
;  APPLICANT:  International Paper Co.
;  APPLICANT:  Echt, Craig. S
;  APPLICANT:  Nelson, C. Dana
;  TITLE OF INVENTION:  MICROSATELITE DNA MARKERS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE:  4481/1E188US1
;  CURRENT APPLICATION NUMBER: US/09/232,785
;  CURRENT FILING DATE:  1999-01-19
;  PRIOR APPLICATION NUMBER:  09/232,884
;  PRIOR FILING DATE:  1999-01-15
;  NUMBER OF SEQ ID NOS:  397
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 218
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Pinus taeda L.
US-09-232-785-218

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        228 GGAGCAGCAATGGGA 242
              ||||||| ||||||||
Db         20 GGAGCAACAATGGGA 6


RESULT 3124
US-09-784-674-553
; Sequence 553, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,674
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: No. US20030054346A1 available
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/021,701
;             FILING DATE: 10-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Choi, Wendy A.
;             REGISTRATION NUMBER: 36,697
;             REFERENCE/DOCKET NUMBER: 10971464-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-236-2386
;             TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 553:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 553:
US-09-784-674-553

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||| ||||||||
Db          6 TTTTTTCTTTTTTAA 20


RESULT 3125
US-09-949-427-228
; Sequence 228, Application US/09949427
; Publication No. US20030054418A1
; GENERAL INFORMATION:
;  APPLICANT: Bodnar, Jackie S.
;  APPLICANT:  Castellani, Lawrence W.
;  APPLICANT:  Chatterjee, Aurobindo
;  APPLICANT:  de Jong, Pieter
;  APPLICANT:  Lusis, Aldons J.
;  APPLICANT:  Ohmen, Jeff
;  APPLICANT:  Ross, David
;  APPLICANT:  Tafuri, Sherrie
;  APPLICANT:  Wu, Chenyan
;  TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
;  FILE REFERENCE: 02810.0014.NPUS02
;  CURRENT APPLICATION NUMBER: US/09/949,427
;  CURRENT FILING DATE:  2001-09-07
;  PRIOR APPLICATION NUMBER: 60/231,322
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Primer
US-09-949-427-228

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2427 TGGTGCACTTCTTAC 2441
```

```
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-I
;  CURRENT APPLICATION NUMBER: US/09/898,234
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hybridization
;   OTHER INFORMATION: probe
US-09-898-234-42

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1964 TAAATATTTACCTTG 1978
                || ||||||||||||
Db         15 TATATATTTACCTTG 1


RESULT 3120
US-09-899-429A-52/c
; Sequence 52, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98-385-J
;  CURRENT APPLICATION NUMBER: US/09/899,429A
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/792,356
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1955-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: hybridization
;   OTHER INFORMATION: probe
US-09-899-429A-52

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1964 TAAATATTTACCTTG 1978
                || ||||||||||||
Db         15 TATATATTTACCTTG 1


RESULT 3121
US-09-792-356-42/c
; Sequence 42, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-G
;  CURRENT APPLICATION NUMBER: US/09/792,356
;  CURRENT FILING DATE:  2001-08-17
;  PRIOR APPLICATION NUMBER: 08/477,639
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hybridization
;   OTHER INFORMATION: probe
US-09-792-356-42

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1964 TAAATATTTACCTTG 1978
                || ||||||||||||
Db         15 TATATATTTACCTTG 1


RESULT 3122
US-09-824-322B-467/c
; Sequence 467, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Butler, Madeline M.
;  APPLICANT:  Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALP
;  TITLE OF INVENTION:  ALPHA) EXPRESSION
;  FILE REFERENCE: ISPH-0501
;  CURRENT APPLICATION NUMBER: US/09/824,322B
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 09/313,932
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: US 09/166,186
;  PRIOR FILING DATE: 1998-10-05
```

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;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US 09/290,640
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-802-669-78

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2441 CGACTTTTTTGAGAC 2455
              || ||||||||||||
Db          1 CGGCTTTTTTGAGAC 15


RESULT 3116
US-09-854-883-130
; Sequence 130, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/09/854,883
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 130
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-130

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2003 CTTCTTCAGAGATCA 2017
              | ||||||||||||||
Db          6 CATCTTCAGAGATCA 20


RESULT 3117
US-09-854-883-210/c
; Sequence 210, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/09/854,883
;  CURRENT FILING DATE:  2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 210
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-210

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        479 GGCCGCCAGAGCCAG 493
              ||||||||||||| ||
Db         18 GGCCGCCAGAGCGAG 4


RESULT 3118
US-09-899-422-42/c
; Sequence 42, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
;  APPLICANT:  Himmler, Adolph
;  APPLICANT:  Maurer-Fogy, Ingrid
;  APPLICANT:  Stratowa, Christian
;  TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
;  TITLE OF INVENTION:  Them
;  FILE REFERENCE: 98,385-H
;  CURRENT APPLICATION NUMBER: US/09/899,422
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 09/525,998
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 08/383,676
;  PRIOR FILING DATE: 1995-02-01
;  PRIOR APPLICATION NUMBER: 08/153,287
;  PRIOR FILING DATE: 1993-11-17
;  PRIOR APPLICATION NUMBER: 07/821,750
;  PRIOR FILING DATE: 1992-01-02
;  PRIOR APPLICATION NUMBER: 07/511,430
;  PRIOR FILING DATE: 1990-04-20
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Hybridization
;   OTHER INFORMATION: probe
US-09-899-422-42

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1964 TAAATATTTACCTTG 1978
              || ||||||||||||
Db         15 TATATATTTACCTTG 1


RESULT 3119
US-09-898-234-42/c
; Sequence 42, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
;  APPLICANT: Hauptmann, Rudolph
```

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Qy       1492 GGAGAAAATGGAGAA 1506
              ||||||||||||| |
Db         15 GGAGAAAATGGAGCA 1


RESULT 3112
US-09-734-846-16/c
; Sequence 16, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Dean, Nicholas M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Nickoloff, Brian J.
;  APPLICANT:  Zhang, QingQing
;  TITLE OF INVENTION:  Antisense Modulation of bcl-x Expression
;  FILE REFERENCE:  ISPH-0528
;  CURRENT APPLICATION NUMBER: US/09/734,846
;  CURRENT FILING DATE:  2000-12-12
;  PRIOR APPLICATION NUMBER:      09/277,020
;  PRIOR FILING DATE:      1998-03-26
;  PRIOR APPLICATION NUMBER:      09/167,921
;  PRIOR FILING DATE:      1998-10-07
;  PRIOR APPLICATION NUMBER:  09/323,743
;  PRIOR FILING DATE:  1999-06-02
;  NUMBER OF SEQ ID NOS:  74
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-734-846-16

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2104 CGGGGGCCTTCTGGT 2118
              ||||| |||||||||
Db         20 CGGGGTCCTTCTGGT 6


RESULT 3113
US-09-752-983-214/c
; Sequence 214, Application US/09752983
; Patent No. US20010016575A1
;  GENERAL INFORMATION:
;    APPLICANT:  Loren J. Miraglia, Pamela Nero, Mark J.
;    APPLICANT:  Graham, Brett P. Monia
;    TITLE OF INVENTION:  ANTISENSE MODULATION OF HUMAN MDM2
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  271
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Jane Massey Licata
;      STREET:  66 East Main Street
;      CITY:  Marlton
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  08053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  WORDPERFECT 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/752,983
;      FILING DATE:  02-Jan-2001
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/280,805
;      FILING DATE:  <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Licata, Jane Massey
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  ISPH-0346
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-810-1515
;      TELEFAX:  609-810-1454
;  INFORMATION FOR SEQ ID NO:  214:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    ANTI-SENSE:  Yes
US-09-752-983-214

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2520 TTTATTCATATATAT 2534
              |||||||| ||||||
Db         15 TTTATTCACATATAT 1


RESULT 3114
US-09-758-881-100/c
; Sequence 100, Application US/09758881
; Patent No. US20010029250A1
; GENERAL INFORMATION:
;  APPLICANT:  Karras, James G
;  TITLE OF INVENTION:  Antisense Oligonucleotide Modulation of STAT3
;  TITLE OF INVENTION:  Expression
;  FILE REFERENCE:  ISPH-0532
;  CURRENT APPLICATION NUMBER: US/09/758,881
;  CURRENT FILING DATE:  2001-01-11
;  PRIOR APPLICATION NUMBER:  PCT/US00/09054
;  PRIOR FILING DATE:  2000-04-06
;  PRIOR APPLICATION NUMBER:  09/288,461
;  PRIOR FILING DATE:  1999-04-08
;  NUMBER OF SEQ ID NOS:  152
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 100
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-100

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2673 AGTGTGTGTGGGTGA 2687
              |||| ||||||||||
Db         16 AGTGAGTGTGGGTGA 2


RESULT 3115
US-09-802-669-78
; Sequence 78, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
;  APPLICANT: Dean, Nicholas M.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Wyatt, Jacqueline
;  APPLICANT:  Zhang, Hong
;  TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
;  FILE REFERENCE: ISPH-545
;  CURRENT APPLICATION NUMBER: US/09/802,669
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: US 09/665,615
```

```
;  PRIOR APPLICATION NUMBER: 09/389,283
;  PRIOR FILING DATE: 1999-09-02
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-352-586-33

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3109
US-10-352-586-33/c
; Sequence 33, Application US/10352586
; Publication No. US20030187240A1
; GENERAL INFORMATION:
;  APPLICANT: Cook, Phillip Dan
;  APPLICANT:  Kawasaki, Andrew
;  TITLE OF INVENTION: 2'-Modified Oligonucleotides
;  FILE REFERENCE: ISIS5137
;  CURRENT APPLICATION NUMBER: US/10/352,586
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 09/389,283
;  PRIOR FILING DATE: 1999-09-02
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-10-352-586-33

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3110
US-10-400-382-87/c
; Sequence 87, Application US/10400382
; Publication No. US20030190659A1
; GENERAL INFORMATION:
;  APPLICANT: LaCasse, Eric
;  APPLICANT:  McManus, Daniel
;  APPLICANT:  Durkin, Jonathan P.
;  TITLE OF INVENTION: Antisense IAP Nucleobase Oligomers and
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 07891/025004
;  CURRENT APPLICATION NUMBER: US/10/400,382
;  CURRENT FILING DATE:  2003-03-27
;  PRIOR APPLICATION NUMBER: US 60/367,853
;  PRIOR FILING DATE: 2002-03-27
;  NUMBER OF SEQ ID NOS: 460
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: based on Homo sapiens.
;   OTHER INFORMATION: Each nucleobase may be part of a ribonucleotide,
;   OTHER INFORMATION: deoxyribonucleotide, or nucleotide analog
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 4, 13, 17
;   OTHER INFORMATION: n = T or U
US-10-400-382-87

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTTT 2177
              || ||| ||||||||  |
Db         19 TTNTCCNTTTTTTTTNCT 2


RESULT 3111
US-08-908-453-9/c
; Sequence 9, Application US/08908453
; Publication No. US20010016332A1
;  GENERAL INFORMATION:
;    APPLICANT:  Ruvkun, Gary
;    APPLICANT:  Morris, Jason
;    APPLICANT:  Tissenbaum, Heidi
;    TITLE OF INVENTION:  AGE-1 POLYPEPTIDES AND RELATED
;    TITLE OF INVENTION:  MOLECULES AND METHODS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/908,453
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US97/13914
;      FILING DATE:  07-AUG-1997
;      APPLICATION NUMBER:  60/023,382
;      FILING DATE:  07-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  08472/704WO2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other
US-08-908-453-9

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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```
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 19 bases
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-996-263-33

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3105
US-09-370-541-4
; Sequence 4, Application US/09370541
; Publication No. US20030088079A1
; GENERAL INFORMATION:
;  APPLICANT: Manoharan, Muthiah
;  APPLICANT: Cook, Phillip Dan
;  APPLICANT: Prakash, Thazha P
;  APPLICANT: Kawasaki, Andrew M
;  TITLE OF INVENTION: Aminoxxy-Modified Nucleosidic Compounds And Oligomeric
;  TITLE OF INVENTION: Compounds Prepared Therefrom
;  FILE REFERENCE: ISIS3993
;  CURRENT APPLICATION NUMBER: US/09/370,541
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: 09/130,973
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 09/016,520
;  EARLIER FILING DATE: 1998-01-30
;  EARLIER APPLICATION NUMBER: 60/037,143
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: 09/344,260
;  EARLIER FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: antisense
;   OTHER INFORMATION: sequence
US-09-370-541-4

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3106
US-09-370-541-4/c
; Sequence 4, Application US/09370541
; Publication No. US20030088079A1
; GENERAL INFORMATION:
;  APPLICANT: Manoharan, Muthiah
;  APPLICANT: Cook, Phillip Dan
;  APPLICANT: Prakash, Thazha P
;  APPLICANT: Kawasaki, Andrew M
;  TITLE OF INVENTION: Aminoxxy-Modified Nucleosidic Compounds And Oligomeric
;  TITLE OF INVENTION: Compounds Prepared Therefrom
;  FILE REFERENCE: ISIS3993
;  CURRENT APPLICATION NUMBER: US/09/370,541
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: 09/130,973
;  EARLIER FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: 09/016,520
;  EARLIER FILING DATE: 1998-01-30
;  EARLIER APPLICATION NUMBER: 60/037,143
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: 09/344,260
;  EARLIER FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: antisense
;   OTHER INFORMATION: sequence
US-09-370-541-4

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3107
US-09-791-190A-16/c
; Sequence 16, Application US/09791190A
; Publication No. US20030104372A1
; GENERAL INFORMATION:
;  APPLICANT: Pyrosequencing AB
;  APPLICANT:  Ahmadian, Afshin
;  APPLICANT:  Lundeberg, Joakim
;  APPLICANT:  Nyren, Pal
;  TITLE OF INVENTION: Allele Specific Primer Extension Assay
;  FILE REFERENCE: Docket 14259
;  CURRENT APPLICATION NUMBER: US/09/791,190A
;  CURRENT FILING DATE:  2002-09-25
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Primer
US-09-791-190A-16

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        431 CCCCTGCACCAGCCG 445
              ||||||||||||| |
Db         16 CCCCTGCACCAGCAG 2


RESULT 3108
US-10-352-586-33
; Sequence 33, Application US/10352586
; Publication No. US20030187240A1
; GENERAL INFORMATION:
;  APPLICANT: Cook, Phillip Dan
;  APPLICANT:  Kawasaki, Andrew
;  TITLE OF INVENTION: 2'-Modified Oligonucleotides
;  FILE REFERENCE: ISIS5137
;  CURRENT APPLICATION NUMBER: US/10/352,586
;  CURRENT FILING DATE:  2003-01-28
```

```
;  CURRENT APPLICATION NUMBER: US/09/969,373
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 09/754,853
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 09/760,427
;  PRIOR FILING DATE: 2001-01-13
;  PRIOR APPLICATION NUMBER: US 09/855,768
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2979
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-969-373-2979

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGTC 2331
              |||| ||||||||||
Db          5 TTGTAGCTGCTTGTC 19


RESULT 3102
US-09-969-373-3523
; Sequence 3523, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
;  APPLICANT: Effertz, Roger J.
;  APPLICANT:  Hauge, Brian M.
;  TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
;  FILE REFERENCE: 38-10(52679)A
;  CURRENT APPLICATION NUMBER: US/09/969,373
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 09/754,853
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 09/760,427
;  PRIOR FILING DATE: 2001-01-13
;  PRIOR APPLICATION NUMBER: US 09/855,768
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3523
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-969-373-3523

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1189 ACGAAATGAGATGGC 1203
              || ||||||||||||
Db          2 ACCAAATGAGATGGC 16


RESULT 3103
US-09-996-263-33
; Sequence 33, Application US/09996263
; Publication No. US20030004325A1
;   GENERAL INFORMATION:
;        APPLICANT: Phillip Dan Cook
;                   Andrew Kawasaki
;        TITLE OF INVENTION: Sugar Modified Oligonucleotides
;        NUMBER OF SEQUENCES: 37
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325A1ris
;             STREET: One Liberty Place - 46th Floor
;             CITY: Philadelphia
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch disk, 720 Kb
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WordPerfect 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/996,263
;             FILING DATE: 28-No. US20030004325A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/471,973
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Joseph Lucci
;             REGISTRATION NUMBER: 33,307
;             REFERENCE/DOCKET NUMBER: ISIS-2005
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-568-3100
;             TELEFAX: 215-568-3439
;   INFORMATION FOR SEQ ID NO: 33:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 19 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-996-263-33

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3104
US-09-996-263-33/c
; Sequence 33, Application US/09996263
; Publication No. US20030004325A1
;   GENERAL INFORMATION:
;        APPLICANT: Phillip Dan Cook
;                   Andrew Kawasaki
;        TITLE OF INVENTION: Sugar Modified Oligonucleotides
;        NUMBER OF SEQUENCES: 37
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325A1ris
;             STREET: One Liberty Place - 46th Floor
;             CITY: Philadelphia
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch disk, 720 Kb
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WordPerfect 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/996,263
;             FILING DATE: 28-No. US20030004325A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/471,973
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Joseph Lucci
;             REGISTRATION NUMBER: 33,307
;             REFERENCE/DOCKET NUMBER: ISIS-2005
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-568-3100
;             TELEFAX: 215-568-3439
;   INFORMATION FOR SEQ ID NO: 33:
```

```
;   ORGANISM: Homo sapiens
US-10-138-674-1503

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   60.0%;  Pred. No. 2.9e+03;
  Matches    9;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1340 CATTTCAGCCTGATT 1354
              ||:::|||||:|| :
Db          1 CAUUUCAGCCUGAAU 15


RESULT 3097
US-10-680-341-14/c
; Sequence 14, Application US/10680341
; Publication No. US20040091923A1
; GENERAL INFORMATION:
;  APPLICANT: Reyes, Antonio A.
;  APPLICANT:  Wallace, Robert B.
;  APPLICANT:  Ugozzoli, Luis A
;  TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
;  FILE REFERENCE: 3239-0105P
;  CURRENT APPLICATION NUMBER: US/10/680,341
;  CURRENT FILING DATE:  2003-10-06
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Description of Combined DNA/RNA Molecule: URACIL
;   OTHER INFORMATION: NUCLEOSIDE IS A RIBONUCLEOSIDE
US-10-680-341-14

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1936 TAAGGTAATGGTTGG 1950
              ||||| |||||||||
Db         18 TAAGGGAATGGTTGG 4


RESULT 3098
US-10-680-341-16/c
; Sequence 16, Application US/10680341
; Publication No. US20040091923A1
; GENERAL INFORMATION:
;  APPLICANT: Reyes, Antonio A.
;  APPLICANT:  Wallace, Robert B.
;  APPLICANT:  Ugozzoli, Luis A
;  TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
;  FILE REFERENCE: 3239-0105P
;  CURRENT APPLICATION NUMBER: US/10/680,341
;  CURRENT FILING DATE:  2003-10-06
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-680-341-16

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1936 TAAGGTAATGGTTGG 1950
              ||||| |||||||||
Db         18 TAAGGGAATGGTTGG 4


RESULT 3099
US-10-287-949A-1414/c
; Sequence 1414, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1414
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1414

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        474 GGCCCGGCCGCCAGA 488
              | ||||||||||||||
Db         15 GACCCGGCCGCCAGA 1


RESULT 3100
US-10-287-949A-1503
; Sequence 1503, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1503
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1503

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   60.0%;  Pred. No. 2.9e+03;
  Matches    9;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1340 CATTTCAGCCTGATT 1354
              ||:::|||||:|| :
Db          1 CAUUUCAGCCUGAAU 15


RESULT 3101
US-09-969-373-2979
; Sequence 2979, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
;  APPLICANT: Effertz, Roger J.
;  APPLICANT:  Hauge, Brian M.
;  TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
;  FILE REFERENCE: 38-10(52679)A
```

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-10-108-260A-4912

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1944 TGGTTGGTTTTTGTG 1958
              ||||||| |||||||
Db          3 TGGTTGGATTTTGTG 17


RESULT 3093
US-10-349-143-4649/c
; Sequence 4649, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4649
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..18
;   OTHER INFORMATION: upstream amplification primer 99-16740 for SEQ 715,
US-10-349-143-4649

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1501 GGAGAAACACAGGAA 1515
              ||||||||| |||||
Db         16 GGAGAAACAGAGGAA 2


RESULT 3094
US-10-349-143-7270
; Sequence 7270, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7270
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..18
;   OTHER INFORMATION: upstream amplification primer 99-3373 for SEQ 3336,
US-10-349-143-7270

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1907 CAGATCAACAATACC 1921
              ||| ||||||||||
Db          3 CAGCTCAACAATACC 17


RESULT 3095
US-10-138-674-1414/c
; Sequence 1414, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1414
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-1414

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        474 GGCCCGGCCGCCAGA 488
              | ||||||||||||||
Db         15 GACCCGGCCGCCAGA 1


RESULT 3096
US-10-138-674-1503
; Sequence 1503, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1503
;   LENGTH: 18
;   TYPE: RNA
```

```
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: CAH oligo 7 for mutation site 2
US-10-152-297-77

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        108 TTGGGGGCTGGGGGG 122
              ||||||||||| |||
Db         17 TTGGGGGCTGGAGGG 3


RESULT 3089
US-10-156-433-69/c
; Sequence 69, Application US/10156433
; Publication No. US20030144489A1
; GENERAL INFORMATION:
;  APPLICANT: Burgin, Alex
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Bellon, Laurent
;  APPLICANT:  Zinnen, Shawn
;  APPLICANT:  Ribozyme Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
;  FILE REFERENCE: MBHB00-943-E (500.007)
;  CURRENT APPLICATION NUMBER: US/10/156,433
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: US 10/112,814
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: US 09/216,584
;  PRIOR FILING DATE: 1998-12-18
;  PRIOR APPLICATION NUMBER: US 09/094,381
;  PRIOR FILING DATE: 1998-06-09
;  PRIOR APPLICATION NUMBER: US 60/068,212
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: US 60/049,002
;  PRIOR FILING DATE: 1997-06-09
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Position X18 of library synthesis
US-10-156-433-69

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        676 GCCTCACCAGATGGA 690
              |||||| ||||||||
Db         17 GCCTCATCAGATGGA 3


RESULT 3090
US-10-297-068-21/c
; Sequence 21, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
;  APPLICANT: INOKO, Hidetoshi
;  APPLICANT:  KAGIYA, Taeko
;  APPLICANT:  ICHIHARA, Tatsuo
;  APPLICANT:  Matsumura, Yoshiyuki
;  APPLICANT:  MORIYA, Shogo
;  APPLICANT:  NISHIDA, Michio
;  TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
;  FILE REFERENCE: 1314OP1174
;  CURRENT APPLICATION NUMBER: US/10/297,068
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: JP 2000-164798
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 1298
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-21

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1326 AGAACTGCTTGTCTC 1340
              ||||||||| |||||
Db         18 AGAACTGCTCGTCTC 4


RESULT 3091
US-10-297-068-1061/c
; Sequence 1061, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
;  APPLICANT: INOKO, Hidetoshi
;  APPLICANT:  KAGIYA, Taeko
;  APPLICANT:  ICHIHARA, Tatsuo
;  APPLICANT:  Matsumura, Yoshiyuki
;  APPLICANT:  MORIYA, Shogo
;  APPLICANT:  NISHIDA, Michio
;  TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
;  FILE REFERENCE: 1314OP1174
;  CURRENT APPLICATION NUMBER: US/10/297,068
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: JP 2000-164798
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 1298
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1061
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1061

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        619 CCACGCACACGCCCT 633
              |||||||| ||||||
Db         18 CCACGCACTCGCCCT 4


RESULT 3092
US-10-108-260A-4912
; Sequence 4912, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20040005560A1el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4912
;   LENGTH: 18
;   TYPE: DNA
```

```
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-239-912-16

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2176
              ||||||||  ||||||
Db         15 CTCCTTTTGTTTTTT 1


RESULT 3085
US-10-239-912-22/c
; Sequence 22, Application US/10239912
; Publication No. US20030212012A1
; GENERAL INFORMATION:
;  APPLICANT: Henry, James L
;  APPLICANT:  Fundytus, Marian E
;  APPLICANT:  Vaudreuil, Terrasse
;  TITLE OF INVENTION: Oligonucleotide For Metabotropic Glutamate Receptor
;  TITLE OF INVENTION:  Type 1 (MGLUR1)
;  FILE REFERENCE: 457-107PCT
;  CURRENT APPLICATION NUMBER: US/10/239,912
;  CURRENT FILING DATE:  2002-09-26
;  PRIOR APPLICATION NUMBER: 60/144,004
;  PRIOR FILING DATE: 1999-07-15
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-239-912-22

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2176
              ||||||||  ||||||
Db         15 CTCCTTTTGTTTTTT 1


RESULT 3086
US-10-239-912-33/c
; Sequence 33, Application US/10239912
; Publication No. US20030212012A1
; GENERAL INFORMATION:
;  APPLICANT: Henry, James L
;  APPLICANT:  Fundytus, Marian E
;  APPLICANT:  Vaudreuil, Terrasse
;  TITLE OF INVENTION: Oligonucleotide For Metabotropic Glutamate Receptor
;  TITLE OF INVENTION:  Type 1 (MGLUR1)
;  FILE REFERENCE: 457-107PCT
;  CURRENT APPLICATION NUMBER: US/10/239,912
;  CURRENT FILING DATE:  2002-09-26
;  PRIOR APPLICATION NUMBER: 60/144,004
;  PRIOR FILING DATE: 1999-07-15
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-239-912-33

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2176
              ||||||||  ||||||
Db         15 CTCCTTTTGTTTTTT 1


RESULT 3087
US-10-403-902A-78/c
; Sequence 78, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
;  APPLICANT: Braun, Andreas
;  APPLICANT:  Bansal, Aruna
;  APPLICANT:  Kleyn, Patrick
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE AND THEIR USE
;  FILE REFERENCE: 24736-2048B
;  CURRENT APPLICATION NUMBER: US/10/403,902A
;  CURRENT FILING DATE:  2003-07-21
;  PRIOR APPLICATION NUMBER: 09/802,640
;  PRIOR FILING DATE: 2001-03-09
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-403-902A-78

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        647 CTGGCCGAGAACCTG 661
              ||||||||||  ||||
Db         15 CTGGCCGAGATCCTG 1


RESULT 3088
US-10-152-297-77/c
; Sequence 77, Application US/10152297
; Publication No. US20030077621A1
; GENERAL INFORMATION:
;  APPLICANT: Shultz, John W
;  APPLICANT:  Lewis, Martin K.
;  APPLICANT:  Lieppe, Donna
;  APPLICANT:  Mandrekar, Michelle
;  APPLICANT:  Kephart, Daniel
;  APPLICANT:  Rhodes, Richard B.
;  APPLICANT:  Andrews, Christine A.
;  APPLICANT:  Hartnett, James R.
;  APPLICANT:  Gu, Trent
;  APPLICANT:  Olson, Ryan J.
;  APPLICANT:  Wood, Keith W.
;  APPLICANT:  Welch, Roy
;  TITLE OF INVENTION: Nucleic Acid Detection
;  FILE REFERENCE: PRO-104 6868/75529
;  CURRENT APPLICATION NUMBER: US/10/152,297
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: US/09/383,316
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: 09/252,436
;  PRIOR FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: 09/042,287
;  PRIOR FILING DATE: 1998-03-13
;  PRIOR APPLICATION NUMBER: 09/358,972
;  PRIOR FILING DATE: 1999-07-21
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
```

```
  Best Local Similarity   82.4%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1241 TGTAAAGAATTCACAGA 1257
              ||||||||| ||: |||
Db         17 TGTAAAGAACTCRTAGA 1


RESULT 3081
US-10-027-632-52415/c
; Sequence 52415, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52415
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-52415

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1241 TGTAAAGAATTCACAGA 1257
              ||||||||| ||: |||
Db         17 TGTAAAGAACTCRTAGA 1


RESULT 3082
US-09-804-014A-59/c
; Sequence 59, Application US/09804014A
; Publication No. US20030064489A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Li
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Spaderna, Steven
;  APPLICANT:  Majumder, Kumud
;  TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
;  FILE REFERENCE: 15966-721 US
;  CURRENT APPLICATION NUMBER: US/09/804,014A
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: 60/188,316
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: 60/188,277
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: 60/189,139
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: 60/189,140
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: 60/190,401
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/190,231
;  PRIOR FILING DATE: 2000-03-17
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide primer
US-09-804-014A-59

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1602 TCCTGGCCTGGGGGA 1616
              ||||||||||| ||||
Db         17 TCCTGGCCTGTGGGA 3


RESULT 3083
US-10-239-912-5/c
; Sequence 5, Application US/10239912
; Publication No. US20030212012A1
; GENERAL INFORMATION:
;  APPLICANT: Henry, James L
;  APPLICANT:  Fundytus, Marian E
;  APPLICANT:  Vaudreuil, Terrasse
;  TITLE OF INVENTION: Oligonucleotide For Metabotropic Glutamate Receptor
;  TITLE OF INVENTION:  Type 1 (MGLUR1)
;  FILE REFERENCE: 457-107PCT
;  CURRENT APPLICATION NUMBER: US/10/239,912
;  CURRENT FILING DATE:  2002-09-26
;  PRIOR APPLICATION NUMBER: 60/144,004
;  PRIOR FILING DATE: 1999-07-15
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-239-912-5

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2176
              |||||||| ||||||
Db         15 CTCCTTTTGTTTTTT 1


RESULT 3084
US-10-239-912-16/c
; Sequence 16, Application US/10239912
; Publication No. US20030212012A1
; GENERAL INFORMATION:
;  APPLICANT: Henry, James L
;  APPLICANT:  Fundytus, Marian E
;  APPLICANT:  Vaudreuil, Terrasse
;  TITLE OF INVENTION: Oligonucleotide For Metabotropic Glutamate Receptor
;  TITLE OF INVENTION:  Type 1 (MGLUR1)
;  FILE REFERENCE: 457-107PCT
;  CURRENT APPLICATION NUMBER: US/10/239,912
;  CURRENT FILING DATE:  2002-09-26
;  PRIOR APPLICATION NUMBER: 60/144,004
;  PRIOR FILING DATE: 1999-07-15
;  NUMBER OF SEQ ID NOS: 39
```

```
; GENERAL INFORMATION:
;  APPLICANT: COLOSI, Peter
;  TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE IN RECOMBINANT ADENO-ASSOCIATED VIRUS
;  TITLE OF INVENTION:  VIRION PRODUCTION
;  FILE REFERENCE: 0800-0023
;  CURRENT APPLICATION NUMBER: US/09/839,583
;  CURRENT FILING DATE:  2001-04-20
;  PRIOR APPLICATION NUMBER: 60/200,453
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: oligo
US-09-839-583-5

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2057 ACTAGTTAATAAGTG 2071
             ||||||||||.||||
Db         18 ACTAGTTAATTAGTG 4


RESULT 3078
US-10-027-632-52400/c
; Sequence 52400, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52400
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-52400

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1241 TGTAAAGAATTCACAGA 1257
             |||||||||.||:.|||
Db         17 TGTAAAGAACTCRTAGA 1


RESULT 3079
US-10-027-632-52400/c
; Sequence 52400, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52400
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-52400

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1241 TGTAAAGAATTCACAGA 1257
             |||||||||.||:.|||
Db         17 TGTAAAGAACTCRTAGA 1


RESULT 3080
US-10-027-632-52415/c
; Sequence 52415, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52415
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-52415

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
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;  APPLICANT:  Hong, Zhi
;  APPLICANT:  Ferrari, Eric
;  TITLE OF INVENTION: HCV REPLICASE COMPLEXES
;  FILE REFERENCE: IN01165
;  CURRENT APPLICATION NUMBER: US/09/828,034
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: U.S. 60/195,852
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-15

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTT 2179
              || |||||||||||||
Db         15 CTGTTTTTTTTTTTT 1


RESULT 3074
US-09-802-640-78/c
; Sequence 78, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
;  APPLICANT: Braun, Andreas
;  APPLICANT:  Bonsal Aruna
;  APPLICANT:  Kleyn Patrick
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE AND THEIR USE
;  FILE REFERENCE: 24736-2048
;  CURRENT APPLICATION NUMBER: US/09/802,640
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-802-640-78

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        647 CTGGCCGAGAACCTG 661
              ||||||||||| ||||
Db         15 CTGGCCGAGATCCTG 1


RESULT 3075
US-09-924-981-24/c
; Sequence 24, Application US/09924981
; Publication No. US20030049624A1
; GENERAL INFORMATION:
;  APPLICANT: Andrews, Christine N.
;  APPLICANT:  Olson, Ryan J.
;  APPLICANT:  Shultz, John W.
;  TITLE OF INVENTION: Pyrophosphorolysis and Incorporation of Nucleotide
;  TITLE OF INVENTION:  Method for Nucleic Acid Detection
;  FILE REFERENCE: 6868/82379
;  CURRENT APPLICATION NUMBER: US/09/924,981
;  CURRENT FILING DATE:  2001-08-07
;  PRIOR APPLICATION NUMBER: 09/358,972
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: 09/788,847
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 09/406,064
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: 09/252,436
;  PRIOR FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: 09/042,287
;  PRIOR FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-924-981-24

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        108 TTGGGGGCTGGGGGG 122
              ||||||||||| |||
Db         17 TTGGGGGCTGGAGGG 3


RESULT 3076
US-09-788-847-27/c
; Sequence 27, Application US/09788847
; Publication No. US20030194699A1
; GENERAL INFORMATION:
;  APPLICANT: Shultz, John W
;  APPLICANT:  Lewis, Martin K.
;  APPLICANT:  Leippe, Donna
;  APPLICANT:  Mandrekar, Michelle
;  APPLICANT:  Kephart, Daniel
;  APPLICANT:  Rhodes, Richard B
;  APPLICANT:  Andrews, Christine A.
;  APPLICANT:  Hartnett, James R.
;  APPLICANT:  Gu, Trent
;  APPLICANT:  Wood, Keith V.
;  APPLICANT:  Welch, Roy
;  TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
;  FILE REFERENCE: PRO-107.0 (6868/75532)
;  CURRENT APPLICATION NUMBER: US/09/788,847
;  CURRENT FILING DATE:  2001-02-20
;  PRIOR APPLICATION NUMBER: 09/406,064
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: 09/252,436
;  PRIOR FILING DATE: 1999-02-18
;  PRIOR APPLICATION NUMBER: 09/042,287
;  PRIOR FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-788-847-27

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        108 TTGGGGGCTGGGGGG 122
              ||||||||||| |||
Db         17 TTGGGGGCTGGAGGG 3


RESULT 3077
US-09-839-583-5/c
; Sequence 5, Application US/09839583
; Publication No. US20020052485A1
```

```
;  CURRENT FILING DATE:  2003-11-13
;  PRIOR APPLICATION NUMBER: US/09/653,225
;  PRIOR FILING DATE: 2000-08-31
;  PRIOR APPLICATION NUMBER: 60/197,769
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/150,713
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 5586
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 703
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-712-672-703

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        626 CACGCCCTGGATGCC 640
              || |||||:|||:|||
Db          2 CAGGCCCUGGAUGCC 16


RESULT 3070
US-10-712-672-1121/c
; Sequence 1121, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
;  FILE REFERENCE: MBHB00-882-C (400/019)
;  CURRENT APPLICATION NUMBER: US/10/712,672
;  CURRENT FILING DATE:  2003-11-13
;  PRIOR APPLICATION NUMBER: US/09/653,225
;  PRIOR FILING DATE: 2000-08-31
;  PRIOR APPLICATION NUMBER: 60/197,769
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/150,713
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 5586
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1121
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-712-672-1121

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        458 AGCCAGCAGCAGGCC 472
              | |||||||||||||
Db         16 ATCCAGCAGCAGGCC 2


RESULT 3071
US-10-712-672-1841
; Sequence 1841, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
;  FILE REFERENCE: MBHB00-882-C (400/019)
;  CURRENT APPLICATION NUMBER: US/10/712,672
;  CURRENT FILING DATE:  2003-11-13
;  PRIOR APPLICATION NUMBER: US/09/653,225
;  PRIOR FILING DATE: 2000-08-31
;  PRIOR APPLICATION NUMBER: 60/197,769
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/150,713
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 5586
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1841
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-712-672-1841

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        288 GCCCCGCGCCACCCC 302
              |||||| ||||||||
Db          3 GCCCCGGGCCACCCC 17


RESULT 3072
US-09-790-417-220/c
; Sequence 220, Application US/09790417
; Patent No. US20010031470A1
; GENERAL INFORMATION:
;  APPLICANT: Shultz, John W
;  APPLICANT:  Lewis, Martin K.
;  APPLICANT:  Lieppe, Donna
;  APPLICANT:  Mandrekar, Michelle
;  APPLICANT:  Kephart, Daniel
;  APPLICANT:  Rhodes, Richard B.
;  APPLICANT:  Andrews, Christine A.
;  APPLICANT:  Hartnett, James R.
;  APPLICANT:  Gu, Trent
;  APPLICANT:  Olson, Ryan J.
;  APPLICANT:  Wood, Keith W.
;  APPLICANT:  Welch, Roy
;  TITLE OF INVENTION: Nucleic Acid Detection
;  FILE REFERENCE: Pro-103 6868/75528
;  CURRENT APPLICATION NUMBER: US/09/790,417
;  CURRENT FILING DATE:  2001-02-22
;  PRIOR APPLICATION NUMBER: 09/358,972
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: 09/042,287
;  PRIOR FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 290
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: CAH oligo 7 for mutation site 2
US-09-790-417-220

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 2.9e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        108 TTGGGGGCTGGGGGG 122
              |||||||||| |||
Db         17 TTGGGGGCTGGAGGG 3


RESULT 3073
US-09-828-034-15/c
; Sequence 15, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
;  APPLICANT: Zhong, Weidong
```

```
RESULT 3065
US-10-287-949A-1634
; Sequence 1634, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1634
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-1634

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   60.0%;  Pred. No. 2.7e+03;
  Matches    9;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2698 TGGAATTGAACTCTC 2712
              :||||::||||: :|
Db          3 UGGAAUUGAACUAUC 17


RESULT 3066
US-10-287-949A-3296/c
; Sequence 3296, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3296
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus musculus
US-10-287-949A-3296

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2488 GTGATGGGGTAATCT 2502
              ||||||| |||||||
Db         15 GTGATGGAGTAATCT 1


RESULT 3067
US-10-287-949A-6327
; Sequence 6327, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6327
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-6327

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 2.7e+03;
  Matches   13;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAAT 1517
              ||| |||||||||||:
Db          3 AGAGACACAGGAAAU 17


RESULT 3068
US-10-712-672-702
; Sequence 702, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
;  FILE REFERENCE: MBHB00-882-C (400/019)
;  CURRENT APPLICATION NUMBER: US/10/712,672
;  CURRENT FILING DATE:  2003-11-13
;  PRIOR APPLICATION NUMBER: US/09/653,225
;  PRIOR FILING DATE: 2000-08-31
;  PRIOR APPLICATION NUMBER: 60/197,769
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/150,713
;  PRIOR FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 5586
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 702
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-712-672-702

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        626 CACGCCCTGGATGCC 640
              || |||||:|||:|||
Db          3 CAGGCCCUGGAUGCC 17


RESULT 3069
US-10-712-672-703
; Sequence 703, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
;  FILE REFERENCE: MBHB00-882-C (400/019)
;  CURRENT APPLICATION NUMBER: US/10/712,672
```

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;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6327
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-6327

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 2.7e+03;
  Matches   13;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAAT 1517
              ||| ||||||||||:
Db          3 AGAGACACAGGAAAU 17


RESULT 3061
US-10-287-949A-577/c
; Sequence 577, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 577
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-577

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              |||||||||| ||||
Db         17 GACTGCAAAAGTCCT 3


RESULT 3062
US-10-287-949A-578/c
; Sequence 578, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 578
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-578

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              |||||||||| ||||
Db         16 GACTGCAAAAGTCCT 2


RESULT 3063
US-10-287-949A-579/c
; Sequence 579, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 579
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-579

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              |||||||||| ||||
Db         15 GACTGCAAAAGTCCT 1


RESULT 3064
US-10-287-949A-734
; Sequence 734, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 734
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-734

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   13.3%;  Pred. No. 2.7e+03;
  Matches    2;  Conservative   12;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTAACT 2190
              :::::::::: ||:
Db          1 UUUUUUUUUUGACU 15
```

```
Qy       1561 GACTGCAAAAATCCT 1575
              ||||||||||  ||||
Db         16 GACTGCAAAAGTCCT 2
```

RESULT 3056
US-10-138-674-579/c
; Sequence 579, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 579
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-579

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1561 GACTGCAAAAATCCT 1575
              ||||||||||  ||||
Db         15 GACTGCAAAAGTCCT 1
```

RESULT 3057
US-10-138-674-734
; Sequence 734, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 734
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-734

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 13.3%; Pred. No. 2.7e+03;
Matches 2; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2176 TTTTTTTTTTTAACT 2190
              ::::::::::: ||:
Db          1 UUUUUUUUUUUGACU 15
```

RESULT 3058
US-10-138-674-1634
; Sequence 1634, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1634
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1634

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2698 TGGAATTGAACTCTC 2712
              :||||::||||: :|
Db          3 UGGAAUUGAACUAUC 17
```

RESULT 3059
US-10-138-674-3296/c
; Sequence 3296, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3296
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3296

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2488 GTGATGGGGTAATCT 2502
              ||||||| |||||||
Db         15 GTGATGGAGTAATCT 1
```

RESULT 3060
US-10-138-674-6327
; Sequence 6327, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

```
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 1298
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1167
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1167

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        619 CCACGCACACGCCCT 633
              ||||||||| |||||
Db         17 CCACGCACAGGCCCT 3


RESULT 3052
US-10-297-068-1168/c
; Sequence 1168, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
;  APPLICANT: INOKO, Hidetoshi
;  APPLICANT:  KAGIYA, Taeko
;  APPLICANT:  ICHIHARA, Tatsuo
;  APPLICANT:  Matsumura, Yoshiyuki
;  APPLICANT:  MORIYA, Shogo
;  APPLICANT:  NISHIDA, Michio
;  TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
;  FILE REFERENCE: 1314OP1174
;  CURRENT APPLICATION NUMBER: US/10/297,068
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: JP 2000-164798
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 1298
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1168
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1168

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        619 CCACGCACACGCCCT 633
              ||||||| ||||||
Db         17 CCACGCACGCGCCCT 3


RESULT 3053
US-10-608-062-26
; Sequence 26, Application US/10608062
; Publication No. US20040014122A1
; GENERAL INFORMATION:
;  APPLICANT: BREEN, ALEXANDER
;  APPLICANT:  SINGLETON, FREDDIE
;  TITLE OF INVENTION: DETECTION OF SPORE FORMING BACTERIA
;  FILE REFERENCE: B1113P
;  CURRENT APPLICATION NUMBER: US/10/608,062
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US 09/356,677
;  PRIOR FILING DATE: 1999-07-20
;  PRIOR APPLICATION NUMBER: US 09/085,359
;  PRIOR FILING DATE: 1998-05-27
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: clostridium thermoaceticum
US-10-608-062-26

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        368 GCCTACTCCCAGTCG 382
              | ||||||||||||||
Db          3 GACTACTCCCAGTCG 17


RESULT 3054
US-10-138-674-577/c
; Sequence 577, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 577
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-577

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              |||||||||| ||||
Db         17 GACTGCAAAAGTCCT 3


RESULT 3055
US-10-138-674-578/c
; Sequence 578, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 578
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-578

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Fosnaugh, Kathy
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
;  FILE REFERENCE: 400/056 (MBHB01-1110)
;  CURRENT APPLICATION NUMBER: US/10/230,006
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US 60/315,315
;  PRIOR FILING DATE: 2001-08-28
;  NUMBER OF SEQ ID NOS: 2678
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2220
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-230-006-2220

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2002 GCTTCTTCAGAGATC 2016
              ||||||||||||  ||
Db         16 GCTTCTTCAGAGGTC 2


RESULT 3048
US-10-230-006-2223/c
; Sequence 2223, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Fosnaugh, Kathy
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
;  FILE REFERENCE: 400/056 (MBHB01-1110)
;  CURRENT APPLICATION NUMBER: US/10/230,006
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US 60/315,315
;  PRIOR FILING DATE: 2001-08-28
;  NUMBER OF SEQ ID NOS: 2678
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2223
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-230-006-2223

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        828 CTGAGGTCTTCTGCT 842
              | ||||||||||||||
Db         16 CGGAGGTCTTCTGCT 2


RESULT 3049
US-10-297-068-1062/c
; Sequence 1062, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
;  APPLICANT: INOKO, Hidetoshi
;  APPLICANT:  KAGIYA, Taeko
;  APPLICANT:  ICHIHARA, Tatsuo
;  APPLICANT:  Matsumura, Yoshiyuki
;  APPLICANT:  MORIYA, Shogo
;  APPLICANT:  NISHIDA, Michio
;  TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
;  FILE REFERENCE: 1314OP1174
;  CURRENT APPLICATION NUMBER: US/10/297,068
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: JP 2000-164798
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 1298
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1062
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1062

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        619 CCACGCACACGCCCT 633
              ||||||||| |||||
Db         17 CCACGCACAGGCCCT 3


RESULT 3050
US-10-297-068-1165/c
; Sequence 1165, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
;  APPLICANT: INOKO, Hidetoshi
;  APPLICANT:  KAGIYA, Taeko
;  APPLICANT:  ICHIHARA, Tatsuo
;  APPLICANT:  Matsumura, Yoshiyuki
;  APPLICANT:  MORIYA, Shogo
;  APPLICANT:  NISHIDA, Michio
;  TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
;  FILE REFERENCE: 1314OP1174
;  CURRENT APPLICATION NUMBER: US/10/297,068
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: JP 2000-164798
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 1298
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1165
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1165

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        619 CCACGCACACGCCCT 633
              |||||||| ||||||
Db         17 CCACGCACTCGCCCT 3


RESULT 3051
US-10-297-068-1167/c
; Sequence 1167, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
;  APPLICANT: INOKO, Hidetoshi
;  APPLICANT:  KAGIYA, Taeko
;  APPLICANT:  ICHIHARA, Tatsuo
;  APPLICANT:  Matsumura, Yoshiyuki
;  APPLICANT:  MORIYA, Shogo
;  APPLICANT:  NISHIDA, Michio
;  TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
;  FILE REFERENCE: 1314OP1174
;  CURRENT APPLICATION NUMBER: US/10/297,068
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: JP 2000-164798
```

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;  CURRENT FILING DATE:  2003-01-07
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 262
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-338-777-262

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2177
              || ||||||||||||
Db          3 TCATTTTTTTTTTTT 17


RESULT 3043
US-10-230-006-616/c
; Sequence 616, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Fosnaugh, Kathy
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
;  FILE REFERENCE: 400/056 (MBHB01-1110)
;  CURRENT APPLICATION NUMBER: US/10/230,006
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US 60/315,315
;  PRIOR FILING DATE: 2001-08-28
;  NUMBER OF SEQ ID NOS: 2678
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 616
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-230-006-616

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        454 AGGCAGCCAGCAGCA 468
              ||||||||||||| ||
Db         17 AGGCAGCCAGCACCA 3


RESULT 3044
US-10-230-006-787/c
; Sequence 787, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Fosnaugh, Kathy
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
;  FILE REFERENCE: 400/056 (MBHB01-1110)
;  CURRENT APPLICATION NUMBER: US/10/230,006
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US 60/315,315
;  PRIOR FILING DATE: 2001-08-28
;  NUMBER OF SEQ ID NOS: 2678
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 787
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-230-006-787

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2002 GCTTCTTCAGAGATC 2016
              ||||||||||||  ||
Db         17 GCTTCTTCAGAGGTC 3


RESULT 3045
US-10-230-006-1313/c
; Sequence 1313, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Fosnaugh, Kathy
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
;  FILE REFERENCE: 400/056 (MBHB01-1110)
;  CURRENT APPLICATION NUMBER: US/10/230,006
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US 60/315,315
;  PRIOR FILING DATE: 2001-08-28
;  NUMBER OF SEQ ID NOS: 2678
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1313
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-230-006-1313

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        454 AGGCAGCCAGCAGCA 468
              ||||||||||||| ||
Db         15 AGGCAGCCAGCACCA 1


RESULT 3046
US-10-230-006-2137/c
; Sequence 2137, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Fosnaugh, Kathy
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
;  FILE REFERENCE: 400/056 (MBHB01-1110)
;  CURRENT APPLICATION NUMBER: US/10/230,006
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US 60/315,315
;  PRIOR FILING DATE: 2001-08-28
;  NUMBER OF SEQ ID NOS: 2678
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2137
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-230-006-2137

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        454 AGGCAGCCAGCAGCA 468
              ||||||||||||| ||
Db         16 AGGCAGCCAGCACCA 2


RESULT 3047
US-10-230-006-2220/c
; Sequence 2220, Application US/10230006
; Publication No. US20030191077A1
```

US-10-238-700-2758

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||| |||
Db 17 GGCGGGGGCGGGGGC 3

RESULT 3038
US-10-238-700-2800
; Sequence 2800, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2800
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-2800

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGGCGGCG 65
||||||| |||||||
Db 3 GCGGCGGCGGCGGCG 17

RESULT 3039
US-10-238-700-2802
; Sequence 2802, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2802
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-2802

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 52 CGGCGGGGGCGGCGG 66
|||||| ||||||||
Db 1 CGGCGGCGGCGGCGG 15

RESULT 3040
US-10-339-782-472
; Sequence 472, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-000110US
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 472
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-472

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2113 TCTGGTTTTAGGAAA 2127
|||||| ||||||||
Db 3 TCTGGTATTAGGAAA 17

RESULT 3041
US-10-339-793-92
; Sequence 92, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
; FILE REFERENCE: 37-000310US
; CURRENT APPLICATION NUMBER: US/10/339,793
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 443
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-793-92

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1475 GATTCTAACAAAACC 1489
||| ||||||||||
Db 1 GATCCTAACAAAACC 15

RESULT 3042
US-10-338-777-262
; Sequence 262, Application US/10338777
; Publication No. US20030188343A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: United States Department of Agriculture
; APPLICANT: Bowen, Benjamin A
; APPLICANT: Haudenschild, Christian D
; APPLICANT: Buckler, Edward S
; TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants
; FILE REFERENCE: 37-000510US
; CURRENT APPLICATION NUMBER: US/10/338,777

```
Qy       1425 TGATTGTCATAGACA 1439
             ||||||| |||||||
Db         15 TGATTGTAATAGACA 1


RESULT 3033
US-10-287-919-1504
; Sequence 1504, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
;  APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
;  TITLE OF INVENTION: Methanococcus jannaschii complete genome.
;  FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
;  CURRENT APPLICATION NUMBER: US/10/287,919
;  CURRENT FILING DATE:  2002-11-05
;  NUMBER OF SEQ ID NOS: 2706
;  SOFTWARE: Proprietary
; SEQ ID NO 1504
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Methanococcus jannaschii complete genome.
;   FEATURE:
;   LOCATION: (806407)...(806423)
;   OTHER INFORMATION: Chromosome = 1  Strand = negative  ConnectronObjectNumber =  1896
US-10-287-919-1504

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTTT 2192
             ||||| |||||||||
Db          2 TTTTTGTTTAACTTT 16


RESULT 3034
US-10-163-552-852/c
; Sequence 852, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
;  TITLE OF INVENTION:  HER2
;  FILE REFERENCE: MBHB01-1653-A (400/014)
;  CURRENT APPLICATION NUMBER: US/10/163,552
;  CURRENT FILING DATE:  2002-06-06
;  NUMBER OF SEQ ID NOS: 1997
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 852
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-163-552-852

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1784 ACCCCATTCTTTCCT 1798
             ||||||||||| |||
Db         15 ACCCCATTCTTCCCT 1


RESULT 3035
US-10-156-306-3486
; Sequence 3486, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of IKK-Gamma and PKR
;  FILE REFERENCE: MBHB01-664-A (400/050)
;  CURRENT APPLICATION NUMBER: US/10/156,306
;  CURRENT FILING DATE:  2002-05-28
;  NUMBER OF SEQ ID NOS: 8013
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3486
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-156-306-3486

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCG 65
              ||||||| |||||||
Db          1 GCGGCGGCGGCGGCG 15


RESULT 3036
US-10-238-700-2710/c
; Sequence 2710, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels
;  FILE REFERENCE: 400/057  (MBHB01-1158-A)
;  CURRENT APPLICATION NUMBER: US/10/238,700
;  CURRENT FILING DATE:  2002-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 02/16840
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/318,471
;  PRIOR FILING DATE: 2001-09-10
;  NUMBER OF SEQ ID NOS: 4666
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2710
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-238-700-2710

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        288 GCCCCGCGCCACCCC 302
              ||||||| |||||||
Db         15 GCCCCGCCCCACCCC 1


RESULT 3037
US-10-238-700-2758/c
; Sequence 2758, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels
;  FILE REFERENCE: 400/057  (MBHB01-1158-A)
;  CURRENT APPLICATION NUMBER: US/10/238,700
;  CURRENT FILING DATE:  2002-09-18
;  PRIOR APPLICATION NUMBER: PCT/US 02/16840
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: US 60/318,471
;  PRIOR FILING DATE: 2001-09-10
;  NUMBER OF SEQ ID NOS: 4666
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2758
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
```

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;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 580
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-580

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        193 CAAGTACGAAGAGGA 207
              |||| ||||||||||
Db          1 CAAGGACGAAGAGGA 15


RESULT 3030
US-10-060-756A-1561/c
; Sequence 1561, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1561
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1561

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1425 TGATTGTCATAGACA 1439
              ||||||| |||||||
Db         17 TGATTGTAATAGACA 3


RESULT 3031
US-10-060-756A-1562/c
; Sequence 1562, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1562
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1562

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1425 TGATTGTCATAGACA 1439
              ||||||| |||||||
Db         16 TGATTGTAATAGACA 2


RESULT 3032
US-10-060-756A-1563/c
; Sequence 1563, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1563
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1563

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        451 CACAGGCAGCCAGCA 465
              ||||||  ||||||||
Db          3 CACAGGTAGCCAGCA 17
```

RESULT 3026
US-10-675-685-657
; Sequence 657, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 657
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-657

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        452 ACAGGCAGCCAGCAG 466
              |||||  |||||||||
Db          1 ACAGGTAGCCAGCAG 15
```

RESULT 3027
US-10-060-756A-578
; Sequence 578, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 578
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-578

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        193 CAAGTACGAAGAGGA 207
              ||||  ||||||||||
Db          3 CAAGGACGAAGAGGA 17
```

RESULT 3028
US-10-060-756A-579
; Sequence 579, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 579
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-579

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        193 CAAGTACGAAGAGGA 207
              ||||  ||||||||||
Db          2 CAAGGACGAAGAGGA 16
```

RESULT 3029
US-10-060-756A-580
; Sequence 580, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

```
                    ||||||||||| |||
Db          17 CCGCGGTGTCTCCCC 3


RESULT 3022
US-09-817-879-1379/c
; Sequence 1379, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Hepatitis C Virus Infection
;  FILE REFERENCE: MBHB00-801-F
;  CURRENT APPLICATION NUMBER: US/09/817,879
;  CURRENT FILING DATE:  2001-03-26
;  NUMBER OF SEQ ID NOS: 9703
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1379
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1379

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        220 CCACGACGGGAGCAG 234
                ||||  ||||||||||
Db         15 CCACCACGGGAGCAG 1


RESULT 3023
US-09-817-879-3735
; Sequence 3735, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Hepatitis C Virus Infection
;  FILE REFERENCE: MBHB00-801-F
;  CURRENT APPLICATION NUMBER: US/09/817,879
;  CURRENT FILING DATE:  2001-03-26
;  NUMBER OF SEQ ID NOS: 9703
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3735
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-3735

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   73.3%;  Pred. No. 2.7e+03;
  Matches   11;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1385 GCCGCGGTGTCTGCC 1399
              |||||||:|:|: ||
Db          3 GCCGCGGUGUCUCCC 17


RESULT 3024
US-09-982-835A-6/c
; Sequence 6, Application US/09982835A
; Publication No. US20030235819A1
;   GENERAL INFORMATION:
;        APPLICANT: RABIN, Mark B.
;        TITLE OF INVENTION: MUTATIONS IN THE BRCA1 GENE
;        NUMBER OF SEQUENCES: 10
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Morgan, Lewis & Bockius LLP
;             STREET: 1111 Pennsylvania Avenue, N.W.
;             CITY: Washington
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/982,835A
;             FILING DATE: 30-Sep-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/038,946
;             FILING DATE: 1998-03-12
;             APPLICATION NUMBER: US 09/697,149
;             FILING DATE: 2000-10-27
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Michael S. Tuscan, Ph.D.
;             REGISTRATION NUMBER: 43,210
;             REFERENCE/DOCKET NUMBER: 44921-5047-02-US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-739-3000
;             TELEFAX: 202-739-3001
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 17 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-982-835A-6

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1918 TACCTTTTTTTTCAG 1932
              |||||||||||||  |
Db         15 TACCTTTTTTTTCTG 1


RESULT 3025
US-10-675-685-654
; Sequence 654, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: PB0114
;  CURRENT APPLICATION NUMBER: US/10/675,685
;  CURRENT FILING DATE:  2003-09-30
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 654
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-675-685-654

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
```

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;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,983
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 2992
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1098
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid
US-09-776-474-1098

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1654 ACTGGTTCTGCATCA 1668
              ||||||||||||| |
Db         16 ACTGGTTCTGCATGA 2


RESULT 3018
US-09-740-332-819/c
; Sequence 819, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Hepatitis C Virus Infection
;  FILE REFERENCE: RPI 400/003
;  CURRENT APPLICATION NUMBER: US/09/740,332
;  CURRENT FILING DATE:  2001-03-26
;  NUMBER OF SEQ ID NOS: 9704
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 819
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-819

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1386 CCGCGGTGTCTGCCC 1400
              ||||||||||| |||
Db         17 CCGCGGTGTCTCCCC 3


RESULT 3019
US-09-740-332-1379/c
; Sequence 1379, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Hepatitis C Virus Infection
;  FILE REFERENCE: RPI 400/003
;  CURRENT APPLICATION NUMBER: US/09/740,332
;  CURRENT FILING DATE:  2001-03-26
;  NUMBER OF SEQ ID NOS: 9704
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1379
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1379

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        220 CCACGACGGGAGCAG 234
              |||| ||||||||||
Db         15 CCACCACGGGAGCAG 1


RESULT 3020
US-09-740-332-3735
; Sequence 3735, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relatec
;  TITLE OF INVENTION:  Hepatitis C Virus Infection
;  FILE REFERENCE: RPI 400/003
;  CURRENT APPLICATION NUMBER: US/09/740,332
;  CURRENT FILING DATE:  2001-03-26
;  NUMBER OF SEQ ID NOS: 9704
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3735
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-3735

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   73.3%;  Pred. No. 2.7e+03;
  Matches   11;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1385 GCCGCGGTGTCTGCC 1399
              |||||||:|:|: ||
Db          3 GCCGCGGUGUCUCCC 17


RESULT 3021
US-09-817-879-819/c
; Sequence 819, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relatec
;  TITLE OF INVENTION:  Hepatitis C Virus Infection
;  FILE REFERENCE: MBHB00-801-F
;  CURRENT APPLICATION NUMBER: US/09/817,879
;  CURRENT FILING DATE:  2001-03-26
;  NUMBER OF SEQ ID NOS: 9703
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 819
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-819

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1386 CCGCGGTGTCTGCCC 1400
```

```
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1192
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-1192

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2479 CTTTTAATGGTGATG 2493
              ||| ||||||||||||
Db         16 CTTCTAATGGTGATG 2


RESULT 3014
US-09-780-533A-2234
; Sequence 2234, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2234
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-2234

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   40.0%;  Pred. No. 2.7e+03;
  Matches    6;  Conservative    8;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1822 TTTAGAATCTTTTAA 1836
              ::: |||:|::::||
Db          3 UUUGGAAUCUUUUAA 17


RESULT 3015
US-09-780-533A-2337
; Sequence 2337, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2337
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-2337

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         55 CGGGGGCGGCGGCAG 69
              ||| ||||||||||||
Db          2 CGGCGGCGGCGGCAG 16


RESULT 3016
US-09-776-474-445/c
; Sequence 445, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Jarvis, Thale
;  APPLICANT:  Booher, Robert
;  APPLICANT:  Holman, Patricia
;  APPLICANT:  Fattaey, Ali
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CH
;  TITLE OF INVENTION:  Enzyme
;  FILE REFERENCE: MBHB00-955-A (400/008)
;  CURRENT APPLICATION NUMBER: US/09/776,474
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,983
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 2992
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 445
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid
US-09-776-474-445

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1654 ACTGGTTCTGCATCA 1668
              ||||||||||||| |
Db         17 ACTGGTTCTGCATGA 3


RESULT 3017
US-09-776-474-1098/c
; Sequence 1098, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Jarvis, Thale
;  APPLICANT:  Booher, Robert
;  APPLICANT:  Holman, Patricia
;  APPLICANT:  Fattaey, Ali
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CH
;  TITLE OF INVENTION:  Enzyme
;  FILE REFERENCE: MBHB00-955-A (400/008)
;  CURRENT APPLICATION NUMBER: US/09/776,474
```

```
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,674
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: No. US20030054346A1 available
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/021,701
;             FILING DATE: 10-FEB-1998
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Choi, Wendy A.
;             REGISTRATION NUMBER: 36,697
;             REFERENCE/DOCKET NUMBER: 10971464-1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-236-2386
;             TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 112:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 17 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-784-674-112

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       141 GACTGTTTTGGGGGA 155
             | ||||||||||||||
Db         1 GTCTGTTTTGGGGGA 15


RESULT 3010
US-09-956-857-9/c
; Sequence 9, Application US/09956857
; Publication No. US20030054356A1
; GENERAL INFORMATION:
;  APPLICANT: Jacobson, James W.
;  APPLICANT:  Burroughs, Jennifer  L.
;  APPLICANT:  Oliver, Kerry  G.
;  TITLE OF INVENTION: Multiple Reporter Read-Out Bioassays
;  FILE REFERENCE: 215063.01001
;  CURRENT APPLICATION NUMBER: US/09/956,857
;  CURRENT FILING DATE:  2001-09-21
;  PRIOR APPLICATION NUMBER: 60/234,430
;  PRIOR FILING DATE: 2000-09-21
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-956-857-9

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1918 TACCTTTTTTTTCAG 1932
             ||||||||||||| |
Db        15 TACCTTTTTTTTCTG 1


RESULT 3011
US-09-780-533A-398
; Sequence 398, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 398
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-398

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   40.0%;  Pred. No. 2.7e+03;
  Matches    6;  Conservative    8;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1822 TTTAGAATCTTTTAA 1836
             ::: |||:|::::||
Db         1 UUUGGAAUCUUUUAA 15


RESULT 3012
US-09-780-533A-929/c
; Sequence 929, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 929
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-533A-929

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       558 TGGAGGCGGGCGCGG 572
             |||||| ||||||||
Db        16 TGGAGGGGGGCGCGG 2


RESULT 3013
US-09-780-533A-1192/c
; Sequence 1192, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
```

```
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        164 GCCATGTTGTGGAAA 178
              ||||||||| |||||
Db         15 GCCATGTTGAGGAAA 1


RESULT 3007
US-09-784-674-110
; Sequence 110, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,674
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: No. US20030054346A1 available
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/021,701
;             FILING DATE: 10-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Choi, Wendy A.
;             REGISTRATION NUMBER: 36,697
;             REFERENCE/DOCKET NUMBER: 10971464-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-236-2386
;             TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 110:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 17 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-09-784-674-110

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        141 GACTGTTTTGGGGGA 155
              | ||||||||||||||
Db          3 GTCTGTTTTGGGGGA 17


RESULT 3008
US-09-784-674-111
; Sequence 111, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,674
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: No. US20030054346A1 available
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/021,701
;             FILING DATE: 10-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Choi, Wendy A.
;             REGISTRATION NUMBER: 36,697
;             REFERENCE/DOCKET NUMBER: 10971464-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-236-2386
;             TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 111:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 17 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-784-674-111

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        141 GACTGTTTTGGGGGA 155
              | ||||||||||||||
Db          2 GTCTGTTTTGGGGGA 16


RESULT 3009
US-09-784-674-112
; Sequence 112, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
```

```
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 654
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-654

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCA 465
              ||||||  ||||||||
Db          3 CACAGGTAGCCAGCA 17


RESULT 3003
US-09-827-998-657
; Sequence 657, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 657
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-657

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        452 ACAGGCAGCCAGCAG 466
              |||||  |||||||||
Db          1 ACAGGTAGCCAGCAG 15


RESULT 3004
US-09-730-289B-139/c
; Sequence 139, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
;  FILE REFERENCE: MBHB00-864-A (400/006)
;  CURRENT APPLICATION NUMBER: US/09/730,289B
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/169,100
;  PRIOR FILING DATE: 1999-12-06
;  NUMBER OF SEQ ID NOS: 3897
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-730-289B-139

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        164 GCCATGTTGTGGAAA 178
              |||||||||  |||||
Db         17 GCCATGTTGAGGAAA 3


RESULT 3005
US-09-730-289B-936
; Sequence 936, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
;  FILE REFERENCE: MBHB00-864-A (400/006)
;  CURRENT APPLICATION NUMBER: US/09/730,289B
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/169,100
;  PRIOR FILING DATE: 1999-12-06
;  NUMBER OF SEQ ID NOS: 3897
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 936
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-730-289B-936

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2286 GTAAACTTGAAAAGG 2300
              |:|||| :|||||||
Db          3 GUAAACAUGAAAAGG 17


RESULT 3006
US-09-730-289B-943/c
; Sequence 943, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
;  FILE REFERENCE: MBHB00-864-A (400/006)
;  CURRENT APPLICATION NUMBER: US/09/730,289B
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: US 60/169,100
;  PRIOR FILING DATE: 1999-12-06
;  NUMBER OF SEQ ID NOS: 3897
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 943
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-730-289B-943

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
```

```
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10726
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-10726

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2554 GAGGATGCTGGGCTC 2568
              | ||||||||||||||
Db          3 GGGGATGCTGGGCTC 17


RESULT 3000
US-09-866-108-10727
; Sequence 10727, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10727
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-10727

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2554 GAGGATGCTGGGCTC 2568
              | ||||||||||||||
Db          2 GGGGATGCTGGGCTC 16


RESULT 3001
US-09-866-108-10728
; Sequence 10728, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10728
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-10728

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2554 GAGGATGCTGGGCTC 2568
              | ||||||||||||||
Db          1 GGGGATGCTGGGCTC 15


RESULT 3002
US-09-827-998-654
; Sequence 654, Application US/09827998
; Patent No. US20020102252A1
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;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2672
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-2672

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         47 GCGCGCGGCGGGGGC 61
              |||||||||||||| |
Db          2 GGGCGCGGCGGGGGC 16


RESULT 2998
US-09-866-108-2673
; Sequence 2673, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2673
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-2673

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         47 GCGCGCGGCGGGGGC 61
              |||||||||||||| |
Db          1 GGGCGCGGCGGGGGC 15


RESULT 2999
US-09-866-108-10726
; Sequence 10726, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
```

```
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2060
;    LENGTH: 17
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-866-108-2060

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1367 GGCAGCCAGGCCATC 1381
              ||||| |||||||||
Db         17 GGCAGGCAGGCCATC 3


RESULT 2996
US-09-866-108-2061/c
; Sequence 2061, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2061
;    LENGTH: 17
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-866-108-2061

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1367 GGCAGCCAGGCCATC 1381
              ||||| |||||||||
Db         16 GGCAGGCAGGCCATC 2


RESULT 2997
US-09-866-108-2672
; Sequence 2672, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Aritificial Sequence: Oligonucleotide structure fc
;   OTHER INFORMATION: molecular beacon
US-10-164-915-3

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2180
              ||||||| |||||||
Db         16 TTTTTTTGTTTTTT 2


RESULT 2991
US-09-132-231-18
; Sequence 18, Application US/09132231A
; Publication No. US20030198950A1
; GENERAL INFORMATION:
;  APPLICANT:  HORWITZ, Marshall S.
;  APPLICANT:  LOEB, Lawrence A.
;  TITLE OF INVENTION:  METHOD FOR PRODUCING NOVEL DNA SEQUENCES WITH
;  TITLE OF INVENTION:  BIOLOGICAL ACTIVITY
;  FILE REFERENCE:  032425-001
;  CURRENT APPLICATION NUMBER: US/09/132,231A
;  CURRENT FILING DATE:  1998-08-11
;  PRIOR APPLICATION NUMBER:  US 08/316,415
;  PRIOR FILING DATE:  1994-09-30
;  NUMBER OF SEQ ID NOS:  57
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-09-132-231-18

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GAGCCGCCGATGCGT 20
              |||||||||||  |||
Db          2 GAGCCGCCGATACGT 16


RESULT 2992
US-10-138-674-5864/c
; Sequence 5864, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5864
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-5864

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              |||||||||| ||||
Db         16 GACTGCAAAAGTCCT 2


RESULT 2993
US-10-287-949A-5864/c
; Sequence 5864, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5864
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-5864

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              |||||||||| ||||
Db         16 GACTGCAAAAGTCCT 2


RESULT 2994
US-10-156-306-526/c
; Sequence 526, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relatec
;  TITLE OF INVENTION:  Levels of IKK-Gamma and PKR
;  FILE REFERENCE: MBHB01-664-A (400/050)
;  CURRENT APPLICATION NUMBER: US/10/156,306
;  CURRENT FILING DATE:  2002-05-28
;  NUMBER OF SEQ ID NOS: 8013
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 526
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-156-306-526

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAA 2797
              || ||||||||||||
Db         15 TTTAAAAAAAAAAAA 1


RESULT 2995
US-09-866-108-2060/c
; Sequence 2060, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
```

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;  PRIOR APPLICATION NUMBER: US/09/531,488B
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: 08/638,941
;  PRIOR FILING DATE: 1996-04-25
;  PRIOR APPLICATION NUMBER: UK 8515686
;  PRIOR FILING DATE: 1985-06-20
;  PRIOR APPLICATION NUMBER: UK 8600754
;  PRIOR FILING DATE: 1986-01-14
;  PRIOR APPLICATION NUMBER: 08/370,356
;  PRIOR FILING DATE: 1995-01-09
;  PRIOR APPLICATION NUMBER: 08/073,043
;  PRIOR FILING DATE: 1993-06-08
;  PRIOR APPLICATION NUMBER: 07/385,952
;  PRIOR FILING DATE: 1989-07-28
;  PRIOR APPLICATION NUMBER: 06/875,880
;  PRIOR FILING DATE: 1986-06-18
;  NUMBER OF SEQ ID NOS: 88
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: synthetic DNA
US-10-279-061-15

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1264 CAGCCAAGACCGGAC 1278
              ||||| |||||||||
Db          1 CAGCCCAGACCGGAC 15


RESULT 2988
US-10-360-275-12
; Sequence 12, Application US/10360275
; Publication No. US20040014644A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Choob, Mikhail
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: AM102.P.1.1.1US
;  CURRENT APPLICATION NUMBER: US/10/360,275
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US 10/072,975
;  PRIOR FILING DATE: 2002-02-09
;  PRIOR APPLICATION NUMBER: US 09/805,296
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Construct
;    FEATURE:
;    NAME/KEY: misc_feature
;    OTHER INFORMATION: Synthetic Sequence
US-10-360-275-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||| |||||||
Db          1 TTTTTTTCTTTTTTT 15


RESULT 2989
US-10-360-275-12/c
; Sequence 12, Application US/10360275
; Publication No. US20040014644A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Choob, Mikhail
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: AM102.P.1.1.1US
;  CURRENT APPLICATION NUMBER: US/10/360,275
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US 10/072,975
;  PRIOR FILING DATE: 2002-02-09
;  PRIOR APPLICATION NUMBER: US 09/805,296
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;    LENGTH: 15
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Construct
;    FEATURE:
;    NAME/KEY: misc_feature
;    OTHER INFORMATION: Synthetic Sequence
US-10-360-275-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||| |||||||
Db         15 AAAAAAAGAAAAAAA 1


RESULT 2990
US-10-164-915-3/c
; Sequence 3, Application US/10164915
; Publication No. US20030148391A1
; GENERAL INFORMATION:
;  APPLICANT: Salafsky, Joshua S.
;  TITLE OF INVENTION: Method Using a Surface-Selective No. US20030148391A1linear Optic
;  TITLE OF INVENTION:  for Detection of Interactions Involving a Conformational Change
;  FILE REFERENCE: 11100-035-999
;  CURRENT APPLICATION NUMBER: US/10/164,915
;  CURRENT FILING DATE:  2002-06-06
;  PRIOR APPLICATION NUMBER: 60/253,862
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: 60/260,249
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/265,775
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: 60/278,941
;  PRIOR FILING DATE: 2001-01-27
;  NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 3
;    LENGTH: 16
;    TYPE: DNA
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RESULT 2984
US-10-072-975-12/c
; Sequence 12, Application US/10072975
; Publication No. US20030059789A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF US
;  FILE REFERENCE: AM102.P.1.1US
;  CURRENT APPLICATION NUMBER: US/10/072,975
;  CURRENT FILING DATE:  2002-02-09
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: 09/805,296
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: PCT/US01/0811
;  PRIOR FILING DATE: 2001-03-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Synthetic Sequence
US-10-072-975-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||| |||||||
Db         15 AAAAAAAGAAAAAAA 1


RESULT 2985
US-10-051-436-12
; Sequence 12, Application US/10051436
; Publication No. US20030138045A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF US
;  FILE REFERENCE: AM102.P.1US
;  CURRENT APPLICATION NUMBER: US/10/051,436
;  CURRENT FILING DATE:  2002-01-18
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Synthetic Sequence
US-10-051-436-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||| |||||||
Db          1 TTTTTTTCTTTTTTT 15


RESULT 2986
US-10-051-436-12/c
; Sequence 12, Application US/10051436
; Publication No. US20030138045A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
;  FILE REFERENCE: AM102.P.1US
;  CURRENT APPLICATION NUMBER: US/10/051,436
;  CURRENT FILING DATE:  2002-01-18
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Synthetic Sequence
US-10-051-436-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||| |||||||
Db         15 AAAAAAAGAAAAAAA 1


RESULT 2987
US-10-279-061-15
; Sequence 15, Application US/10279061
; Publication No. US20030170811A1
; GENERAL INFORMATION:
;  APPLICANT: UEDA, IKUO
;  APPLICANT:  NIWA, MINEO
;  APPLICANT:  SAITO, YOSHIMASA
;  APPLICANT:  YAMADA, HISASHI
;  APPLICANT:  ISHII, YOSHINORI
;  TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF ALPHA-HUMAN ATRIAL NATRIURETIC POLYI
;  FILE REFERENCE: 0018-1100-0CONT
;  CURRENT APPLICATION NUMBER: US/10/279,061
;  CURRENT FILING DATE:  2002-10-24
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RESULT 2981
US-09-805-296D-12/c
; Sequence 12, Application US/09805296D
; Patent No. US20020155989A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF US
;  FILE REFERENCE: AM102.P.1US
;  CURRENT APPLICATION NUMBER: US/09/805,296D
;  CURRENT FILING DATE:  2001-03-13
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Synthetic Sequence
US-09-805-296D-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||| |||||||
Db         15 AAAAAAAGAAAAAAA 1


RESULT 2982
US-10-132-002-13
; Sequence 13, Application US/10132002
; Publication No. US20030022204A1
;   GENERAL INFORMATION:
;        APPLICANT: Lansdorp, Peter
;        TITLE OF INVENTION: Method for Detecting Multiple Copies of
;                            a Repeat Sequence in a Nucleic Acid Molecule
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: HOWSON & HOWSON
;             STREET: 321 No. US20030022204A1ristown Road
;             CITY: Spring House
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/132,002
;             FILING DATE: 25-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/730,635
;             FILING DATE: 11-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: B&P7USA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 540-9200
;             TELEFAX: (215) 540-5818
;             TELEX: N/A
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-132-002-13

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||| |||||||||
Db          1 GGCGGCGGCGGCGGC 15


RESULT 2983
US-10-072-975-12
; Sequence 12, Application US/10072975
; Publication No. US20030059789A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF US
;  FILE REFERENCE: AM102.P.1.1US
;  CURRENT APPLICATION NUMBER: US/10/072,975
;  CURRENT FILING DATE:  2002-02-09
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: 09/805,296
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: PCT/US01/0811
;  PRIOR FILING DATE: 2001-03-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Synthetic Sequence
US-10-072-975-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||| |||||||
Db          1 TTTTTTTCTTTTTTT 15
```

```
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)..(6)
;   OTHER INFORMATION: The residue between C at position 5 and T at position 6 is acridi
;   OTHER INFORMATION: ne
US-10-239-595-6

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 22;
  Best Local Similarity   80.0%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
                ||| |||||| | ||| |||
Db         21 GAAGAAAAAAGAGAAAGAAA 2


RESULT 2978
US-09-504-231A-824/c
; Sequence 824, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/504,231A
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 09/274,553
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3242
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 824
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-504-231A-824

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2204 CTTCAAATGGGAGAC 2218
                ||||||| ||||||
Db         15 CTTCAAATAGGAGAC 1


RESULT 2979
US-09-274-553D-824/c
; Sequence 824, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
;  APPLICANT: Blatt, Lawrence
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Roberts, Beth
;  APPLICANT:  Pavco, Pamela
;  APPLICANT:  Macejak, Dennis
;  TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
;  TITLE OF INVENTION:  HEPATITIS C VIRUS INFECTION
;  FILE REFERENCE: rpi 247/282
;  CURRENT APPLICATION NUMBER: US/09/274,553D
;  CURRENT FILING DATE:  1999-03-23
;  PRIOR APPLICATION NUMBER: 09/257,608
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/100,842
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/083,217
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 3148
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 824
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid Target
US-09-274-553D-824

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2204 CTTCAAATGGGAGAC 2218
                ||||||| ||||||
Db         15 CTTCAAATAGGAGAC 1


RESULT 2980
US-09-805-296D-12
; Sequence 12, Application US/09805296D
; Patent No. US20020155989A1
; GENERAL INFORMATION:
;  APPLICANT: Active Motif
;  APPLICANT:  Efimov, Vladimir
;  APPLICANT:  Fernandez, Joseph
;  APPLICANT:  Archdeacon, Dorothy
;  APPLICANT:  Archdeacon, John
;  APPLICANT:  Chakhmakhcheau, Oksana
;  APPLICANT:  Buryakova, Alla
;  APPLICANT:  Choob, Mikhail
;  APPLICANT:  Hondorp, Kyle
;  TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USI
;  FILE REFERENCE: AM102.P.1US
;  CURRENT APPLICATION NUMBER: US/09/805,296D
;  CURRENT FILING DATE:  2001-03-13
;  PRIOR APPLICATION NUMBER: US 60/189,190
;  PRIOR FILING DATE: 2000-03-14
;  PRIOR APPLICATION NUMBER: US 60/250,334
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Synthetic Sequence
US-09-805-296D-12

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||| |||||||
Db          1 TTTTTTTCTTTTTTT 15
```

```
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2467
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2467

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              || ||| | |||| ||||||
Db         20 TTGTTTCTGTTTTGTTTTTA 1


RESULT 2974
US-10-688-706-2843/c
; Sequence 2843, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2843
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2843

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTT 2173
              |||| |||||  ||| ||||
Db         20 ATTTGTTTCTGTTTTGTTTT 1


RESULT 2975
US-10-688-706-2908/c
; Sequence 2908, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2908
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2908

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTT 2174
              ||| |||||  ||| |||||
Db         20 TTTGTTTCTGTTTTGTTTTT 1


RESULT 2976
US-10-239-595-5/c
; Sequence 5, Application US/10239595
; Publication No. US20030211612A1
; GENERAL INFORMATION:
;  APPLICANT: Seidman, Michael M
;  APPLICANT:  Majumdar, Alokes
;  TITLE OF INVENTION: ESTABLISHMENT OF CELLULAR MANIPULATIONS WHICH ENHANCE OLIGO-MEDIA
;  TITLE OF INVENTION:  TARGETING
;  FILE REFERENCE: 4239-63915
;  CURRENT APPLICATION NUMBER: US/10/239,595
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: PCT/US01/09218
;  PRIOR FILING DATE: 2001-03-22
;  PRIOR APPLICATION NUMBER: US 60/191,996
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)..(6)
;   OTHER INFORMATION: The residue between C at position 5 and T at position 6 is pyrene
US-10-239-595-5

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 22;
  Best Local Similarity   80.0%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||| |||||| | ||| |||
Db         21 GAAGAAAAAAGAGAAAGAAA 2


RESULT 2977
US-10-239-595-6/c
; Sequence 6, Application US/10239595
; Publication No. US20030211612A1
; GENERAL INFORMATION:
;  APPLICANT: Seidman, Michael M
;  APPLICANT:  Majumdar, Alokes
;  TITLE OF INVENTION: ESTABLISHMENT OF CELLULAR MANIPULATIONS WHICH ENHANCE OLIGO-MEDIA
;  TITLE OF INVENTION:  TARGETING
;  FILE REFERENCE: 4239-63915
;  CURRENT APPLICATION NUMBER: US/10/239,595
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: PCT/US01/09218
;  PRIOR FILING DATE: 2001-03-22
;  PRIOR APPLICATION NUMBER: US 60/191,996
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 15
```

```
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2110

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2801
              ||| ||||| |||| | |||
Db          1 ATTTAAAAACAAAACAGAAA 20


RESULT 2969
US-10-688-706-2110/c
; Sequence 2110, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2110
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2110

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              ||| | |||| ||||||| |
Db         20 TTTCTGTTTTGTTTTTAAAT 1


RESULT 2970
US-10-688-706-2269/c
; Sequence 2269, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2269
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2269

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAA 2188
              | ||| | |||| |||||||
Db         20 TGTTTCTGTTTTGTTTTTAA 1


RESULT 2971
US-10-688-706-2404/c
; Sequence 2404, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2404
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2404

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2255 TTTATTTGCATATTTATTTC 2274
              |||||||  | |||| ||||
Db         20 TTTATTTTGAAATTTGTTTC 1


RESULT 2972
US-10-688-706-2457/c
; Sequence 2457, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2457
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-2457

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1176 CTCATCTTGGAGGACGAAAT 1195
              || | | |||| ||||||||
Db         20 CTGAGCATGGATGACGAAAT 1


RESULT 2973
US-10-688-706-2467/c
; Sequence 2467, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
```

```
Db         20 CTCTTTAGCTGAACCTCTCT 1


RESULT 2964
US-10-304-124-43/c
; Sequence 43, Application US/10304124
; Publication No. US20040102404A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lawrence Panasci
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF KU86 EXPRESSION
;  FILE REFERENCE: HTS-0015
;  CURRENT APPLICATION NUMBER: US/10/304,124
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-124-43

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1238 CTGTGTAAAGAATTCACAGA 1257
              ||||| || |||| |||| |
Db         20 CTGTGGAATGAATACACACA 1


RESULT 2965
US-10-304-124-77
; Sequence 77, Application US/10304124
; Publication No. US20040102404A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lawrence Panasci
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF KU86 EXPRESSION
;  FILE REFERENCE: HTS-0015
;  CURRENT APPLICATION NUMBER: US/10/304,124
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 77
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-304-124-77

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1238 CTGTGTAAAGAATTCACAGA 1257
              ||||| || |||| |||| |
Db          1 CTGTGGAATGAATACACACA 20


RESULT 2966
US-10-688-706-385
; Sequence 385, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 385
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-385

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2592 TTTAATTGAAACTCTCTGTT 2611
              |||||| | | |||| ||||
Db          1 TTTAATAGCAGCTCTGTGTT 20


RESULT 2967
US-10-688-706-394
; Sequence 394, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 394
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human GFAT antisense
US-10-688-706-394

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2591 ATTTAATTGAAACTCTCTGT 2610
              ||||||| | | |||| |||
Db          1 ATTTAATAGCAGCTCTGTGT 20


RESULT 2968
US-10-688-706-2110
; Sequence 2110, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Broschat, Kay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
;  FILE REFERENCE: 01393/1
;  CURRENT APPLICATION NUMBER: US/10/688,706
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/419,268
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 3071
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2110
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
```

```
Qy       2643 GGGCTGAACCCTAAGGTGAG 2662
              |||||||||| | |  |||
Db         20 GGGCTGAACCCAAGGCAGAG 1


RESULT 2959
US-10-302-027-17
; Sequence 17, Application US/10302027
; Publication No. US20040102391A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION
;  FILE REFERENCE: PTS-0068
;  CURRENT APPLICATION NUMBER: US/10/302,027
;  CURRENT FILING DATE:  2002-11-21
;  NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-302-027-17

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1919 ACCTTTTTTTTCAGTGTTAA 1938
              || |||| |||||| || ||
Db          1 ACATTTTATTTCAGAGTAAA 20


RESULT 2960
US-10-303-420-27
; Sequence 27, Application US/10303420
; Publication No. US20040102398A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF B7H EXPRESSION
;  FILE REFERENCE: RTS-0417
;  CURRENT APPLICATION NUMBER: US/10/303,420
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 271
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-420-27

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        587 GATGCCTACCGCCGCTCCGA 606
              | ||||||||  ||||| ||
Db          1 GCTGCCTACCATCGCTCTGA 20


RESULT 2961
US-10-303-420-183/c
; Sequence 183, Application US/10303420
; Publication No. US20040102398A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF B7H EXPRESSION
;  FILE REFERENCE: RTS-0417
;  CURRENT APPLICATION NUMBER: US/10/303,420
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 271
; SEQ ID NO 183
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-303-420-183

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        587 GATGCCTACCGCCGCTCCGA 606
              | ||||||||  ||||| ||
Db         20 GCTGCCTACCATCGCTCTGA 1


RESULT 2962
US-10-304-113-49
; Sequence 49, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
;  FILE REFERENCE: RTS-0415
;  CURRENT APPLICATION NUMBER: US/10/304,113
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 49
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-113-49

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2589 CTATTTAATTGAAACTCTCT 2608
              || ||||  |||| ||||||
Db          1 CTCTTTAGCTGAACCTCTCT 20


RESULT 2963
US-10-304-113-127/c
; Sequence 127, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
;  FILE REFERENCE: RTS-0415
;  CURRENT APPLICATION NUMBER: US/10/304,113
;  CURRENT FILING DATE:  2002-11-23
;  NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 127
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-304-113-127

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2589 CTATTTAATTGAAACTCTCT 2608
              || ||||  |||| ||||||
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```
Qy        458 AGCCAGCAGCAGGCCTGGCC 477
              |||||| | | |||||| ||
Db          1 AGCCAGTATCTGGCCTGCCC 20


RESULT 2954
US-10-637-009-43
; Sequence 43, Application US/10637009
; Publication No. US20040091920A1
; GENERAL INFORMATION:
;  APPLICANT: TSUJI, Toru
;  APPLICANT:  YANAGAWA, Hiroshi
;  TITLE OF INVENTION: Method of Constructing DNA Library and Utilization Thereof
;  FILE REFERENCE: P24048
;  CURRENT APPLICATION NUMBER: US/10/637,009
;  CURRENT FILING DATE:  2003-08-08
;  PRIOR APPLICATION NUMBER: PCT 2000-293692
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: US 10/396334
;  PRIOR FILING DATE: 2003-03-26
;  PRIOR APPLICATION NUMBER: PCT 2001-29138
;  PRIOR FILING DATE: 2001-02-06
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-637-009-43

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        596 CGCCGCTCCGACCTGCTGCT 615
              | || ||  ||||||||||
Db          1 CCCCTCTATGACCTGCTGCT 20


RESULT 2955
US-10-298-404-21/c
; Sequence 21, Application US/10298404
; Publication No. US20040097443A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF JERKY-LIKE 1 EXPRESSION
;  FILE REFERENCE: HTS-0011
;  CURRENT APPLICATION NUMBER: US/10/298,404
;  CURRENT FILING DATE:  2002-11-16
;  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 21
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-298-404-21

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1720 TTTGGACCTATTATCAGAAG 1739
              |||| ||  || ||||||||
Db         20 TTTGTACAGATAATCAGAAG 1


RESULT 2956
US-10-298-404-56
; Sequence 56, Application US/10298404
; Publication No. US20040097443A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF JERKY-LIKE 1 EXPRESSION
;  FILE REFERENCE: HTS-0011
;  CURRENT APPLICATION NUMBER: US/10/298,404
;  CURRENT FILING DATE:  2002-11-16
;  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-298-404-56

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1720 TTTGGACCTATTATCAGAAG 1739
              |||| ||  || ||||||||
Db          1 TTTGTACAGATAATCAGAAG 20


RESULT 2957
US-10-299-089-76
; Sequence 76, Application US/10299089
; Publication No. US20040097447A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF INTERLEUKIN 22 RECEPTOR EXPRESSION
;  FILE REFERENCE: RTS-0440
;  CURRENT APPLICATION NUMBER: US/10/299,089
;  CURRENT FILING DATE:  2002-11-16
;  NUMBER OF SEQ ID NOS: 144
; SEQ ID NO 76
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-299-089-76

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2643 GGGCTGAACCCTAAGGTGAG 2662
              |||||||||||| | |  |||
Db          1 GGGCTGAACCCAAGGCAGAG 20


RESULT 2958
US-10-299-089-136/c
; Sequence 136, Application US/10299089
; Publication No. US20040097447A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF INTERLEUKIN 22 RECEPTOR EXPRESSION
;  FILE REFERENCE: RTS-0440
;  CURRENT APPLICATION NUMBER: US/10/299,089
;  CURRENT FILING DATE:  2002-11-16
;  NUMBER OF SEQ ID NOS: 144
; SEQ ID NO 136
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-299-089-136

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

RESULT 2949
US-10-280-183A-421
; Sequence 421, Application US/10280183A
; Publication No. US20040081964A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Bachmanov, Alexander A
; APPLICANT: Beauchamp, Gary K.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: De Jong, Pieter J.
; APPLICANT: Li, Shanru
; APPLICANT: Li, Xia
; APPLICANT: Ohmen, Jeffrey D
; APPLICANT: Reed, Danielle R.
; APPLICANT: Ross, David
; APPLICANT: Tordoff, Michael G.
; TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
; TITLE OF INVENTION: CARBOHYDRATE COMPOUNDS AND OTHER SWEETNERS
; FILE REFERENCE: PC18306A
; CURRENT APPLICATION NUMBER: US/10/280,183A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/200,794
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 421
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mouse
US-10-280-183A-421

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1562 ACTGCAAAAATCCTTCTCCA 1581
|||||||| ||| |||||
Db 1 ACTGCAAATGTCCAACTCCA 20

RESULT 2950
US-10-292-849-60/c
; Sequence 60, Application US/10292849
; Publication No. US20040092463A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: MODULATION OF PIM-1 EXPRESSION
; FILE REFERENCE: RTS-0170
; CURRENT APPLICATION NUMBER: US/10/292,849
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-292-849-60

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1260 TTCTCAGCCAAGACCGGACA 1279
||| |||||||||| |||
Db 20 TTCAAAGCCAAGACCTCACA 1

RESULT 2951
US-10-292-849-118
; Sequence 118, Application US/10292849
; Publication No. US20040092463A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: MODULATION OF PIM-1 EXPRESSION
; FILE REFERENCE: RTS-0170
; CURRENT APPLICATION NUMBER: US/10/292,849
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-292-849-118

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1260 TTCTCAGCCAAGACCGGACA 1279
||| |||||||||| |||
Db 1 TTCAAAGCCAAGACCTCACA 20

RESULT 2952
US-10-293-864-36/c
; Sequence 36, Application US/10293864
; Publication No. US20040092465A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-864-36

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 458 AGCCAGCAGCAGGCCTGGCC 477
|||||| | | |||||| ||
Db 20 AGCCAGTATCTGGCCTGCCC 1

RESULT 2953
US-10-293-864-113
; Sequence 113, Application US/10293864
; Publication No. US20040092465A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 113
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-293-864-113

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
; Sequence 169, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook II, John P.
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Chillakuru, Rajeev A.
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gerlach, Valerie L.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Gould-Rothberg, Bonnie E.
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Jeffers, Michael E.
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Li, Li
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Murphey, Ryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Starling, Gary
;  APPLICANT:  Taupier, Raymond J.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-502A
;  CURRENT APPLICATION NUMBER: US/10/309,290
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/336,600
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: 60/338,285
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: 60/341,346
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: 60/341,477
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 60/341,540
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 60/342,592
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/344,297
;  PRIOR FILING DATE: 2001-12-27
;  PRIOR APPLICATION NUMBER: 60/344,903
;  PRIOR FILING DATE: 2001-12-31
;  PRIOR APPLICATION NUMBER: 60/373,288
;  PRIOR FILING DATE: 2002-04-17
;  PRIOR APPLICATION NUMBER: 60/380,981
;  PRIOR FILING DATE: 2002-05-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 169
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artifical Sequence:  Primer/Probe
US-10-309-290-169

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1650 CTTCACTGGTTCTGCATCAC 1669
              |||| ||||||  ||| |||
Db          1 CTTCCCTGGTTGAGCACCAC 20
```

```
RESULT 2947
US-10-703-864-64
; Sequence 64, Application US/10703864
; Publication No. US20040077580A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  Susan Murray
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Nicholas M. Dean
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PI3K P85 EXPRESSION
;  FILE REFERENCE: ISIS0057-102 (ISPH-0519)
;  CURRENT APPLICATION NUMBER: US/10/703,864
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: US/09/715,983
;  PRIOR FILING DATE: 2000-11-20
;  NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-703-864-64

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2110 CCTTCTGGTTTTAGGAAACT 2129
              ||| ||||| || ||| |||
Db          1 CCTGCTGGTATTTGGACACT 20
```

```
RESULT 2948
US-10-280-183A-236/c
; Sequence 236, Application US/10280183A
; Publication No. US20040081964A1
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Inc.
;  APPLICANT:  Bachmanov, Alexander A
;  APPLICANT:  Beauchamp, Gary K.
;  APPLICANT:  Chatterjee, Aurobindo
;  APPLICANT:  De  Jong, Pieter J.
;  APPLICANT:  Li, Shanru
;  APPLICANT:  Li, Xia
;  APPLICANT:  Ohmen, Jeffrey D
;  APPLICANT:  Reed, Danielle R.
;  APPLICANT:  Ross, David
;  APPLICANT:  Tordoff, Michael G.
;  TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
;  TITLE OF INVENTION:  CARBOHYDRATE COMPOUNDS AND OTHER SWEETNERS
;  FILE REFERENCE: PC18306A
;  CURRENT APPLICATION NUMBER: US/10/280,183A
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: 60/200,794
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 652
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 236
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Mouse
US-10-280-183A-236

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1331 TGCTTGTCTCATTTCAGCCT 1350
              | |||||||  |||| ||||
Db         20 TCCTTGTCTGCTTTCTGCCT 1
```

```
;  PRIOR APPLICATION NUMBER: 60/288,395
;  PRIOR FILING DATE: 2001-05-03
;  PRIOR APPLICATION NUMBER: 60/308,901
;  PRIOR FILING DATE: 2001-07-31
;  PRIOR APPLICATION NUMBER: 60/313,388
;  PRIOR FILING DATE: 2001-08-17
;  PRIOR APPLICATION NUMBER: 60/324,757
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: 60/288,900
;  PRIOR FILING DATE: 2001-05-04
;  NUMBER OF SEQ ID NOS: 203
; SEQ ID NO 171
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-138-588-171

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2396 TTATGCGTAATTTAATGGGG 2415
              |||||| |  || |||||||
Db          1 TTATGCTTGTTTCAATGGGG 20


RESULT 2942
US-10-210-556-34/c
; Sequence 34, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION
;  FILE REFERENCE: PTS-0015
;  CURRENT APPLICATION NUMBER: US/10/210,556
;  CURRENT FILING DATE:  2002-07-31
;  NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-556-34

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1370 AGCCAGGCCATCTGTGCCGC 1389
              | ||||||| |||||  ||
Db         20 ATCCAGGCCACCTGTGAGGC 1


RESULT 2943
US-10-210-556-157
; Sequence 157, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION
;  FILE REFERENCE: PTS-0015
;  CURRENT APPLICATION NUMBER: US/10/210,556
;  CURRENT FILING DATE:  2002-07-31
;  NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 157
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-210-556-157

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1370 AGCCAGGCCATCTGTGCCGC 1389
              | ||||||| |||||  ||
Db          1 ATCCAGGCCACCTGTGAGGC 20


RESULT 2944
US-10-211-179-27
; Sequence 27, Application US/10211179
; Publication No. US20040023906A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRI
;  FILE REFERENCE: PTS-0011
;  CURRENT APPLICATION NUMBER: US/10/211,179
;  CURRENT FILING DATE:  2002-08-01
;  NUMBER OF SEQ ID NOS: 119
; SEQ ID NO 27
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-211-179-27

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2203 TCTTCAAATGGGAGACTCTT 2222
              ||| ||||||||  | ||||
Db          1 TCTGCAAATGGGCCAGTCTT 20


RESULT 2945
US-10-211-179-94/c
; Sequence 94, Application US/10211179
; Publication No. US20040023906A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRI
;  FILE REFERENCE: PTS-0011
;  CURRENT APPLICATION NUMBER: US/10/211,179
;  CURRENT FILING DATE:  2002-08-01
;  NUMBER OF SEQ ID NOS: 119
; SEQ ID NO 94
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-211-179-94

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2203 TCTTCAAATGGGAGACTCTT 2222
              ||| ||||||||  | ||||
Db         20 TCTGCAAATGGGCCAGTCTT 1


RESULT 2946
US-10-309-290-169
```

```
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1578
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-1578

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        903 AAGTACAGAGGCGACTGTCC 922
              ||| || ||||||| | |||
Db          1 AAGAACGGAGGCGATTATCC 20


RESULT 2937
US-10-289-762-2361/c
; Sequence 2361, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2361
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-2361

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1114 CTTTGCCTATGTCTGTGAAG 1133
              ||||||||||     ||||||
Db         20 CTTTGCCTATAGGGGTGAAG 1


RESULT 2938
US-10-289-762-4000/c
; Sequence 4000, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4000
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-4000

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1310 TTGGAGACGAACATACAGAA 1329
              |||  | ||||| |||||||
Db         20 TTGCTGCCGAACCTACAGAA 1


RESULT 2939
US-10-289-762-4383/c
; Sequence 4383, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4383
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-4383

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1114 CTTTGCCTATGTCTGTGAAG 1133
              |||| ||||||| || | ||
Db         20 CTTTCCCTATGTATGGGGAG 1


RESULT 2940
US-10-455-229-12
; Sequence 12, Application US/10455229
; Publication No. US20040016030A1
; GENERAL INFORMATION:
;  APPLICANT: LOWE, BRENDA A.
;  APPLICANT:  CHOMET, PAUL
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF MAIZE LINES
;  TITLE OF INVENTION:  WITH INCREASED TRANSFORMABILITY
;  FILE REFERENCE: DEKM:195US
;  CURRENT APPLICATION NUMBER: US/10/455,229
;  CURRENT FILING DATE:  2003-06-05
;  PRIOR APPLICATION NUMBER: 60/386,522
;  PRIOR FILING DATE: 2002-06-06
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-10-455-229-12

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1084 AGAAGGTGAAGCTGTTCATT 1103
              |||| |||||||||  | ||
Db          1 AGAACGTGAAGCTGAGCGTT 20


RESULT 2941
US-10-138-588-171
; Sequence 171, Application US/10138588
; Publication No. US20040018594A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook et al.
;  TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI
;  TITLE OF INVENTION:  ENCODING THE ANTIGENS, AND METHODS OF USE
;  FILE REFERENCE: 21402-347A
;  CURRENT APPLICATION NUMBER: US/10/138,588
;  CURRENT FILING DATE:  2002-05-01
```

```
  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCCC 308
              |||||| || |||| | |||
Db         20 CCCCGCCCCGCCCCGCCCCC 1


RESULT 2932
US-10-407-449-9/c
; Sequence 9, Application US/10407449
; Publication No. US20040005601A1
; GENERAL INFORMATION:
;  APPLICANT: Siddiqui-Jain, Adam
;  APPLICANT:  Hurley, Laurence
;  APPLICANT:  Farrell, Thomas
;  APPLICANT:  Grand, Cory
;  APPLICANT:  Bearss, David
;  TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
;  FILE REFERENCE: 53223-20004.00
;  CURRENT APPLICATION NUMBER: US/10/407,449
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/404,966
;  PRIOR FILING DATE: 2002-08-04
;  PRIOR APPLICATION NUMBER: US 60/370,358
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: Unknown
;  PRIOR FILING DATE: 2003-03-20
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-407-449-9

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCCC 308
              |||||| || |||| | |||
Db         20 CCCCGCCCCGCCCCGCCCCC 1


RESULT 2933
US-10-188-470-13/c
; Sequence 13, Application US/10188470
; Publication No. US20040005707A1
; GENERAL INFORMATION:
;  APPLICANT: Scott Cooper
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA 5 EXPRESSION
;  FILE REFERENCE: PTS-0024
;  CURRENT APPLICATION NUMBER: US/10/188,470
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-470-13

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2364 AAGAAACAGTGCGTTGAGTG 2383
              |||| | | ||||| |||||
Db         20 AAGAGAGATTGCGTCGAGTG 1


RESULT 2934
US-10-189-267-136
; Sequence 136, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
;  FILE REFERENCE: PTS-0038
;  CURRENT APPLICATION NUMBER: US/10/189,267
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 136
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-136

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        768 CCAAGAACCCTCTGAACCTC 787
              |||||| |||||| ||  ||
Db          1 CCAAGATCCCTCTTAAAATC 20


RESULT 2935
US-10-189-267-258/c
; Sequence 258, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
;  FILE REFERENCE: PTS-0038
;  CURRENT APPLICATION NUMBER: US/10/189,267
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 258
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: M. musculus
;   FEATURE:
US-10-189-267-258

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        768 CCAAGAACCCTCTGAACCTC 787
              |||||| |||||| ||  ||
Db         20 CCAAGATCCCTCTTAAAATC 1


RESULT 2936
US-10-289-762-1578
; Sequence 1578, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prever
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
```

```
US-10-349-143-8908
; Sequence 8908, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8908
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: downstream amplification primer 99-1997 for SEQ 1043, in compleme
US-10-349-143-8908

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        970 AGCCAAATCGAAAAATGGAG 989
              ||||||||  | |||| |||
Db          1 AGCCAAATGAACAAATAGAG 20


RESULT 2929
US-10-349-143-9924
; Sequence 9924, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9924
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: downstream amplification primer 99-8289 for SEQ 2059, in compleme
US-10-349-143-9924

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1493 GAGAAAATGGAGAAACACAG 1512
              || | || ||||| ||||||
Db          1 GATATAAAGGAGATACACAG 20


RESULT 2930
US-10-349-143-10846/c
; Sequence 10846, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10846
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: downstream amplification primer 99-21377 for SEQ 2981, in complem
US-10-349-143-10846

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2124 GAAACTTGTAGAAACGAAGC 2143
              |||||   || |||||||||
Db         20 GAAACCACTATAAACGAAGC 1


RESULT 2931
US-10-407-449-5/c
; Sequence 5, Application US/10407449
; Publication No. US20040005601A1
; GENERAL INFORMATION:
;  APPLICANT: Siddiqui-Jain, Adam
;  APPLICANT:  Hurley, Laurence
;  APPLICANT:  Farrell, Thomas
;  APPLICANT:  Grand, Cory
;  APPLICANT:  Bearss, David
;  TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
;  FILE REFERENCE: 53223-20004.00
;  CURRENT APPLICATION NUMBER: US/10/407,449
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/404,966
;  PRIOR FILING DATE: 2002-08-04
;  PRIOR APPLICATION NUMBER: US 60/370,358
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: Unknown
;  PRIOR FILING DATE: 2003-03-20
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-407-449-5
```

```
; SEQ ID NO 68
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-646-68

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         33 GGACAGCAAGGCCCGCGCGC 52
              |||||| |||| ||| |||
Db          1 GGACAGGAAGGTGCGCACGC 20


RESULT 2924
US-10-188-646-137/c
; Sequence 137, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
;  FILE REFERENCE: RTS-0373
;  CURRENT APPLICATION NUMBER: US/10/188,646
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 137
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-188-646-137

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         33 GGACAGCAAGGCCCGCGCGC 52
              |||||| |||| ||| |||
Db         20 GGACAGGAAGGTGCGCACGC 1


RESULT 2925
US-10-188-779A-64/c
; Sequence 64, Application US/10188779A
; Publication No. US20040005567A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN-DEPENDENT KINASE 4 EXPRESSION
;  FILE REFERENCE: PTS-0042
;  CURRENT APPLICATION NUMBER: US/10/188,779A
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 282
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-779A-64

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1593 GGGAACCCCTCCTGGCCTGG 1612
              | |||||| |||||||  ||
Db         20 GAGAACCCATCCTGGCTGGG 1


RESULT 2926
US-10-188-779A-127
; Sequence 127, Application US/10188779A
; Publication No. US20040005567A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN-DEPENDENT KINASE 4 EXPRESSION
;  FILE REFERENCE: PTS-0042
;  CURRENT APPLICATION NUMBER: US/10/188,779A
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 282
; SEQ ID NO 127
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-779A-127

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2339 AGTCCCCGTGGAGGTTCTGT 2358
              || ||| |||||||| || |
Db          1 AGGCCCGGTGGAGGTGCTTT 20


RESULT 2927
US-10-349-143-5752
; Sequence 5752, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5752
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: upstream amplification primer 99-6613 for SEQ 1818,
US-10-349-143-5752

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1535 AGGTTAGGAGAGTAGGGAAG 1554
              || | ||||| | |||||||
Db          1 AGATGAGGAGTGGAGGGAAG 20


RESULT 2928
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  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2212 GGGAGACTCTTTGAAATGAC 2231
              || | ||  ||||||||||
Db         20 GGAAAACAGTTTGAAATGAC 1


RESULT 2920
US-10-159-856-59/c
; Sequence 59, Application US/10159856
; Publication No. US20030228689A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRE
;  FILE REFERENCE: RTS-0365
;  CURRENT APPLICATION NUMBER: US/10/159,856
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 59
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-856-59

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        794 CAGAAGGAGCTGGTGGGGGC 813
              ||||| ||| |||||| | |
Db         20 CAGAACGAGATGGTGGAGAC 1


RESULT 2921
US-10-167-034-57
; Sequence 57, Application US/10167034
; Publication No. US20030228690A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-1 EXPRESS
;  FILE REFERENCE: PTS-0003
;  CURRENT APPLICATION NUMBER: US/10/167,034
;  CURRENT FILING DATE:  2002-06-10
;  NUMBER OF SEQ ID NOS: 142
; SEQ ID NO 57
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-167-034-57

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        362 CAGCTGGCCTACTCCCAGTC 381
              ||||||||| |  ||||| |
Db          1 CAGCTGGCCCAGGCCCAGGC 20


RESULT 2922
US-10-307-928A-34
; Sequence 34, Application US/10307928A
; Publication No. US20030229016A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John P.
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Guo, Xiaojia (Sasha)
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Li, Li
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Voss, Edward Z.
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS O
;  TITLE OF INVENTION:  THE SAME
;  FILE REFERENCE: 24102-502D
;  CURRENT APPLICATION NUMBER: US/10/307,928A
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/341,477
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 60/341,540
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 60/342,592
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/344,903
;  PRIOR FILING DATE: 2001-12-31
;  PRIOR APPLICATION NUMBER: 60/373,288
;  PRIOR FILING DATE: 2002-04-17
;  PRIOR APPLICATION NUMBER: 60/380,981
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/381,495
;  PRIOR FILING DATE: 2002-05-17
;  PRIOR APPLICATION NUMBER: 60/383,744
;  PRIOR FILING DATE: 2002-05-28
;  PRIOR APPLICATION NUMBER: 60/384,024
;  PRIOR FILING DATE: 2002-05-29
;  PRIOR APPLICATION NUMBER: 60/401,788
;  PRIOR FILING DATE: 2002-08-07
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Primer/Probe
US-10-307-928A-34

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        606 ACCTGCTGCTGCCCCACGCA 625
              ||||||||| |  |||| ||
Db          1 ACCTGCTGCAGGGCCACTCA 20


RESULT 2923
US-10-188-646-68
; Sequence 68, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
;  FILE REFERENCE: RTS-0373
;  CURRENT APPLICATION NUMBER: US/10/188,646
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 153
```

```
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-23

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        903 AAGTACAGAGGCGACTGTCC 922
              | |||||||| || | ||||
Db         20 AGGTACAGAGACGTCAGTCC 1


RESULT 2916
US-10-360-510-183/c
; Sequence 183, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/10/360,510
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US/09/854,883
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 183
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-183

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1590 ACTGGGAACCCCTCCTGGCC 1609
              ||||| | ||| ||||||  |
Db         20 ACTGGAAGCCCTTCCTGGTC 1


RESULT 2917
US-10-360-510-301
; Sequence 301, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/10/360,510
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US/09/854,883
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 301
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-301

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        350 CCTCCCTACCAGCAGCTGGC 369
              |||||  ||||||||   |||
Db          1 CCTCCTTACCAGCAAGAGGC 20


RESULT 2918
US-10-159-834-58
; Sequence 58, Application US/10159834
; Publication No. US20030228688A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ISOPRENYLCYSTEINE CARBOXYL METHYLTRANSFERA
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0299
;  CURRENT APPLICATION NUMBER: US/10/159,834
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 58
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-834-58

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2212 GGGAGACTCTTTGAAATGAC 2231
              || | ||  ||||||||||
Db          1 GGAAAACAGTTTGAAATGAC 20


RESULT 2919
US-10-159-834-117/c
; Sequence 117, Application US/10159834
; Publication No. US20030228688A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ISOPRENYLCYSTEINE CARBOXYL METHYLTRANSFERA
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0299
;  CURRENT APPLICATION NUMBER: US/10/159,834
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 117
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-159-834-117

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
```

```
;  FILE REFERENCE: 2185-0648P
;  CURRENT APPLICATION NUMBER: US/10/148,835
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 213
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Designed
;   OTHER INFORMATION: oligonucleotide probe  for Southern hybridization
US-10-148-835-118

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        365 CTGGCCTACTCCCAGTCGGC 384
              ||||||| |||| | ||||
Db          1 CTGGCCTTGTCCCTGACGGC 20


RESULT 2912
US-10-148-835-119
; Sequence 119, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
;  APPLICANT: SAITO et al.
;  TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
;  FILE REFERENCE: 2185-0648P
;  CURRENT APPLICATION NUMBER: US/10/148,835
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 213
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Designed
;   OTHER INFORMATION: oligonucleotide probe  for Southern hybridization
US-10-148-835-119

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        369 CCTACTCCCAGTCGGCCGAC 388
              |||  |||| | ||||||||
Db          1 CCTTGTCCCTGACGGCCGAC 20


RESULT 2913
US-10-151-612-16
; Sequence 16, Application US/10151612
; Publication No. US20030215872A1
; GENERAL INFORMATION:
;  APPLICANT: Kohn, Leonard D
;  APPLICANT:  Suzuki, Koichi
;  APPLICANT:  Mori-Aoki, Atsumi
;  APPLICANT:  Iishi, Ken
;  APPLICANT:  Klinman, Dennis M
;  APPLICANT:  Rice, John M
;  TITLE OF INVENTION: IMMUNE ACTIVATION BY DOUBLE-STRANDED POLYNUCLEOTIDES
;  FILE REFERENCE: 0079661/0502168
;  CURRENT APPLICATION NUMBER: US/10/151,612
;  CURRENT FILING DATE:  2003-03-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Rattus sp.
US-10-151-612-16

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        829 TGAGGTCTTCTGCTCAGTCC 848
              ||| | ||||||||| | ||
Db          1 TGAAGACTTCTGCTCGGACC 20


RESULT 2914
US-10-310-677-34/c
; Sequence 34, Application US/10310677
; Publication No. US20030219772A1
; GENERAL INFORMATION:
;  APPLICANT: Kuyl v.d., Antoinette C.
;  APPLICANT:  Cornelissen, Marion
;  TITLE OF INVENTION: Means and methods for treatment evaluation
;  FILE REFERENCE: P55190US10
;  CURRENT APPLICATION NUMBER: US/10/310,677
;  CURRENT FILING DATE:  2002-12-05
;  PRIOR APPLICATION NUMBER: EP 01200228.3
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: EP 01203703.2
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US 60/325,722
;  PRIOR FILING DATE: 2001-09-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: TAG004
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(5)
;   OTHER INFORMATION: /note="A  stands for inosine"
US-10-310-677-34

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2343 CCCGTGGAGGTTCTGTATTT 2362
              || |||||||  ||| |||
Db         20 CCAGTGGAGGTCATGTTTTT 1


RESULT 2915
US-10-360-510-23/c
; Sequence 23, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Madeline M. Butler
;  APPLICANT:  Robert McKay
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
;  FILE REFERENCE: ISPH-0576
;  CURRENT APPLICATION NUMBER: US/10/360,510
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: US/09/854,883
;  PRIOR FILING DATE: 2001-05-14
;  PRIOR APPLICATION NUMBER: US 09/629,644
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 09/487,368
;  PRIOR FILING DATE: 2000-01-18
```

```
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2756 TGTATAATAAAAGTATTCTT 2775
              | |||||||||| ||  |||
Db         20 TCTATAATAAAACTAAACTT 1


RESULT 2908
US-10-430-196-67
; Sequence 67, Application US/10430196
; Publication No. US20030194738A1
;   GENERAL INFORMATION:
;        APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
;                   Miraglia; Brenda F. Baker
;        TITLE OF INVENTION: Antisense Oligonucleotide
;                            Compositions and Methods for the Modulation of
;                            Activating Protein 1
;        NUMBER OF SEQUENCES: 139
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Law Offices of Jane Massey Licata
;             STREET: 66 East Main Street
;             CITY: Marlton
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08053
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: WINDOWS 95
;             SOFTWARE: WORDPERFECT 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/430,196
;             FILING DATE: 05-May-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/923,517A
;             FILING DATE: 07-Aug-2001
;             APPLICATION NUMBER: 09/364,416
;             FILING DATE: 1999-07-30
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jane Massey Licata
;             REGISTRATION NUMBER: 32,257
;             REFERENCE/DOCKET NUMBER: ISPH-0209
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (609) 810-1515
;             TELEFAX: (609) 810-1454
;   INFORMATION FOR SEQ ID NO: 67:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20
;             TYPE: Nucleic Acid
;             STRANDEDNESS: Single
;             TOPOLOGY: Linear
;        ANTI-SENSE: Yes
;        SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-430-196-67

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        632 CTGGATGCCGCGGGCCTGGC 651
              ||||||||||    |||| ||
Db          1 CTGGATGCCGGCTGCCTTGC 20


RESULT 2909
US-10-273-557-2/c
; Sequence 2, Application US/10273557
; Publication No. US20030195256A1
; GENERAL INFORMATION:
;  APPLICANT: SINGH, INDERJIT
;  TITLE OF INVENTION: INHIBITORS OF NITRIC OXIDE SYNTHASE
;  FILE REFERENCE: MESC002USD1
;  CURRENT APPLICATION NUMBER: US/10/273,557
;  CURRENT FILING DATE:  2003-01-14
;  PRIOR APPLICATION NUMBER: 09/579,791
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/066,839
;  PRIOR FILING DATE: 1997-11-25
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-10-273-557-2

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1482 ACAAAACCCTGGAGAAAATG 1501
              |||| | ||||||| || ||
Db         20 ACAACATCCTGGAGGAAGTG 1


RESULT 2910
US-10-005-344-215/c
; Sequence 215, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
;  APPLICANT: Loren J. Miraglia
;  APPLICANT:  Pamela Nero
;  APPLICANT:  Mark J. Graham
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Erich Koller
;  APPLICANT:  MingYi Chiang
;  APPLICANT:  Mano Manoharan
;  TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
;  FILE REFERENCE: ISPH-0622
;  CURRENT APPLICATION NUMBER: US/10/005,344
;  CURRENT FILING DATE:  2001-12-04
;  PRIOR APPLICATION NUMBER: US 09/048,810
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: US 09/280,805
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 379
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 215
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-005-344-215

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2520 TTTATTCATATATATACAGG 2539
              |||||||| ||||||  | |
Db         20 TTTATTCACATATATCAAAG 1


RESULT 2911
US-10-148-835-118
; Sequence 118, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
;  APPLICANT: SAITO et al.
;  TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
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;  TITLE OF INVENTION:  METHOD FOR ASSESSMENT OF GENE EXPRESSION IN SMALL BIOLOGICAL SAM
;  FILE REFERENCE: 01154/2001-203
;  CURRENT APPLICATION NUMBER: US/10/109,349A
;  CURRENT FILING DATE:  2002-06-12
;  NUMBER OF SEQ ID NOS: 282
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-109-349A-167

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        633 TGGATGCCGCGGGCCTGGCC 652
              ||||||| || ||  |||||
Db         20 TGGATGCTGCTGGTGTGGCC 1


RESULT 2905
US-10-356-625-116/c
; Sequence 116, Application US/10356625
; Publication No. US20030186290A1
; GENERAL INFORMATION:
;  APPLICANT: Tournier-Lasserve, Elisabeth
;  APPLICANT:  Joutel, Anne
;  APPLICANT:  Bousser, Marie-Germaine
;  APPLICANT:  Bach, Jean-Francois
;  TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND
;  TITLE OF INVENTION:  THERAPEUTIC APPLICATION
;  FILE REFERENCE: 03715.0048-00000
;  CURRENT APPLICATION NUMBER: US/10/356,625
;  CURRENT FILING DATE:  2003-02-03
;  PRIOR APPLICATION NUMBER: US/09/230,652
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: FR 96 09733
;  PRIOR FILING DATE: 1996-08-01
;  PRIOR APPLICATION NUMBER: FR 97 04680
;  PRIOR FILING DATE: 1997-04-16
;  PRIOR APPLICATION NUMBER: PCT/FR97/01433
;  PRIOR FILING DATE: 1997-07-31
;  NUMBER OF SEQ ID NOS: 163
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-356-625-116

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAACA 1559
              ||||||||  |   |||||||
Db         20 AGGAGAGTGGCACAGGAACA 1


RESULT 2906
US-10-352-615-66/c
; Sequence 66, Application US/10352615
; Publication No. US20030190285A1
;   GENERAL INFORMATION:
;        APPLICANT: VAN DEN VEN, W.J.M.
;                   SCHOENMAKERS, H.F.P.M.
;        TITLE OF INVENTION: MULTIPLE-TUMOR ABERRENT GROWTH
;                            GENES
;        NUMBER OF SEQUENCES: 164
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: The Webb Law Firm
;             STREET: 700 Koppers Building, 436 Seventh Avenue
;             CITY: Pittsburgh
;             STATE: PA
;             COUNTRY: USA
;             ZIP: 15219-1818
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/352,615
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/894,454
;             FILING DATE: 15-AUG-1997
;             APPLICATION NUMBER: PCT/EP/00716
;             FILING DATE: 19-FEB-1996
;             APPLICATION NUMBER: 95200390.3
;             FILING DATE: 17-FEB-1995
;             APPLICATION NUMBER: 95201951.1
;             FILING DATE: 14-JUL-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Johnson, Barbara E
;             REGISTRATION NUMBER: 31,198
;             REFERENCE/DOCKET NUMBER: 702-971100
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 412-471-8815
;             TELEFAX: 412-471-4094
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 66:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-352-615-66

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2672 CAGTGTGTGTGGGTGAAATG 2691
              ||  ||||||||  ||| |||
Db         20 CATTGTGTGTGCCTGAGATG 1


RESULT 2907
US-10-080-979-47/c
; Sequence 47, Application US/10080979
; Publication No. US20030191075A1
; GENERAL INFORMATION:
;  APPLICANT: Cook,  Philip Dan
;  APPLICANT:  Manoharan, Muthiah
;  APPLICANT:  Bennett, Frank C.
;  TITLE OF INVENTION: Oligonucleotide Conjugates For Hepatic Delivery
;  FILE REFERENCE: Isis-5028
;  CURRENT APPLICATION NUMBER: US/10/080,979
;  CURRENT FILING DATE:  2002-02-22
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-080-979-47

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02024
US-10-367-470-17

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db         20 TTTTTTTAGAATTTTTTTTT 1


RESULT 2901
US-10-173-805-1
; Sequence 1, Application US/10173805
; Publication No. US20030170240A1
; GENERAL INFORMATION:
;  APPLICANT: SAKANO, Katsuichi
;  APPLICANT:  HIGASHIHASHI, No. US20030170240A1uyuki
;  APPLICANT:  HASHIMOTO, Ryuji
;  TITLE OF INVENTION: Method for Elevating the Concentration of Free
;  TITLE OF INVENTION:  Insulin-Like Growth Factor
;  FILE REFERENCE: Q54313
;  CURRENT APPLICATION NUMBER: US/10/173,805
;  CURRENT FILING DATE:  2002-06-19
;  PRIOR APPLICATION NUMBER: US/09/331,851
;  PRIOR FILING DATE: 1999-06-28
;  PRIOR APPLICATION NUMBER: JP P1996-349968
;  PRIOR FILING DATE: 1996-12-27
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: STS
;   LOCATION: (1)..(20)
;   OTHER INFORMATION: One of PCR primers for cloning of the 5' end of
;   OTHER INFORMATION: IGFBP-3 gene from rat pancreas cDNA library
;   OTHER INFORMATION: The Sequence is described at page 38, line 19
;   OTHER INFORMATION: of the specification.
;  PUBLICATION INFORMATION:
;   AUTHORS: Shimasaki, S.
;   JOURNAL: Biochem. Biophys. Res. Commun.
;   VOLUME: 165
;   PAGES: 907-
;   DATE: 1989
US-10-173-805-1

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        628 CGCCCTGGATGCCGCGGGCC 647
              |||| || || ||||| |||
Db          1 CGCCATGCATCCCGCGCGCC 20


RESULT 2902
US-10-055-728-34/c
; Sequence 34, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
;  APPLICANT: van der Kuyl, Antoinette C.
;  APPLICANT:  Cornelissen, Marion
;  TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
;  FILE REFERENCE: 5244US (REN/P55190US00)
;  CURRENT APPLICATION NUMBER: US/10/055,728
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/325,722
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 0120373.2
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: EP 01200228.3
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 156
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(5)
;   OTHER INFORMATION: a stands for inosine
US-10-055-728-34

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2343 CCCGTGGAGGTTCTGTATTT 2362
              || |||||||  ||| |||
Db         20 CCAGTGGAGGTCATGTTTTT 1


RESULT 2903
US-10-053-645A-26
; Sequence 26, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
;  APPLICANT: Robert E. Klem
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
;  TITLE OF INVENTION:  CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
;  TITLE OF INVENTION:  ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
;  FILE REFERENCE: 10412-022-999
;  CURRENT APPLICATION NUMBER: US/10/053,645A
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: 60/263,244
;  PRIOR FILING DATE: 2001-01-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
;   OTHER INFORMATION: Oligionucleotide
US-10-053-645A-26

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         49 GCGCGGCGGGGGCGGCGGCA 68
              |||||||||| | |  ||||
Db          1 GCGCGGCGGGCGGGCGGGCA 20


RESULT 2904
US-10-109-349A-167/c
; Sequence 167, Application US/10109349A
; Publication No. US20030186246A1
; GENERAL INFORMATION:
;  APPLICANT: Medical College of Ohio
;  APPLICANT:  Willey, James C.
;  APPLICANT:  Crawford, Erin L.
;  TITLE OF INVENTION: MULTIPLEX STANDARDIZED REVERSE TRANSCRIPTASE-POLYMERASE CHAIN REAC
```

```
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02013
US-10-367-470-10

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 2897
US-10-367-470-11
; Sequence 11, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02014
US-10-367-470-11

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 2898
US-10-367-470-12/c
; Sequence 12, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Complement DNA oligo AGT02009
US-10-367-470-12

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db         20 TTTTTTTAAAATTTTTTTTT 1


RESULT 2899
US-10-367-470-14/c
; Sequence 14, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligo AGT02021
US-10-367-470-14

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db         20 TTTTTTTACAATTTTTTTTT 1


RESULT 2900
US-10-367-470-17/c
; Sequence 17, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
```

```
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: US 08/624,447
;  PRIOR FILING DATE: 1996-08-19
;  PRIOR APPLICATION NUMBER: PCT/US94/11279
;  PRIOR FILING DATE: 1994-10-06
;  PRIOR APPLICATION NUMBER: US 08/133,963
;  PRIOR FILING DATE: 1993-10-07
;  NUMBER OF SEQ ID NOS: 145
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 89
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Amycolatopsis mediterranei
US-10-267-255-89

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        507 TGCCCTCGCACCACGGGCGC 526
              ||| | |||| ||||| |||
Db         20 TGCGCGCGCAGCACGGACGC 1


RESULT 2893
US-10-267-255-90
; Sequence 90, Application US/10267255
; Publication No. US20030124689A1
; GENERAL INFORMATION:
;  APPLICANT: Sherman, D
;  APPLICANT:  Mao, Y
;  APPLICANT:  Varoglu, M
;  APPLICANT:  He, M
;  APPLICANT:  Sheldon, P
;  TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
;  FILE REFERENCE: 600.456US1
;  CURRENT APPLICATION NUMBER: US/10/267,255
;  CURRENT FILING DATE:  2002-10-09
;  PRIOR APPLICATION NUMBER: US 09/266,965
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: US 08/624,447
;  PRIOR FILING DATE: 1996-08-19
;  PRIOR APPLICATION NUMBER: PCT/US94/11279
;  PRIOR FILING DATE: 1994-10-06
;  PRIOR APPLICATION NUMBER: US 08/133,963
;  PRIOR FILING DATE: 1993-10-07
;  NUMBER OF SEQ ID NOS: 145
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 90
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Amycolatopsis mediterranei
US-10-267-255-90

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        507 TGCCCTCGCACCACGGGCGC 526
              ||| | |||| ||||| |||
Db          1 TGCGCGCGCAGCACGGACGC 20


RESULT 2894
US-10-367-470-8
; Sequence 8, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02008
US-10-367-470-8

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTT 20


RESULT 2895
US-10-367-470-9
; Sequence 9, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: US 09/616,761
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide AGT02012
US-10-367-470-9

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTT 20


RESULT 2896
US-10-367-470-10
; Sequence 10, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
;  APPLICANT: Applied Gene Technologies, Inc.
;  APPLICANT:  Dattagupta, Nanibhushan
;  TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 47541-20004.20
;  CURRENT APPLICATION NUMBER: US/10/367,470
;  CURRENT FILING DATE:  2003-02-13
;  PRIOR APPLICATION NUMBER: US/09/823,647B
```

```
;  TITLE OF INVENTION: Proteins
;  FILE REFERENCE: 2543-1-028
;  CURRENT APPLICATION NUMBER: US/10/227,616
;  CURRENT FILING DATE:  2002-08-23
;  PRIOR APPLICATION NUMBER: GB 0004576.5
;  PRIOR FILING DATE: 2000-02-25
;  PRIOR APPLICATION NUMBER: GB 0031341.1
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY:
;   OTHER INFORMATION: Primer
US-10-227-616-88

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        849 CTGGAAGATTGTCGCTCCTC 868
              ||||| |||||||  | |||
Db          1 CTGGAGGATTGTCAATACTC 20


RESULT 2889
US-10-161-229-99
; Sequence 99, Application US/10161229
; Publication No. US20030100527A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules for
;  TITLE OF INVENTION:  Activating Dendritic Cells
;  FILE REFERENCE: C01039/70061
;  CURRENT APPLICATION NUMBER: US/10/161,229
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: US 09/191,170
;  PRIOR FILING DATE: 1998-11-13
;  PRIOR APPLICATION NUMBER: US 08/960,774
;  PRIOR FILING DATE: 1997-10-30
;  PRIOR APPLICATION NUMBER: US 08/738,652
;  PRIOR FILING DATE: 1996-10-30
;  PRIOR APPLICATION NUMBER: US 08/386,063
;  PRIOR FILING DATE: 1995-02-07
;  PRIOR APPLICATION NUMBER: US 08/276,358
;  PRIOR FILING DATE: 1994-07-15
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-161-229-99

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAAAA 1985
              || ||  || ||||||||||
Db          1 AAAATCAACGTTGAAAAAAA 20


RESULT 2890
US-10-003-354-67/c
; Sequence 67, Application US/10003354
; Publication No. US20030114400A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINAS
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0348
;  CURRENT APPLICATION NUMBER: US/10/003,354
;  CURRENT FILING DATE:  2001-12-06
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-354-67

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2620 AATAACTTTGTCTCGTTCCT 2639
              || ||| || |||| |||||
Db         20 AAGAACCTTCTCTCCTTCCT 1


RESULT 2891
US-10-279-186-70/c
; Sequence 70, Application US/10279186
; Publication No. US20030114407A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR
;  TITLE OF INVENTION:  ETBR-LP-2 EXPRESSION
;  FILE REFERENCE: RTS-0346
;  CURRENT APPLICATION NUMBER: US/10/279,186
;  CURRENT FILING DATE:  2002-10-23
;  PRIOR APPLICATION NUMBER: US/10/003,126
;  PRIOR FILING DATE: 2001-12-06
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 70
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-279-186-70

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        250 GGTCCCCCACCTCTCCTCCG 269
              |||  || |||||||| |||
Db         20 GGTGGCCTACCTCTCCACCG 1


RESULT 2892
US-10-267-255-89/c
; Sequence 89, Application US/10267255
; Publication No. US20030124689A1
; GENERAL INFORMATION:
;  APPLICANT: Sherman, D
;  APPLICANT:  Mao, Y
;  APPLICANT:  Varoglu, M
;  APPLICANT:  He, M
;  APPLICANT:  Sheldon, P
;  TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
;  FILE REFERENCE: 600.456US1
;  CURRENT APPLICATION NUMBER: US/10/267,255
;  CURRENT FILING DATE:  2002-10-09
;  PRIOR APPLICATION NUMBER: US 09/266,965
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RESULT 2884
US-10-017-995-855/c
; Sequence 855, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 855
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-855

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
             ||||||||||   |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 2885
US-10-173-539-19
; Sequence 19, Application US/10173539
; Publication No. US20030059812A1
; GENERAL INFORMATION:
;  APPLICANT: Richon, Victoria
;  APPLICANT:  Zhou, Xianbo
;  APPLICANT:  Rifkind, Richard A.
;  APPLICANT:  Marks, Paul A.
;  TITLE OF INVENTION: HDAC9 Polypeptides and Polynucleotides
;  TITLE OF INVENTION:  and Uses Thereof
;  FILE REFERENCE: 3254.1000-003
;  CURRENT APPLICATION NUMBER: US/10/173,539
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/298,173
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: 60/311,686
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/316,995
;  PRIOR FILING DATE: 2001-09-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer used to amplify human DNA
US-10-173-539-19

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGGCT 2567
             |||  | ||||||||||| |
Db          1 AATGTACAGGATGCTGGGGT 20


RESULT 2886
US-10-181-107-164
; Sequence 164, Application US/10181107
; Publication No. US20030083295A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
;  FILE REFERENCE: RTSP-0325
;  CURRENT APPLICATION NUMBER: US/10/181,107
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00888
;  PRIOR FILING DATE: 2001-01-11
;  PRIOR APPLICATION NUMBER: 09/484,617
;  PRIOR FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 164
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-107-164

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1742 GACAAGTACTGGCTCTTTAT 1761
              ||||  |||| |||| ||||
Db          1 GACAGTTACTTGCTCCTTAT 20


RESULT 2887
US-10-181-846-109/c
; Sequence 109, Application US/10181846
; Publication No. US20030083297A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
;  FILE REFERENCE: RTSP-0363
;  CURRENT APPLICATION NUMBER: US/10/181,846
;  CURRENT FILING DATE:  2002-07-17
;  PRIOR APPLICATION NUMBER: PCT/US01/01416
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: 09/490,692
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 109
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-846-109

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1992 TGTGTATCTAGCTTCTTCAG 2011
              ||||| ||| || ||| |||
Db         20 TGTGTTTCTGGCCTCTGCAG 1


RESULT 2888
US-10-227-616-88
; Sequence 88, Application US/10227616
; Publication No. US20030099662A1
; GENERAL INFORMATION:
;  APPLICANT: Boyd, Robert Simon
;  APPLICANT:  Stamps, Alasdair Craig
;  APPLICANT:  Terrett, Jonathan Alexander
```

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;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 749
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-749

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAAAA 1985
              || ||  || ||||||||||
Db          1 AAAATCAACGTTGAAAAAAA 20


RESULT 2880
US-10-112-653-826/c
; Sequence 826, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 826
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-826

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 2881
US-10-017-995-353/c
; Sequence 353, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 353
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-353

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1543 AGAGTAGGGAAGGAACAGGA 1562
              ||| |  |||||||||| |||
Db         20 AGACTGAGGAAGGAACTGGA 1


RESULT 2882
US-10-017-995-525/c
; Sequence 525, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 525
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-525

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 2883
US-10-017-995-776
; Sequence 776, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-776

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAAAA 1985
              || ||  || ||||||||||
Db          1 AAAATCAACGTTGAAAAAAA 20
```

```
RESULT 2875
US-10-060-301-120/c
; Sequence 120, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA, Yusuke  et al.
;  TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
;  FILE REFERENCE: 1254-0195p
;  CURRENT APPLICATION NUMBER: US/10/060,301
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: JP 2001-25700
;  PRIOR FILING DATE: 2001-02-01
;  NUMBER OF SEQ ID NOS: 200
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Reverse Primer for SNP ID 60
US-10-060-301-120

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2094 CGTGTTCAAACGGGGGCCTT 2113
              ||| |||||| | ||||||
Db         20 CGTTCTCAAACTGTGGCCTT 1


RESULT 2876
US-10-125-181-17
; Sequence 17, Application US/10125181
; Publication No. US20020187954A1
; GENERAL INFORMATION:
;  APPLICANT: WRIGHT, Jim A.
;  APPLICANT:  YOUNG, Aiping H.
;  APPLICANT:  LEE, Yoon S.
;  TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE
;  TITLE OF INVENTION:  OLIGONUCLEOTIDE
;  TITLE OF INVENTION:  SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL
;  TITLE OF INVENTION:  GROWTH
;  FILE REFERENCE: 032396-046
;  CURRENT APPLICATION NUMBER: US/10/125,181
;  CURRENT FILING DATE:  2002-04-17
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/295,593
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,791
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-23
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Human
US-10-125-181-17

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        251 GTCCCCCACCTCTCCTCCGC 270
              |||| ||| ||| || ||||
Db          1 GTCCACCAGCTCCCCGCCGC 20


RESULT 2877
US-10-112-653-342/c
; Sequence 342, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-342

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1543 AGAGTAGGGAAGGAACAGGA 1562
              ||| |  |||||||| |||
Db         20 AGACTGAGGAAGGAACTGGA 1


RESULT 2878
US-10-112-653-502/c
; Sequence 502, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 502
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-502

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 2879
US-10-112-653-749
; Sequence 749, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
```

```
US-10-314-578-855/c
; Sequence 855, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Schetter, Christian
;  APPLICANT:  Vollmer, Jorg
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids
;  FILE REFERENCE: C1039/7035 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/314,578
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 60/156,113
;  PRIOR FILING DATE: 1999-09-25
;  PRIOR APPLICATION NUMBER: US 60/156,135
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: US 60/227,436
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 1145
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 855
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-314-578-855

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 2872
US-10-287-971-307
; Sequence 307, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, et al
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-480A
;  CURRENT APPLICATION NUMBER: US/10/287,971
;  CURRENT FILING DATE:  2002-11-05
;  PRIOR APPLICATION NUMBER: 09/997,425
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: 10/035,568
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: 60/338,626
;  PRIOR FILING DATE: 2001-11-05
;  PRIOR APPLICATION NUMBER: 60/401,479
;  PRIOR FILING DATE: 2002-08-06
;  PRIOR APPLICATION NUMBER: 60/333,072
;  PRIOR FILING DATE: 2001-11-06
;  PRIOR APPLICATION NUMBER: 60/348,283
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: 60/393,262
;  PRIOR FILING DATE: 2002-07-02
;  PRIOR APPLICATION NUMBER: 60/406,181
;  PRIOR FILING DATE: 2002-08-26
;  NUMBER OF SEQ ID NOS: 397
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 307
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artifical Sequence:  Primer/Probe
US-10-287-971-307

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1459 AGACCAGAGTCCAGCTGATT 1478
              ||||||   ||||||| ||
Db          1 AGACCAAGCTCCAGCTGTTT 20


RESULT 2873
US-10-403-902A-80/c
; Sequence 80, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
;  APPLICANT: Braun, Andreas
;  APPLICANT:  Bansal, Aruna
;  APPLICANT:  Kleyn, Patrick
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE AND THEIR USE
;  FILE REFERENCE: 24736-2048B
;  CURRENT APPLICATION NUMBER: US/10/403,902A
;  CURRENT FILING DATE:  2003-07-21
;  PRIOR APPLICATION NUMBER: 09/802,640
;  PRIOR FILING DATE: 2001-03-09
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-403-902A-80

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        642 CGGGCCTGGCCGAGAACCTG 661
              | |  |||||||||| ||||
Db         20 CAGCACTGGCCGAGATCCTG 1


RESULT 2874
US-10-060-301-94
; Sequence 94, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA, Yusuke  et al.
;  TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
;  FILE REFERENCE: 1254-0195p
;  CURRENT APPLICATION NUMBER: US/10/060,301
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: JP 2001-25700
;  PRIOR FILING DATE: 2001-02-01
;  NUMBER OF SEQ ID NOS: 200
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Reverse Primer for SNP ID 47
US-10-060-301-94

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1197 AGATGGCAGCTAGGAAGAAC 1216
              |||  ||||| |||||| ||
Db          1 AGAACGCAGCAAGGAAGCAC 20
```

```
Qy       1051 AGCCGCTCATGTGACTCTCC 1070
              | |  |||||| ||||||||
Db         20 ACCACCTCATGAGACTCTCC 1


RESULT 2867
US-10-144-140-14
; Sequence 14, Application US/10144140
; Publication No. US20030211606A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DYRK4 EXPRESSION
;  FILE REFERENCE: RTS-0362
;  CURRENT APPLICATION NUMBER: US/10/144,140
;  CURRENT FILING DATE:  2002-05-10
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-144-140-14

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        530 GCCGGCCTACTGCCCCACCT 549
              || ||||  |||| ||||||
Db          1 GCAGGCCAGCTGCTCCACCT 20


RESULT 2868
US-10-314-578-353/c
; Sequence 353, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Schetter, Christian
;  APPLICANT:  Vollmer, Jorg
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids
;  FILE REFERENCE: C1039/7035 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/314,578
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 60/156,113
;  PRIOR FILING DATE: 1999-09-25
;  PRIOR APPLICATION NUMBER: US 60/156,135
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: US 60/227,436
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 1145
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 353
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-314-578-353

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1543 AGAGTAGGGAAGGAACAGGA 1562
              |||  |  |||||||||  |||
Db         20 AGACTGAGGAAGGAACTGGA 1


RESULT 2869
US-10-314-578-525/c
; Sequence 525, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Schetter, Christian
;  APPLICANT:  Vollmer, Jorg
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids
;  FILE REFERENCE: C1039/7035 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/314,578
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 60/156,113
;  PRIOR FILING DATE: 1999-09-25
;  PRIOR APPLICATION NUMBER: US 60/156,135
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: US 60/227,436
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 1145
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 525
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-314-578-525

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 2870
US-10-314-578-776
; Sequence 776, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Schetter, Christian
;  APPLICANT:  Vollmer, Jorg
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids
;  FILE REFERENCE: C1039/7035 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/314,578
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 60/156,113
;  PRIOR FILING DATE: 1999-09-25
;  PRIOR APPLICATION NUMBER: US 60/156,135
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: US 60/227,436
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 1145
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-314-578-776

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAAAA 1985
              || ||  || ||||||||||
Db          1 AAAATCAACGTTGAAAAAAA 20


RESULT 2871
```

```
Db          1 CTGGAGGATTGTCAATACTC 20


RESULT 2862
US-09-771-355-5
; Sequence 5, Application US/09771355
; Publication No. US20020086840A1
; GENERAL INFORMATION:
;  APPLICANT: Reddy, Gurucharan
;  APPLICANT:  Zarling, David A.
;  TITLE OF INVENTION: USE OF RAD51 INHIBITORS FOR p53 GENE THERAPY
;  FILE REFERENCE: A-68872-1/RFT/RMS/BTC
;  CURRENT APPLICATION NUMBER: US/09/771,355
;  CURRENT FILING DATE:  2001-01-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Antisense
;   OTHER INFORMATION: oligonucleotide
US-09-771-355-5

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        563 GCGGGCGCGGTGAGCGCCCG 582
              ||||||| ||   |||||||
Db          1 GCGGGCGTGGCACGCGCCCG 20


RESULT 2863
US-10-144-488-57
; Sequence 57, Application US/10144488
; Publication No. US20030212017A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF FARNESYL TRANSFERASE BETA SUBUNIT EXPRESS
;  FILE REFERENCE: RTS-0363
;  CURRENT APPLICATION NUMBER: US/10/144,488
;  CURRENT FILING DATE:  2002-05-10
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-144-488-57

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        782 AACCTCCCCTGTCAGAAGGA 801
              | || | |||| ||||||||
Db          1 AGCCCCGCCTGCCAGAAGGA 20


RESULT 2864
US-10-163-272-13
; Sequence 13, Application US/10163272
; Publication No. US20030224517A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME 2 EXPRESSIO
;  FILE REFERENCE: RTS-0378
;  CURRENT APPLICATION NUMBER: US/10/163,272
;  CURRENT FILING DATE:  2002-06-04
;  NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-163-272-13

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2340 GTCCCCGTGGAGGTTCTGTA 2359
              |||||| || ||||| | ||
Db          1 GTCCCCCTGCAGGTTGTCTA 20


RESULT 2865
US-10-163-272-90/c
; Sequence 90, Application US/10163272
; Publication No. US20030224517A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME 2 EXPRESSIO
;  FILE REFERENCE: RTS-0378
;  CURRENT APPLICATION NUMBER: US/10/163,272
;  CURRENT FILING DATE:  2002-06-04
;  NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 90
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-163-272-90

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2340 GTCCCCGTGGAGGTTCTGTA 2359
              |||||| || ||||| | ||
Db         20 GTCCCCCTGCAGGTTGTCTA 1


RESULT 2866
US-10-181-873A-19/c
; Sequence 19, Application US/10181873A
; Publication No. US20030212019A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF COT ONCOGENE EXPRESSION
;  FILE REFERENCE: RTSP-0346
;  CURRENT APPLICATION NUMBER: US/10/181,873A
;  CURRENT FILING DATE:  2002-12-13
;  PRIOR APPLICATION NUMBER: PCT/US01/01417
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: 09/489,868
;  PRIOR FILING DATE: 2000-01-20
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-873A-19

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Wyatt, Jacqueline
;  APPLICANT:  Zhang, Hong
;  TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
;  FILE REFERENCE: ISPH-545
;  CURRENT APPLICATION NUMBER: US/10/619,220
;  CURRENT FILING DATE:  2003-07-14
;  PRIOR APPLICATION NUMBER: 09/802,669
;  PRIOR FILING DATE: 2001-03-01
;  PRIOR APPLICATION NUMBER: US 09/665,615
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US 09/290,640
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-619-220-67

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        231 GCAGCAATGGGAATCCGCGG 250
              ||||||| || || | ||||
Db          1 GCAGCAAGGGAAAACAGCGG 20


RESULT 2859
US-09-984-637-7
; Sequence 7, Application US/09984637
; Publication No. US20040048246A1
; GENERAL INFORMATION:
;  APPLICANT: Tosoh Corporation
;  TITLE OF INVENTION: OLIGONUCLEOTIDE FOR DETECTION OF HIV-1 AND DETECTION METHOD
;  FILE REFERENCE: PA211-0315
;  CURRENT APPLICATION NUMBER: US/09/984,637
;  CURRENT FILING DATE:  2001-10-30
;  NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide hybridizable with a specific site of HIV-1 RNA
US-09-984-637-7

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||  | ||||| ||||
Db          1 TTTTTTCTTACTTTTGTTTT 20


RESULT 2860
US-09-923-517-67
; Sequence 67, Application US/09923517
; Publication No. US20020039741A1
;   GENERAL INFORMATION:
;        APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
;                   Miraglia; Brenda F. Baker
;        TITLE OF INVENTION: Antisense Oligonucleotide
;                            Compositions and Methods for the Modulation of
;                            Activating Protein 1
;        NUMBER OF SEQUENCES: 139
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Law Offices of Jane Massey Licata
;             STREET: 66 East Main Street
;             CITY: Marlton
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08053
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
;             COMPUTER: IBM PS/2
;             OPERATING SYSTEM: WINDOWS 95
;             SOFTWARE: WORDPERFECT 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/923,517
;             FILING DATE: 07-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/364,416
;             FILING DATE: 1999-07-30
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jane Massey Licata
;             REGISTRATION NUMBER: 32,257
;             REFERENCE/DOCKET NUMBER: ISPH-0209
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (609) 810-1515
;             TELEFAX: (609) 810-1454
;   INFORMATION FOR SEQ ID NO: 67:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20
;             TYPE: Nucleic Acid
;             STRANDEDNESS: Single
;             TOPOLOGY: Linear
;        ANTI-SENSE: Yes
;        SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-923-517-67

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        632 CTGGATGCCGCGGGCCTGGC 651
              ||||||||||   |||| ||
Db          1 CTGGATGCCGGCTGCCTTGC 20


RESULT 2861
US-09-792-440B-9
; Sequence 9, Application US/09792440B
; Publication No. US20030017456A1
; GENERAL INFORMATION:
;  APPLICANT: Boyd, Robert Simon
;  APPLICANT:  Stamps, Alasdair Craig
;  APPLICANT:  Terrett, Jonathan Alexander
;  APPLICANT:  Tyson, Kerry Louise
;  TITLE OF INVENTION: Diagnosis and Treatment and Related
;  TITLE OF INVENTION:  Preparations
;  FILE REFERENCE: 2543-1-006N
;  CURRENT APPLICATION NUMBER: US/09/792,440B
;  CURRENT FILING DATE:  2002-05-21
;  PRIOR APPLICATION NUMBER: GB 0004576.5
;  PRIOR FILING DATE: 2000-02-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: human
US-09-792-440B-9

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        849 CTGGAAGATTGTCGCTCCTC 868
              ||||| |||||||  | |||
```

```
RESULT 2856
US-10-188-248-184/c
; Sequence 184, Application US/10188248
; Publication No. US20040029790A1
; GENERAL INFORMATION:
;  APPLICANT: Patturajan, Meera
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Taupier Jr., Raymond J.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Guo, Xiaojia Sasha
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Hjalt, Tord
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Li, Li
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R.
;  TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS O
;  TITLE OF INVENTION:  THE SAME
;  FILE REFERENCE: 21402-297D
;  CURRENT APPLICATION NUMBER: US/10/188,248
;  CURRENT FILING DATE:  2002-07-02
;  PRIOR APPLICATION NUMBER: 60/303,046
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/303,828
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/358,932
;  PRIOR FILING DATE: 2002-02-22
;  PRIOR APPLICATION NUMBER: 60/304,502
;  PRIOR FILING DATE: 2001-07-11
;  PRIOR APPLICATION NUMBER: 60/305,011
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/305,262
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: 60/307,536
;  PRIOR FILING DATE: 2001-07-24
;  PRIOR APPLICATION NUMBER: 60/306,085
;  PRIOR FILING DATE: 2001-07-17
;  PRIOR APPLICATION NUMBER: 60/308,228
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/323,449
;  PRIOR FILING DATE: 2001-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 184
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artifical Sequence:  Primer/Probe
US-10-188-248-184

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1082 GTAGAAGGTGAAGCTGTTCA 1101
              | | ||||||||| ||| |||
Db         20 GGACAAGGTGAATCTGCTCA 1

RESULT 2857
US-10-072-012-1014
; Sequence 1014, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE:  2002-01-31
;  PRIOR APPLICATION NUMBER: 60/265,102
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,395
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1391
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1014
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Ag2956 Reverse
US-10-072-012-1014

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1069 CCTGACATCCTTAGTAGAAG 1088
              || || |||||| | |||||
Db          1 CCAGAGATCCTTGGCAGAAG 20

RESULT 2858
US-10-619-220-67
; Sequence 67, Application US/10619220
; Publication No. US20040033979A1
; GENERAL INFORMATION:
;  APPLICANT: Dean, Nicholas M.
```

```
;  NUMBER OF SEQ ID NOS: 153
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Amycolatopsis mediterranei
US-09-953-348-89

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        507 TGCCCTCGCACCACGGGCGC 526
              ||| | |||| ||||| |||
Db         20 TGCGCGCGCAGCACGGACGC 1


RESULT 2853
US-09-953-348-90
; Sequence 90, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
;  APPLICANT: Sherman, David. H
;  APPLICANT:  Mao, Yingqing
;  APPLICANT:  Varoglu, Mustafa
;  APPLICANT:  He, Min
;  APPLICANT:  Sheldon, Paul
;  TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
;  FILE REFERENCE: 600.530US1
;  CURRENT APPLICATION NUMBER: US/09/953,348
;  CURRENT FILING DATE:  2001-09-12
;  PRIOR APPLICATION NUMBER: PCT/US00/06394
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: 09/266965
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 153
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Amycolatopsis mediterranei
US-09-953-348-90

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        507 TGCCCTCGCACCACGGGCGC 526
              ||| | |||| ||||| |||
Db          1 TGCGCGCGCAGCACGGACGC 20


RESULT 2854
US-09-875-211-5
; Sequence 5, Application US/09875211
; Publication No. US20030207266A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Caifu
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Haff, Lawrence
;  TITLE OF INVENTION: ASYNCHRONOUS PRIMED PCR
;  FILE REFERENCE: 4563US
;  CURRENT APPLICATION NUMBER: US/09/875,211
;  CURRENT FILING DATE:  2001-06-05
;  PRIOR APPLICATION NUMBER: 60/209,883
;  PRIOR FILING DATE: 2000-06-06
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: synthetic construct
US-09-875-211-5

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        247 GCGGGTCCCCCACCTCTCCT 266
              || ||||||  | ||||||
Db          1 GCTGGTCCCCGTCTTCTCCT 20


RESULT 2855
US-10-643-130-37/c
; Sequence 37, Application US/10643130
; Publication No. US20040072786A1
;   GENERAL INFORMATION:
;        APPLICANT: Monia, B.P., Cowsert, L.M. and Manoharan, M.
;        TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of ras
;        NUMBER OF SEQUENCES: 55
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Jane Massey Licata
;             STREET: 66 East Main Street
;             CITY: Marlton
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08053
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;             COMPUTER: IBM COMPATIBLE
;             OPERATING SYSTEM: WINDOWS 95
;             SOFTWARE: WORDPERFECT 6.1 for WINDOWS
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/643,130
;             FILING DATE: 18-Aug-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/575,554
;             FILING DATE: 22-May-2000
;             APPLICATION NUMBER: 09/128,494
;             FILING DATE: August 3, 1998
;             APPLICATION NUMBER: 08/411,734
;             FILING DATE: April 3, 1995
;             APPLICATION NUMBER: PCT/US93/09346
;             FILING DATE: October 1, 1993
;             APPLICATION NUMBER: 07/958,134
;             FILING DATE: October 5, 1992
;             APPLICATION NUMBER: 08/007,996
;             FILING DATE: January 21, 1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jane Massey Licata
;             REGISTRATION NUMBER: 32,257
;             REFERENCE/DOCKET NUMBER: ISPH-0463
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (856) 810-1515
;             TELEFAX: (856) 810-1454
;   INFORMATION FOR SEQ ID NO: 37:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20
;             TYPE: Nucleic Acid
;             STRANDEDNESS: Single
;             TOPOLOGY: Linear
;        ANTI-SENSE: Yes
;        SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-643-130-37

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         69 GACGCCTGGTCACCGTGACC 88
              | |||||||| || ||| ||
Db         20 GCCGCCTGGTTACTGTGTCC 1
```

; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-776

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1966 AATATTTACCTTGAAAAAAA 1985
|| || || ||||||||||
Db 1 AAAATCAACGTTGAAAAAAA 20

RESULT 2849
US-09-776-479-855/c
; Sequence 855, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 855
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-855

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1776 TTTTTTGAACCCCATTCTTT 1795
|||||||||| ||| |||
Db 20 TTTTTTGAACGTCATGTTTT 1

RESULT 2850
US-09-776-479-855/c
; Sequence 855, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 855
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-855

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1776 TTTTTTGAACCCCATTCTTT 1795
|||||||||| ||| |||
Db 20 TTTTTTGAACGTCATGTTTT 1

RESULT 2851
US-09-993-731-85/c
; Sequence 85, Application US/09993731
; Publication No. US20030105040A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B-R EXPRESSION
; FILE REFERENCE: RTS-0302
; CURRENT APPLICATION NUMBER: US/09/993,731
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 85
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-993-731-85

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1081 AGTAGAAGGTGAAGCTGTTC 1100
|| || |||||||||| |
Db 20 AGCAGTGGGTGAAGCTGTAC 1

RESULT 2852
US-09-953-348-89/c
; Sequence 89, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, David. H
; APPLICANT: Mao, Yingqing
; APPLICANT: Varoglu, Mustafa
; APPLICANT: He, Min
; APPLICANT: Sheldon, Paul
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: 600.530US1
; CURRENT APPLICATION NUMBER: US/09/953,348
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/06394
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/266965
; PRIOR FILING DATE: 1999-03-12

```
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1543 AGAGTAGGGAAGGAACAGGA 1562
              ||| |  ||||||||| |||
Db         20 AGACTGAGGAAGGAACTGGA 1


RESULT 2844
US-09-776-479-353/c
; Sequence 353, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 353
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-353

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1543 AGAGTAGGGAAGGAACAGGA 1562
              ||| |  ||||||||| |||
Db         20 AGACTGAGGAAGGAACTGGA 1


RESULT 2845
US-09-776-479-525/c
; Sequence 525, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 525
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-525

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 2846
US-09-776-479-525/c
; Sequence 525, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 525
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-525

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 2847
US-09-776-479-776
; Sequence 776, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-776

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAAAA 1985
              ||  ||  ||  ||||||||||
Db          1 AAAATCAACGTTGAAAAAAA 20


RESULT 2848
US-09-776-479-776
; Sequence 776, Application US/09776479
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RESULT 2840
US-09-784-674-776/c
; Sequence 776, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,674
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: No. US20030054346A1 available
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/021,701
;             FILING DATE: 10-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Choi, Wendy A.
;             REGISTRATION NUMBER: 36,697
;             REFERENCE/DOCKET NUMBER: 10971464-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-236-2386
;             TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 776:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 776:
US-09-784-674-776

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2801
              ||||| | || |||||| ||
Db         20 ATTGACAGAAGAAAAAATAA 1


RESULT 2841
US-09-915-485-34/c
; Sequence 34, Application US/09915485
; Publication No. US20030083281A1
; GENERAL INFORMATION:
;  APPLICANT: Mark J. Graham
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
;  FILE REFERENCE: RTS-0251
;  CURRENT APPLICATION NUMBER: US/09/915,485
;  CURRENT FILING DATE:  2001-07-25
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 34
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-915-485-34

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1390 GGTGTCTGCCCTGCAGAACT 1409
              |||||||| |||| ||||
Db         20 GGTGTCTGGGCTGCTAAACT 1


RESULT 2842
US-09-918-187-62
; Sequence 62, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
;  APPLICANT: Rosanne M. Crooke
;  APPLICANT:  Mark J. Graham
;  TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
;  FILE REFERENCE: ISPH-0590
;  CURRENT APPLICATION NUMBER: US/09/918,187
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 62
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-62

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        484 CCAGAGCCAGGAGGGAGCGG 503
              || |||||||||| ||  ||
Db          1 CCCGAGCCAGGAGAGAAAGG 20


RESULT 2843
US-09-776-479-353/c
; Sequence 353, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 353
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-353

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
```

```
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-236-2386
;            TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 551:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 20 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       SEQUENCE DESCRIPTION: SEQ ID NO: 551:
US-09-784-674-551

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTT 2178
              || ||  |||||| ||||||
Db          1 TTACTGATTTTTTCTTTTTT 20


RESULT 2838
US-09-784-674-774/c
; Sequence 774, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;       APPLICANT: Shannon, Karen W.
;                  Wolber, Paul K.
;                  Delenstarr, Glenda C.
;                  Webb, Peter G.
;                  Kincaid, Robert H.
;       TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                           probe sequences
;       NUMBER OF SEQUENCES: 1165
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                       Company M/S 20BO
;            STREET: 3000 Hanover Street
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94304
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/784,674
;            FILING DATE: 15-Feb-2001
;            CLASSIFICATION: No. US20030054346A1 available
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/021,701
;            FILING DATE: 10-FEB-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Choi, Wendy A.
;            REGISTRATION NUMBER: 36,697
;            REFERENCE/DOCKET NUMBER: 10971464-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-236-2386
;            TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 774:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 20 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       SEQUENCE DESCRIPTION: SEQ ID NO: 774:
US-09-784-674-774

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              ||| | || |||||| ||||
Db         20 TGACAGAAGAAAAAATAAAA 1


RESULT 2839
US-09-784-674-775/c
; Sequence 775, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;       APPLICANT: Shannon, Karen W.
;                  Wolber, Paul K.
;                  Delenstarr, Glenda C.
;                  Webb, Peter G.
;                  Kincaid, Robert H.
;       TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                           probe sequences
;       NUMBER OF SEQUENCES: 1165
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                       Company M/S 20BO
;            STREET: 3000 Hanover Street
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94304
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/784,674
;            FILING DATE: 15-Feb-2001
;            CLASSIFICATION: No. US20030054346A1 available
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/021,701
;            FILING DATE: 10-FEB-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Choi, Wendy A.
;            REGISTRATION NUMBER: 36,697
;            REFERENCE/DOCKET NUMBER: 10971464-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-236-2386
;            TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 775:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 20 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       SEQUENCE DESCRIPTION: SEQ ID NO: 775:
US-09-784-674-775

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              |||| | || |||||| |||
Db         20 TTGACAGAAGAAAAAATAAA 1
```

```
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: phosphodiester backbone
US-09-888-326-542

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1543 AGAGTAGGGAAGGAACAGGA 1562
              ||| |  ||||||||| |||
Db         20 AGACTGAGGAAGGAACTGGA 1


RESULT 2835
US-09-802-640-80/c
; Sequence 80, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
;  APPLICANT: Braun, Andreas
;  APPLICANT:  Bonsal Aruna
;  APPLICANT:  Kleyn Patrick
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE AND THEIR USE
;  FILE REFERENCE: 24736-2048
;  CURRENT APPLICATION NUMBER: US/09/802,640
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-802-640-80

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        642 CGGGCCTGGCCGAGAACCTG 661
              | |  |||||||||| ||||
Db         20 CAGCACTGGCCGAGATCCTG 1


RESULT 2836
US-09-784-674-354/c
; Sequence 354, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,674
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: No. US20030054346A1 available
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/021,701
;             FILING DATE: 10-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Choi, Wendy A.
;             REGISTRATION NUMBER: 36,697
;             REFERENCE/DOCKET NUMBER: 10971464-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-236-2386
;             TELEFAX: 650-852-8063
;   INFORMATION FOR SEQ ID NO: 354:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 354:
US-09-784-674-354

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1818 AAGTTTTAGAATCTTTTAAA 1837
              || | |||||  ||||||||
Db         20 AAATCTTAGAGCCTTTTAAA 1


RESULT 2837
US-09-784-674-551
; Sequence 551, Application US/09784674
; Publication No. US20030054346A1
;   GENERAL INFORMATION:
;        APPLICANT: Shannon, Karen W.
;                   Wolber, Paul K.
;                   Delenstarr, Glenda C.
;                   Webb, Peter G.
;                   Kincaid, Robert H.
;        TITLE OF INVENTION: Methods for evaluating oligonucleotide
;                            probe sequences
;        NUMBER OF SEQUENCES: 1165
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
;                        Company M/S 20BO
;             STREET: 3000 Hanover Street
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
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